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Interaction of Phytohormones with Cotton Fiber Cell Development

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Abstract

Cotton is a vital part of the global textile industry, because of its mature fibers rich in cellulose. The study of these fibers provides a significant understanding of the mechanisms controlling single-cell differentiation and proliferation. Furthermore, these processes are focus points in programs aiming at increasing fiber development. Plant hormones play critical roles in a wide range of plant developmental processes, even when present in small amounts within plants. Hormones also affecting the production of cotton fibers, as well as other developmental activities such as exogenous hormone treatment, has been proven in studies to speed up the initiation and elongation of fiber cells. This article provides an overview of genes associated with hormone biosynthesis and signaling pathways. It also investigates the methods by which these phytohormones control the initial development and elongation of cotton fiber cells. Most of the hormones involved in fiber production are beneficial while cytokinin and abscisic acid have been demonstrated to be harmful.

Keyword

Fiber elongation, Signaling pathway, Fiber initiation, Phytohormone, Trichome, Gibberellins

Introduction

Cotton is a vital part of the global textile industry, as it is used for paper products, textiles, and cottonseed oil. It's grown in over 80 countries and produces lint around 20 million tons each year. Cotton belongs to the Malvaceae family and genus Gossypium. There are around 50 species in the genus of Gossypium, and only four of them are commercially grown. Two of these are diploid, while the other two are tetraploid (Ahmed et al., 2018). Cotton is a highly diverse crop with various parts having valuable uses and byproducts. Among them, lint is the most valuable product of cotton (Khanpara & Vala, 2023). The lint is obtained from cotton fibers while cottonseed oil is used for culinary purposes. Cotton benefits humans by producing sticks, fibers, seeds, and oil as basic products, and various secondary products by utilizing these cotton components. Cotton's value as a cash crop is mostly defined by its diverse applications. Cotton textile, hosiery manufacturing, and the production of raw and fine cotton goods account for a substantial share of agricultural value addition. Cotton is also used in a variety of surgical items, which adds to its overall importance in a variety of industries (Munir et al., 2020). A single hormone may affect the growth and differentiation of various tissues, multiple hormones may have a direct effect on a single cell type and fiber development. These signaling molecules are capable of targeting specific transcriptional regulators of gene expression. All cotton-producing countries have the priority to improve crop yield. One way to improve yield is to increase the number of fiber and its quality with each developing seed (Xiao et al., 2016). Cotton fiber, which is an extension of epidermal cells, is made up of single cell trichomes. The growth and synthesis of cotton fiber depend heavily on hormones. It is an outgrowth of the ovule integument which undergoes synchronous elongation during fiber expansion (Wang et al., 2019). An isodiametric expansion of ovule epidermal cells is required to initiate cotton fiber cell formation, and this particular phase typically lasts a single day or a short duration depending on the individual fiber cell. It is possible for there to be multiple waves of fiber cell initiation on the ovule surface, it becomes possible to detect this initiation at any given moment within the initial 5 to 6 days following anthesis. Based on data obtained from expressed sequence tags, numerous transcription factors, such as MYB, WRKY, AP2/EREBP, C2H2, and bHLH, have been identified as potentially crucial for initiating fiber cells (Prasad et al., 2022). Like this, the cDNA microarray study discovered three crucial transcription factors that control lint fiber initiation: GhMYB25, GhMYB25-like, and GhHD1. In cotton, silencing GhMYB25 caused shorter fibers, a decrease in the amount of trichomes on leaves, petioles, and petals, and a delay in the onset of new fibers. On the other hand, GhMYB25 overexpression increased both fiber commencement and trichome development. Dynamic regulations of plant channels including turgor pressure and dynamic regulation of plasmodesmata have effect on elongation of fiber cells. Plasmodesmeta have been seen to open between 0 and 9 days after anthesis (DPA), and then reopen at 16 DPA. The morphology of cotton fiber cells is influenced by organization of the cell wall. Cotton fiber cells express high levels of GhRac1 during the elongation phase of their development. As the rate of fiber elongation decreases, GhRac1 expression rapidly declines, indicating that GhRac1/GTPase may be a key player in controlling fiber elongation through modifications to cytoskeletal elements. Four groups of GhACT genes are known to be expressed in cotton tissues, of which *GhACT1* is expressed only in fiber cells and is essential for fiber elongation (Ahmed et al., 2018). Aquaporins, a distinct class of proteins found in the plasma membrane and tonoplast, are essential components of numerous cellular development pathways. In particular, factors related to cotton fiber cell elongation have been discovered to increase the expression of two specific aquaporin genes, GhPIP1-2 and GhTIP1 (Zhang et al., 2017). Phytohormones are biological molecules found in plants. Plant hormones control a plant's overall growth and development. Fiber cells requires plant hormones for growth and development (Davière & Achard, 2016). Auxin, gibberellin, jasmonic acid, ethylene, brassinosteroids, and strigolactones all contribute to the production of fibers, while cytokinin and abscisic acid inhibit fiber growth. Despite the fact that the action mechanisms of these plant hormones are well understood in Arabidopsis, the significance of phytohormone signaling pathways in cotton fiber production remains unexplained (Ahmed et al., 2018). Several hormones have been proven in studies to have critical roles in cellular processes such as cell enlargement, cell expansion, and overall plant growth (Hassan et al., 2021).

Auxin

Auxins play a crucial role in promoting root growth, controlling apical bud dominance, regulating embryonic development, facilitating in vascular tissue transformation and responding to various internal and external signals (Xiao et al., 2019a). The auxin synthesis gene *iaaM* is over-expressed using an ovule-specific promoter, increasing the lint yield and fiber quality by 15%. Literature indicates that the buildup of auxin occurs slowly during the differentiation of fiber cells. The buildup of auxin was prevented during the initiation stage of ovule cultures in vitro due to inhibitors of NPA and BFA auxin transport. This, in turn, had an effect on the formation of fibers. Meanwhile, the application of NOA, an inhibitor of auxin flow, on the ovules did not seem to have any significant impact (Ahmed et al., 2018). Exogenous indole-3-acetic acid (IAA) supplementation shows the ability to overcome limitations on fiber elongation as shown in figure 1. Additionally, the total fiber volume is significantly increased by the external accumulation of IAA, as crucial natural auxin. Auxin accumulation starts before the flowering stage and peaks at about 2-3 days post-anthesis (DPA). Thereafter, it gradually declines until it reaches a baseline level by 10 DPA. The temporal variation in auxin levels correlates with this hormone's important function in promoting the growth of plant fibers (Wang et al., 2020). There is a 15% growth in fiber cells when the MAD FBP7 regulates IAA production from 2 DPA in the trichome to 10 DPA in the ovule (Xiao et al., 2019a).

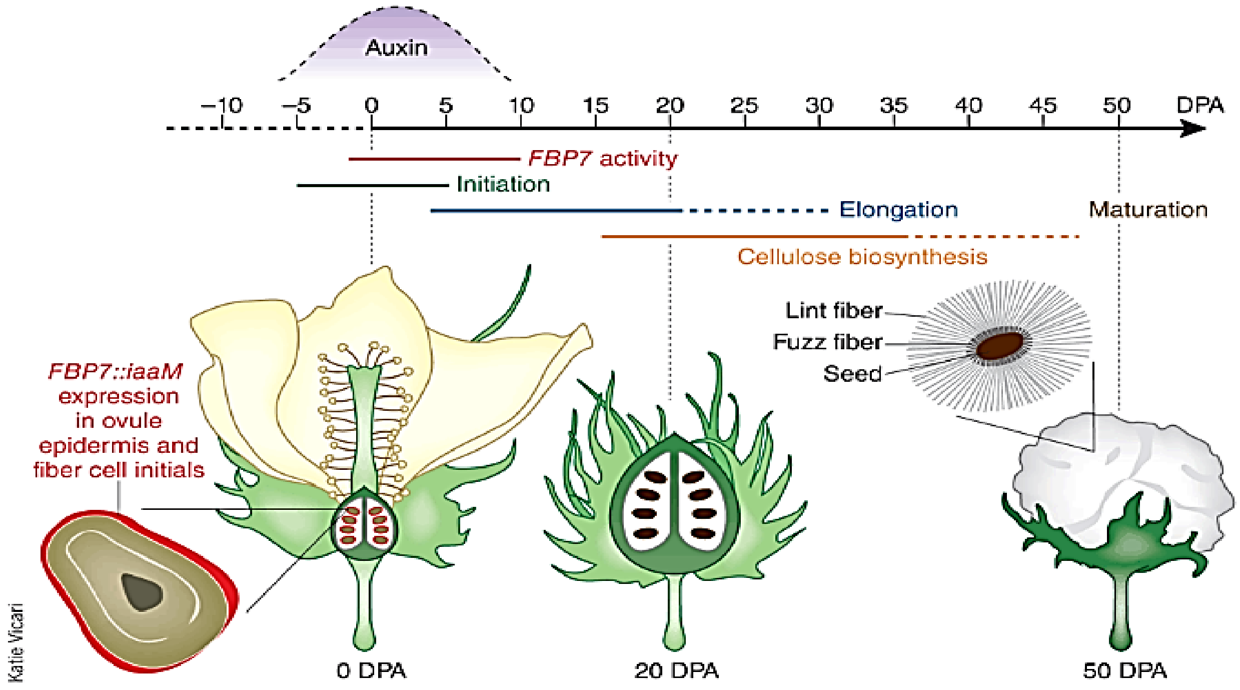

Figure 1: Indole acetic acid expression in ovule epidermis and fiber cell after 10 DPA.

Gibberellic Acid

There are numerous physiological processes in plants that gibberellic acid (GA) regulates, including seed germination, root and stem elongation, flower maturity, fruit ripening, and dormancy regulation. It has been demonstrated that GA external treatment stimulates cotton plant fiber elongation. On the other hand, when a chemical inhibitor of GA production is incorporated during ovulated culture, cotton fiber length and quantity are both decreased (Wang et al., 2018). When cotton of natural color is treated with an exogenous form of GA, the concentrations of two essential hormones increase (IAA and ABA). These hormones play a major role in controlling the fibers elongation during the process of maturation period. The maturation process, durability, micronaire and other fiber properties are all greatly influenced by this hormonal change (Ji et al., 2022). The accumulation of gibberellic acid (GA) and cotton fiber elongation are closely related processes. Since GA is crucial for flower development and fruit maturation, its levels fluctuate during the post-flowering period within fiber cells. Cotton types with longer fibers have significantly greater amounts of endogenous GA3 than with medium and short fiber lengths. The production and length of long fibers are increased when GA20-OXIDASE1 is induced in transgenic cotton. The levels of GA3 and GA4 are significantly increased to produce this effect (Li et al., 2022). DELLA proteins have significant effects on the gibberellic acid (GA) signaling pathway as negative regulators. (Davière & Achard, 2016). The GID1 receptor starts a binding cascade in the presence of gibberellic acid (GA), which sets off a series of events that lead to the ubiquitin-mediated breakdown of DELLA proteins. As a result, crucial transcription factors are released during this degradation process, allowing the activation of genes that respond to GA. Recent research has shown a unique mechanism that uses gibberellic acid (GA) to promote cotton fiber elongation. The GA signaling pathway places a significant emphasis on the transcription factor GhHOX3 (Shan et al., 2014).The DELLA protein GhSLR1 takes part in a specific interaction with GhHOX3, prohibiting GhHOX3 from expressing its regulatory control over the targeted genes when Gibberellic Acid (GA) levels are low. On the other hand, GhSLR1 degrades in the presence of high GA concentrations, releasing *GhHOX3*. The link between GhHOX3 and GhHD1 facilitates this release of GhHOX3, which activates two important genes, GhRDL1 and GhEXPA1 (Xiao et al., 2019a).

Ethylene

It regulates root hair development, hypocotyl extension, and apical trichome development, as well as the production of root hairs (Dubois et al., 2018). Ethylene has been shown to promote fiber cell elongation in cotton, as evidenced by the overexpression of ACO genes during fiber elongation. Using an inhibitor of ethylene synthesis on cotton fiber cells, ethylene substantially increases fiber cell elongation. The ethylene production pathway becomes evident during the fiber elongation stage, as a crucial metabolic mechanism (Wang et al., 2020). It is crucial that GhACO1-3 is effectively expressed at this point because it is associated with an increase in ethylene synthesis in actively elongating fiber cells. Cotton fibers elongation is regulated by this plant growth regulator, which boosts the expression of genes involved in tubulin, sucrose synthase, and expansin. The detection of ethylene in fibers has provided evidence for its existence and effect on fiber elongation. In particular, the fiber elongation stage occurs when genes involved in ethylene production, such as ACO1–3, are expressed. In addition, studies have examined potential associations between the BR (brassinosteroid) and ROS (reactive oxygen species) signaling pathways and ethylene (Ahmed et al., 2018). The production of ethylene may be stimulated by reactive oxygen species (ROS), which in turn appear to increase fiber elongation by affecting the concentration of calcium ions (Ca2+) (Xiao et al., 2019a).

Brassinosteroids

Cotton fibers are individual trichomes that develop from the seeds' epidermal cells (Samuel Yang et al., 2006). The BES1 gene family, which is specific to plants, participates in brassinosteroids signaling (Lu et al., 2018; Zhang et al., 2017). When transcription factors like the BES1 gene family bind to target gene promoters, they help in signal transmission and regulation (Kir et al., 2015; Kono & Yin, 2020). Gh14-3-3 regulatory protein involved in cotton fiber initiation and elongation due to its interaction with GhBZR1, which is an important component of brassinosteroid signaling. (Zhang et al., 2010).

On the other hand, it has been demonstrated that the use of brassinazole, prevents cotton fiber elongation. The most essential transcription factors associated with fiber development are bHLH and HLH (Lu et al., 2018). The bHLH transcription factor GhFP1 was over expressed in Arabidopsis, which increased the length of trichomes (Walford et al., 2012). Over-expression of GhFP1 stimulate the fiber development process. The BR biosynthesis pathway includes the genes GhCPD and GhDWF4, both of which GhFP1 been shown to be capable of directly binding to their promoters as shown in figure 2. An improvement in fiber elongation results from this binding event have beneficial regulatory impact on BR biosynthesis (Liu et al., 2020).

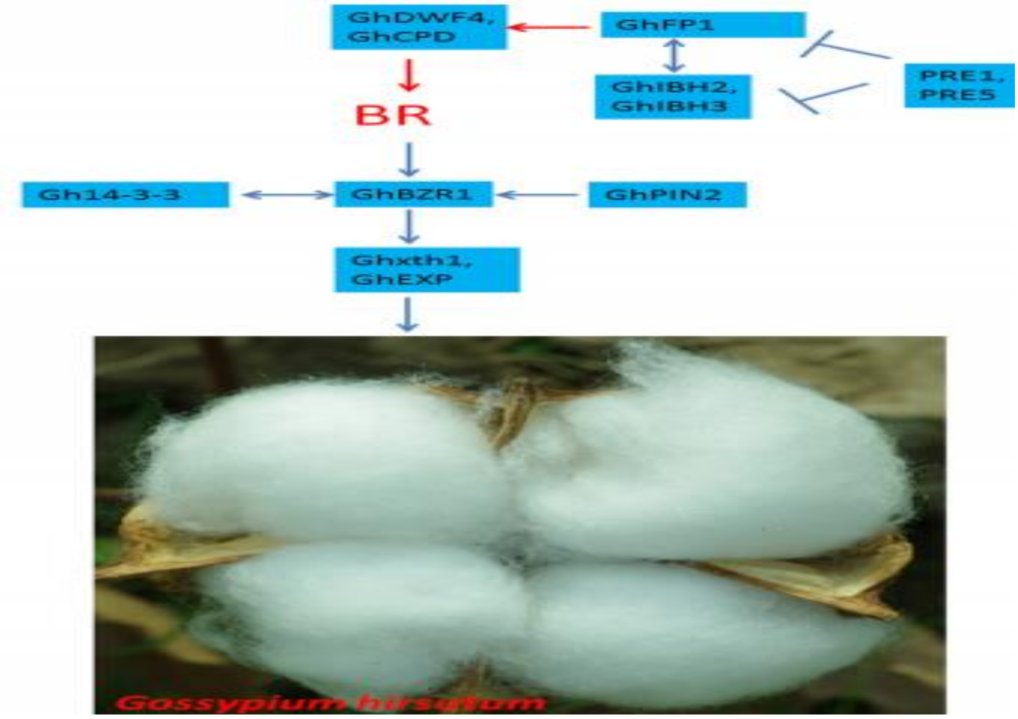

Figure 2: BR biosynthesis of GhBZR1 an active transcription to regulate gene expression

Cytokinin is a phytohormone that plays important roles in plant growth, such as cell division and tissue and organ senescence (Abdelrahman et al., 2018). Cotton fiber is a component of the exterior integument of the ovule (Xiao et al., 2019b). Cytokinin is a crucial hormone that regulates cell proliferation and differentiation in plants. Before flowering, cytokinins function as promoters of fiber initiation, but after flowering, cytokinins inhibit fiber growth (Liu et al., 2017). A high dose of cytokinin induces an auxin gradient in the ovule epidermis, reducing its role in fiber growth growth (Zhang et al., 2017). Genetic modification provides a technique to measure hormone concentrations, such as cytokinin and studying their resulting phenotypes. Overexpression of ITP, a rate-limiting enzyme in cytokinin production, can increase cytokinin levels (Zhang et al., 2022). Cytokinin oxidase/dehydrogenase (CKX) is one of the most important negative regulators of cytokinin (Spallek et al., 2017). Numerous research investigations have been done to establish the role of thidiazuron, a cytokinin-like molecule, in inducing cotton leaf abscission and possibly improving fiber quality. (X. Gao et al., 2020; Leal et al., 2020). Thiadiazuron, a synthetic cytokinin analog, has been shown to regulate the gene expression of cytokinin and abscisic acid biosynthesis (Pesch et al., 2013). The delay in thidiazuron causes the boll to open and results in superior fiber quality (Manghwar et al., 2022). However, its application on commercial scale is not recommended as it costs high and time consuming. Cytokinin provides excellent model for studying ovule and fiber growth (Davière & Achard, 2016). Application of cytokinin to in vitro-cultured ovules, promotes ovule growth, but inhibits fiber development (Li et al., 2004).

Abscisic acid

Abscisic acid (ABA) is essential for controlling seed dormancy and stress responses. As reported by Beasley et al. (1974) and various other studies, when ABA is used in vitro, it not only inhibits the elongation of fiber cells but also reduces the initial development of cotton fibers (Tuan et al., 2018). An increase in ABA concentrations is significantly related to this inhibitory action (Ioannidi et al., 2016). The researcher studied naturally occurring ABA levels in various fiber cells and discovered that ABA accumulation increased gradually during the initial fiber cell development stage (Gilbert et al., 2013). Numerous physiological processes in higher and lower plants are under the control of abscisic acid. If ABA has been given exogenous, cotton fiber exhibits an inhibitory effect. Abscisic acid treatment performed in vitro plays a part in inhibiting cotton fiber growth. The ovules' ability to absorb and release potassium is improved by abscisic acid (Salih et al., 2016). By interfering with the metabolism of malate, ABA prevents the growth of the fiber. In addition, the endogenous administration of ABA supports the formation of short fibers. An abscisic accumulation is evident in the short fiber cotton mutant known as ligon-lintless 1. Then, ABA levels dropped during fiber elongation phase (10–20 DPA), declining until they eventually reverted to their low levels during the maturation stage (30–50 DPA). Short-staple fibers have a much greater ABA content than long-staple fibers throughout development (Ma et al., 2011). The formation of short fibers is also affected by physiological levels of ABA in cotton ovules. All of these findings indicated that ABA is a fiber inhibitor. (Davis & Addicott, 1972).

Jasmonic acid

Jasmonic acid (JA) is one of the most well-known plant hormones which is responsible for regulating plant growth, as well as trichome formation and senescence and other responses to its activation (Ruan et al., 2019). JA stimulates the bHLH transcription factor, which is important for trichome initiation. JAZ is a protein that contains the ZIM domain and work as JA inhibitor (Delker et al., 2006; Song et al., 2013). Jasmonic acid-related metabolism in cotton promotes in the development of the fiber. The JAZ family gene GhJAZ2 is extensively expressed in follicles during the fiber initiation phase, which may impede fiber initiation and potentially reduce cell length (Hu et al., 2016). Starting process of cotton fiber is broke down by the enzyme Allene oxide cyclase (AOC), which is involved in JA production. AOC has a crucial function in fiber development as it manifests in many tissues, organs, and cotton fibers of the TM-1 variety at the fiber beginning stage at -1 DPA. For instance, it has been shown that over expressing the JAZ protein GhJAZ2 has an inhibitory effect on fiber development (Prasad et al., 2022). During the initial phase of fiber synthesis, interactions between the signalling molecules jasmonic acid (JA) and brassinosteroids (BR) take place. Increased fiber production results from the application of JA at lower concentrations (0.001 M), however this process fails at larger concentrations (2.5 M). Jasmonic acid (JA), as shown in earlier research is involved in cell elongation and the development of trichomes (Traw & Bergelson, 2003). These findings offer valuable insights on its contribution to cotton fiber development. It is crucial to emphasize that the external application of JA prevents the growth of new fibers. To give an example, significant amounts of this hormone block the transcription of the genes GL3, EGL3, and KCS12 (Tan et al., 2012).

Future prospectus

The recent development of high-yield sequencing technology has played a critical role in advancing cotton genomic studies. While it is well known that auxin, gibberellic acid (GA), brassinosteroids (BR), ethylene all contribute to the development of cotton fiber cell development, and many different genes have been identified as being involved in the production of cotton fiber, there is still a need for comprehensive studies to fully understand the mechanisms behind cotton fiber formation and development. Understanding the complex mechanisms which influence cotton fiber development and their interconnections is a significant challenge." External application of these hormones, or over-expression of related genes, has shown promise for increasing fiber length and fiber elongation in cotton. However, it is controversial whether certain essential elements within these pathways actively contribute to fiber development or not. Further functional research is required to fill these information gaps. CRISPR-Cas9 is a powerful tool for precise base manipulation that allows for nucleotide substitution in the genome." Its wide spread use in genome editing is due to its low cost and ability to permit targeted genetic alterations (H. Gao et al., 2020). This approach has the potential to significantly improve commercially valuable features in crop species. Therefore, a promising strategy for getting a plant with an abundance of trichomes is simultaneously deleting the negative regulators of trichomes and fiber development inhibitors (Wang et al., 2014).

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Current Selection Indices for Improving Some Economic Traits in Egyptian Cotton Genotypes

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Abstract

The research aimed to evaluate the efficiency of current selection methods in three generations F_2, F_3 and F_4 of the two populations of Egyptian cotton derived from the crosses [(Giza 91 x Giza 90) x Giza 85] x Giza 95 (pop.1) and [(Giza 91 x Giza 90) x Giza 85] x [(Giza 83 x Giza 80) x Giza 89] (pop.2). during three seasons (2021 to 2023) to determine genetic gain of predicted response to selection (pR), realized response to selection (rR), generalized selection (pgR) and selection differential response (ps) as well as heritability, phenotypic (PCV %) and genotypic (GCV %) coefficients of variability for (BW), (LY), (L%), (UHM), (Mic) and (PI). The results showed that the Phenotypic (PCV %) values was higher than genotypic (GCV %) coefficient of variability for studied cotton traits of the two populations on three generations, indicating the magnitude of genetic variability persisting in this material was sufficient for improvement the studied traits through current selection of superior progenies. On the same time high values of PCV% and GCV% were observed for (LY) in F_3 generation (pop.1) and all generations (pop.2), indicating that this trait was less affected by the environmental conditions, hence selection would be effective for this trait. Selected families of the two populations recorded increase mean performances for (BW), (LY) and (L %), while fiber traits revealed low increase mean performances through generations of the two populations, therefore recurrent selection on different generations in two populations will be success and affected in improving yield traits. Mean values of the predicted response to selection effects for (BW) from F_2 to F_3 in two populations were greater than realized response selection through selection cycles indicating that dominance gene effects was involved in the inheritance of (BW). Higher heritability narrow sense estimates (ph^2_{ns}) for (BW) a cross F_2 to F_4 in (pop.2) indicated that the additive gene effects increased in advanced generation and useful selection for (BW). The families selected from F_2, F_3 and F_4 generations had higher mean performances of (LY) in two populations of cycles selected, Predicted heritability estimates (ph^2_{ns}) in narrow sense were higher in two populations for F_2 and in F_4 in (pop.2), it means the current selection was useful to accumulate desirable genes for (LY). Means of selected families for (L%) trait of (pop.1) were higher than the realized mean of F_3 generation in two populations, the same results was obtained in (pop.1) of F_4 generation, while narrow sense heritability (ph^2_{ns}) predicted for (L%) was differed from F_2 generation to F_4 generation, means the current selection would be useful for improving (L%) trait in superior selected plant. (UHM) trait of the (pop.2) in F_2 and F_4 generations recoded low values of (ph^2_{ns}) it could be described to the low magnitude of additive portion and amount of environmental and gene effects. Predicted narrow sense heritability (ph^2_{ns}) of (Mic) value and (PI) were decreased as generation proceeded except for (pop.2) in F_4 generation of (PI) trait, these clarified that dominance gene effects were prevalence in the inheritance of this traits. The two populations of the three cycles showed varied in their response to selection for traits under study of the first population witch showed higher responses for most traits and improving yield traits through cycles of current selection methods.

INTRODUCTION

Cotton breeder objective is to improve yield components and fiber quality of cotton plant through selection process in inbreeding programs for superior plants, therefore the breeder use different selection methods on the genetic materials to improve the different traits of cotton plant (Singh 2004).

The variability for selection efficiency in cotton breeding program depends on the existence of genetic variability for yield and fiber traits in gene pool. The breeding of self-pollinated crops, rapid homozygosity occurs in filial generations by pedigree or bulk selection, thus the number of genes that could be good combinations decreases at the same rate. Selection success is adversely affected by decreasing variation due to successive self-generation (Tokerand Cagirgan 1995).

Recurrent selection popularized was first by Hull (1945) in a cyclic selection generation after generation accompanied with interbreeding of selects to improve frequency of the desired alleles for a trait. Recurrent selection increases genetic variability for further generation (Maich et al., 2000) and also increases the frequency the desirable genes controlling the target of the character and genotypes in the population Abou El-Yazied et al., (2014). Recurrent selection in cotton was successfully applied by Basal et al., (2017) and Parre and Patial (2021) used different procedures of selection from F_2 to F_4 in Upland cotton and they found predominance of additive genetic variance and practiced effective selection for isolating promising lines for studied traits. Al-Hibbiny et al., (2019) studied some selection procedures, i.e. 11 selection indices with pedigree line selection were used to improve lint yield, yield components and fiber properties in early segregations (F_2 and F_3) of cotton cross (Giza86 x Australy13), they found the F_3 generation mean was higher than those of F_2 generation for all studied traits.

The goal of the present study aimed to estimate the mean performances and evaluate the efficiency of selection indices in two segregations F_3 and F_4 after two cycles of current selection as compared to the base population (F_2) for yield and fiber cotton traits to enhance selection of superior cotton plants.

MATERIALS AND METHODS

Three generations of the cotton genotypes (F_2, F_3 and F_4) for two crosses i.e. [(Giza 91 x Giza 90) x Giza 85] x Giza 95 and [(Giza 91 x Giza 90) x Giza 85] x [(Giza 83 x Giza 80) x Giza 89] were used as a material in this study to applied the effect of the current selection methods on cotton traits. The three segregation generations were grown at Seds Experimental Station, Agricultural Research Center, Egypt during 2021 to 2023 seasons.

In 2021 season F_2 generation was growing as single plants and self-pollination was practiced for all F_2 plants. Selection was accomplished on F_2 plants in field witch have desirable yield cotton traits and ideal types of cotton plant to evaluate the studied traits. Selection was used in 5% intensity of the F_2 plants which have the highest performance of traits.

In 2022 season natural seed of F_2 plants selected growing as F_3 families in randomized complete block design with three replications while the selfed seeds were grown as individual plants. Selection was practiced between families and within families to select the best 5% intensity of plants within best families to consist the F_4 seeds.

In 2023 season F_4 generation were grown as F_3 generation, families in experimental design and individual plants, selection was used in 5% intensity of plants within best families to be used as the F_5 seeds.

The studied traits were.

1- Boll weight (BW_{gm}).
2- Lint cotton yield (LY_{gm})
3- Lint percentage (L %).
4- Fiber length (UHM_{mm})
5- Micronaire reading (Mic)
6- Fiber strength (PI)

Statistical analysis

The analyses of variances were according to Singh and Chaudhary (1985). The phenotypic and genotypic variances and heritability values in broad sense were estimated in accordance to Falconer and Mackay (1996) as follows:

- Phenotypic variance (δ^2p): Total phenotypic variance for each generation.
- Environmental variance (δ^2E): The mean variance for the parental varieties.

$\delta^2E = (V\ P1 + V\ P2) / 2.$

- Genotypic variance (δ^2g) is the genetic variance of each generation. $\delta^2g = \delta^2p - \delta^2E$.
- Broad sense heritability (h^2_{bs} %) = $(\delta 2g / \delta 2p)$ x 100

The phenotypic (PCV) and genotypic (GCV) coefficients of variability were calculated as shown by Burton (1952) as follows:

PCV = (δp /X) x 100
GCV = (δ g / X) x 100
Where: δp and δg are standard deviation of phenotypic and genotypic of families. X is the general mean of a trait.

Selection Parameters

Predicted Selection Response:

The expected genetic advance and the realized selection response were calculated as popularized by Sharma (1988) and Falconer (1989) as follows:

1- pS (Predicted / Expected selection differential) pS = i x δp
Where: i: Constant (=2.06 at 5% selection intensity); δp: Phenotypic standard deviation.

2- pR (Predicted / Expected selection response, i.e. Genetic advance) pR= i x h2
b x δp or = h^2_{bs} x pS
Where: h^2_{bs}= heritability in broad sense.

3- pR% (Percentage proportion of pR in X p)
pR% = 100 x pR / X p.
Where: X p=Mean of selected plants in a generation.

4- pgR (Predicted/ expected generalized selection response)
pgR = pR / δp; or = (pS x h^2_{bs}) / δp.

5- ph^2_{ns} (Predicted heritability in narrow-sense)= pR / (i x δp).

Realised Selection Response:

1- rR (Realized selection response) = $X_g - X_0$
Where:
X_g: Mean of selected plants in generation.
X_0: Mean of the same generation.

2- rR% (Percentage proportion) = (rR / F_n) x 100
Where: F_n is the mean of any generation.

3- rgR (Realized generalized selection response in generation) = rR x δp.

4- rh^2_{ns} (Realized heritability in narrow-sense)
rh^2_{ns} = rR / (i x δp).

RESULTS AND DISCUSSION

Genetic improvement of cotton is largely condition by the type and relative amount of genetic variance in the populations, therefore cotton breeder choice the selection methods on genetic materials to improve the different traits of cotton plant.

Heritability broad sense estimates (ph_{bs}%), phenotypic (PCV%), genotypic (GCV%) coefficient of variability and mean performances for all studied traits of the two populations in three generations (F_1, F_2 and F_3) are presented in Table (1). High values of heritability broad sense (ph^2_{bs} %) (over 50%) was found for all traits in different generations of the population1 except for lint yield (LY) in F_2 generation which recorded moderate heritability estimates (30% to 50%). On the other hand fiber length (UHM) and fiber fineness (Mic) in F_3 generation and fiber strength (PI) in F_2 and F_4 generations which showed low broad sense heritability (ph^2_{bs} %) (less than 30%) of the (pop.1) . Heritability (ph^2_{bs}%) results for studied traits in three generations of the (Pop.2) was highly for boll weight (BW) in F_2 and F_3, lint yield (LY) in F_2, F_3 and F_4, lint percentage (L %) in F_2, fiber fineness (Mic) in F_2 and F_3 and fiber strength (PI) in F_3 and F_4 generations. While moderate heritability estimates (ph^2_{ns}%) was noticed of the poulation2 for boll weight (BW) and lint percentage (L%) in F_4. Low broad sense heritability ((ph^2_{ns}%) was recorded for lint percentage (L%) in F_3, fiber length (UHM) in F_2, F_3 and F_4, fiber fineness (Mic) in F_4 and fiber strength (PI) in F_2 Generations. In generally, high heritability estimates (ph^2_{ns}%) indicated that the genotypic variances was greater than environment variances, it means the presence of sufficient amount of genetic variances in the studied material to practice effective selection for superior progenies to improve cotton traits. However, the reduction of heritability (ph^2_{ns}) value for traits within the two populations might be ascribed to the reduction in genetic variability and heterozygosity. The same results were mentioned with those, Abd El-Moghny (2016), Okaz et al., (2017) and Gibely (2021) which detected increasing heritability (ph^2_{ns} %) broad sense values with advancing of generation that was attributed to increase gene additive effects as results of the increase in homozygosiy.

Phenotypic (PCV%) and genotypic (GCV%) coefficient of variation Table (1). (PCV%) values were higher than (GCV%) for studied cotton traits of the two populations on three generations, indicating the magnitude of genetic variability persisting in this material was sufficient for improvement the studied traits through current selection of superior progenies. At the same time high values of (PCV%) and (GCV%) were observed for lint yield (LY) in F_3 generation (pop.1) and all generations (pop.2), indicating that this trait was less affected by the environmental conditions, hence selection would be effective for this trait. Meanwhile the values of (PCV%) and (GCV%) for other traits were differed slightly and narrow range of variability in two populations through generations detected for most traits reflecting efficiency of selection, hence cotton breeder should be create genetic variability through diverse germplasme and hybridization.

Mean performances table (1), the generations of the two populations recorded increase mean performances for boll weight (BW), lint yield (LY) and lint percentage (L%). On the other hand fiber traits revealed low increase mean performances through generations of the two populations, therefore recurrent selection on different generations in two populations will be success and affected in improving yield traits.

Table1. Mean performance, Heritability ($ph^2_{b.s}$ %), phenotypic (PCV %) and genotypic (GCV %) coefficients of variation in generations (F_2, F_3 and F_4) through two populations.

Characters	Generation	Heritability %		GCV%		PCV%		Means± Sd	
		pop.2	pop.1	pop.2	pop.1	pop.2	pop.1	pop.2	pop.1
Boll weight (BW)	F_2	82.3	80.1	2.67	3.29	2.64	2.20	3.15±0.32	2.91±0.28
	F_3	53.3	87.3	0.99	3.59	3.13	0.53	3.16±0.34	2.99±0.17
	F_4	87.1	37.3	3.37	1.01	0.38	2.94	3.24±0.18	3.17±0.33
Lint yield (LY)	F_2	45.2	75.7	3.85	43.43	32.86	1.74	40.93±4.22	39.48±1.23
	F_3	94.9	87.3	41.15	68.06	59.40	39.04	41.39±5.31	39.64±4.04
	F_4	57.4	86.7	4.46	78.18	67.79	2.56	41.59±5.70	43.91±1.40
Lint % (L%)	F_2	67.9	63.5	5.72	9.26	5.88	3.88	38.88±1.90	39.76±1.51
	F_3	72.7	24.7	6.61	4.33	1.07	4.81	40.25±1.32	40.55±1.64
	F_4	63.4	42.2	4.92	5.59	2.36	3.12	40.65±1.51	40.66±1.41
Fiber length (UHM)	F_2	80.8	13.0	4.65	3.57	0.47	3.76	31.03±1.05	30.65±1.19
	F_3	2.2	20.5	0.90	3.91	0.80	0.02	31.04±1.10	30.93±0.53
	F_4	76.8	10.1	3.76	3.43	0.35	2.89	31.28±1.04	31.37±1.09
Fiber fineness (Mic)	F_2	56.3	-80.2	2.84	1.00	-0.80	1.60	4.17±0.20	4.64±0.36
	F_3	13.8	-161.5	2.65	0.67	-1.08	0.37	4.29±0.17	11.19±0.40
	F_4	-52.1	17.4	3.04	2.06	0.36	0.66	4.43±0.30	11.26±0.36
Fiber strength (PI)	F_2	17.2	-5.0	2.84	0.98	-0.05	0.49	9.62±0.31	9.55±0.52
	F_3	75.2	56.3	9.30	2.43	1.37	6.99	9.30±0.48	9.72±0.95
	F_4	25.6	72.8	3.03	2.63	1.91	0.77	9.29±0.49	9.97±0.55

The selection procedures.

The predicted (PR) and realized (rR) responses means to selection for boll weight (BW) in three selection cycles of tow populations are presented in Table(2). Predicted response (PR) selected families for boll weight trait (BW) in selection cycles from F_2 to F_4 generations had higher range of mean performances, the same results obtained from F_4 to F_5 generations in two populations. Mean values of the predicted response to selection effects for boll weight (BW) was greater than realized response selection through selection cycles indicating that dominance gene effects was involved in the inheritance of boll weight (BW). Moreover, percentage proportion for predicted response to selection (pR%), predicted generalized response to selection (pgR) and predicted selection differentials (ps) recorded higher values than realized proportion selection (rR%), realized generalized selection (rgR) and realized differential response (rs) in two population through generations for boll weight (BW), these results indicated that the greater progress improving (BW) trait in cycles selection. Predicted heritability values in narrow sense ($ph^2_{n.s}$) were higher in F2 and F_4 (pop.1) and in F_4 (pop.2). Higher values of narrow sense heritability ($ph^2_{n.s}$) for boll weight (BW) a cross F_2 to F_4 indicated that the additive gene effects increased in advanced generation and useful selection for this trait.

Table2. Predicated and realized response to selection in F_2, F_3 and F_4 generations through populations for boll weight (BW).

Selection Parameters	Predicted response in F_2		Realized response F_3		Predicted response in F_4		Realized response in F_4		Predicted response in F_5	
	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
Selection response ((G.A),PR, rR)	0.47	0.53	0.08	0.01	0.19	0.61	0.18	0.09	0.59	0.14
Percentage proportion (Pr%, rR%)	15.36	16.64	2.52	0.20	6.21	20.20	5.77	2.68	17.99	4.37
Generalized selection response (pgR, rgR)	1.69	1.65	0.44	0.02	1.10	1.80	0.56	0.48	1.79	0.77
Selection differential response (Ps, rs)	0.57	0.66	0.17	0.04	0.35	0.69	0.09	-0.05	0.67	0.37
Heritability narrow sense (ph^2_{ns})	0.82	80.14	0.53	0.10	0.53	87.31	0.03	0.01	87.12	37.34
Mean	2.91	3.15	2.99	3.16	3.17	3.24				
Mean C1	3.08	3.19	3.04	3.00	3.26	3.19				

Means of predicted (pR) and realized (rR) responses to selection for lint yield (LY) in the selection cycles are presented in Table (3). The results showed that the families selected from F_2, F_3 and F_4 generations had higher mean performances in two populations of cycles selected. The predicted (pR) and realized (rR) responses to selection increased as generation progressed due to the efficiency of selection. The predicted expected advance to selection (pR) in F_2 and F4 were greater than realized advance (rR) in F_3 and F_4 generations. The pR in F_4 to F_5 generations were higher in (pop.2). Percentage proportion for predicted response to selection (pR %) were higher than the realized (rR %) in all cases for the two populations over all generations. In addition predicted generalized response to selection (pgR) of F_2 and F_4 generations were higher than realized generalized selection (rgR) in F_3, as well as the predicted selection differential (ps) were higher than the realized differential response (rs) in F_2 of the (pop.2) and in F_4 in two populations. Predicted heritability estimates (ph^2_{ns}) in narrow sense were higher in two populations for F_2 and in F_4 in (pop.2), as well as the Predicted heritability estimates (ph^2_{ns}) in narrow sense in F_5 generation was higher than the realized in F_4 generation in two populations, it means the current selection was useful to accumulate desirable genes for lint yield (LY), Table (3).

Lint percentage trait (L%) in the three cycles of selection for predicted (pR) and realized (rR) response of selection presented in Table (4). The data showed that the means of F_2 selected families of (pop1) were higher than the realized means of F_3 generation in two populations, the same results was obtained in (pop1) of F_4 generation. The results of the first cycle of selection for predicted genetic advance (pR) in F_2 to F_3 generations of populations were greater than realized genetic advanced (rR) in F_3, on the other hand (pR) in F_4 of the (pop.1) was higher than (rR), while the (rR) of the F_3 generation in (pop.2) was greater value than (pR) in F_4 generation of the (pop.2). The predicted generalized (pgR) values of the two populations in F_2 and in F_4 generations (pop.1) were higher than realized generalized selection. Results of predicted selection differential response (ps) in F_2 and F_4 generations in two populations were higher than the realized differential response (rs) in F_3 generation of two populations. Narrow sense heritability (ph^2_{ns}) predicted estimates were gave higher value in two population of F_2 generation, while the (rh^2_{ns}) realized response was higher value only in (pop.2) of the F_3 and F_4 generations. On the other hand F_4 generation of the (pop.2) showed low (ph^2_{ns}) predicted estimates. Narrow sense heritability (ph^2_{ns}) predicted for lint percentage (L %) was differed from F_2 generation to F_4 generation, means the current selection would be useful for improving (L%) trait in superior selected plant, its clarify in predicted response selection of F_5 generation, Table (4).

Table3. Predicated and realized response to selection in F_2, F_3 and F_4 generations through populations for lint yield (LY).

Selection Parameters	**Predicted response in F_2**		**Realized response F_3**		**Predicted response in F_4**		**Realized response in F_4**		**Predicted response in F_5**	
	Pop.1	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**
Selection response ((G.A),PR, rR)	**114.76**	**6.57**	**0.16**	**0.46**	**7.89**	**9.54**	**4.27**	**0.19**	**1.65**	**10.18**
Percentage proportion (Pr%, rR%)	**272.59**	**15.78**	**0.40**	**1.12**	**19.66**	**23.20**	**9.72**	**0.46**	**3.68**	**23.57**
Generalized selection response (pgR, rgR)	**93.05**	**1.56**	**0.04**	**0.09**	**1.95**	**1.80**	**3.05**	**0.03**	**1.18**	**1.79**
Selection differential response (Ps, rs)	**2.54**	**8.69**	**2.62**	**0.72**	**8.32**	**10.93**	**1.05**	**1.62**	**2.88**	**11.75**
Heritability narrow sense (ph^2_{ns})	**45.17**	**75.68**	**0.95**	**118.94**	**0.95**	**87.28**	**2.90**	**0.53**	**57.40**	**86.71**
Mean	**39.48**	**40.93**	**39.64**	**41.39**	**43.91**	**41.59**				
Mean C1	**42.10**	**41.65**	**40.16**	**41.13**	**44.96**	**43.21**				

Table4. Predicated and realized response to selection in F_2, F_3 and F_4 generations through populations for lint percentage (L %).

Selection Parameters	Predicted response in F_2		Realized response F_3		Predicted response in F_4		Realized response in F_4		Predicted response in F_5	
	Pop.1	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**
Selection response ((G.A),PR, rR)	210.90	2.48	0.78	1.36	2.45	0.67	0.12	0.41	1.85	1.31
Percentage proportion (Pr%, rR%)	505.45	6.09	1.94	3.39	6.01	1.65	0.29	1.00	4.50	3.25
Generalized selection response (pgR, rgR)	139.81	1.31	0.48	1.03	1.50	0.51	0.08	0.27	1.31	0.87
Selection differential response (Ps, rs)	3.11	3.91	1.96	1.89	3.37	2.72	0.40	-0.27	2.91	3.11
Heritability narrow sense (ph^2_{ns})	67.87	63.52	0.73	87.48	0.73	24.69	0.08	0.30	63.43	42.20
Mean	39.76	38.88	40.55	40.25	40.66	40.65				
Mean C1	41.73	40.77	40.86	40.61	41.07	40.38				

Regarding to fiber length (UHM) results in Table (5), showed that the mean performances for selected families were higher in F_4 generation of the two populations than F_2 and F_3 generations. Predicted response selection (PR) was higher in F_2 generation of the (pop1). The predicted genetic advance (pr) recorded higher values of F_2 and F_4 generations for (pop.1) and 2, respectively. The predicted generalized (pgR) values of F_2 generation of (pop.1) were higher than other generations (F_3 and F_4) in two populations, its clear that the dominance gene effects controlled in fiber length trait. Selection differential response (ps) results, table (5) revealed that the F_2 and F_4 generations of the two populations recorded higher values than F_3 generation of the two populations, high value of (ps) means additive gene effects were effective in population for improvement this trait. Narrow sense heritability (ph^2_{ns}) predicted estimates showed higher value in F_2 generation in (pop.1), while fiber length trait of the (pop.2) in F_2 and F_4 generations recoded low values of (ph^2_{ns}) for, could be described to the low magnitude of additive portion and amount of environmental and gene effects. The (pop1) in F_5 generation than F_4 generation, Table (5) gives high narrow sense heritability (ph^2_{ns}) predicted estimates indicated that additive gene effects increasing in advanced generation through current selection cycles.

Table5. Predicated and realized response to selection in F_2, F_3 and F_4 generations through populations for fiber length (U.H.M).

Selection Parameters	Predicted response in F_2		Realized response F_3		Predicted response in F_4		Realized response in F_4		Predicted response in F_5	
	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
Selection response ((G.A),PR, rR)	198.85	0.28	0.27	0.001	0.02	0.47	0.45	0.25	1.72	0.22
Percentage proportion (Pr%, rR%)	638.85	0.91	0.89	0.003	0.08	1.51	1.42	0.79	5.36	0.68
Generalized selection response (pgR, rgR)	166.51	0.27	0.52	0.001	0.05	0.42	0.41	0.24	1.58	0.21
Selection differential response (Ps, rs)	2.46	2.17	0.47	0.013	1.09	2.27	0.65	0.13	2.24	2.13
Heritability narrow sense (ph^2_{ns})	80.83	13.05	0.02	0.048	0.02	20.50	0.23	0.12	76.81	10.08
Mean	30.65	31.03	30.93	31.04	31.37	31.28				
Mean C1	31.13	31.05	31.2	30.82	32.03	31.41				

Respecting to Micronair values (Mic) of the two populations in three cycles of selection were presented in Table (6), (Mic) results revealed that the families selected recorded mean performances ranged from 4.2 to 4.4 in two populations at three selection cycles. The realized advance (rR) in

F_3 (pop1) showed negatively values of (Mic) as well as the realized advance (rR), generalized selection response (rR) an selection differential response (sp) showed desirable negative in F_3 and F_4 of the (pop.1) and (pop.2), respectively, Table (6). Negatively predicted response (Mic) value in F_5, means the current selection would be improving fiber fineness (Mic). Heritability (ph^2_{ns}) values of (Mic) were higher in F_2 of two populations and only in F_4 of (pop.2). The heritability (ph^2_{ns}) values were decreased as generation proceeded, these clarified that dominance gene effects were prevalence in the inheritance of (Mic) trait.

Table6. Predicated and realized response to selection in F_2, F_3 and F_4 generations through populations for Micronaire (Mic).

Selection Parameters	**Predicted response in F_2**		**Realized response F_3**		**Predicted response in F_4**		**Realized response in F_4**		**Predicted response in F_5**	
	Pop.1	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**	**Pop.1**	**Pop.2**
Selection response ((G.A),PR, rR)	42.13	-0.34	-0.21	0.11	0.07	-0.56	0.00	0.14	-0.21	0.11
Percentage proportion (Pr%, rR%)	976.16	-8.13	-4.71	2.68	1.67	-13.33	-0.11	3.22	-4.83	2.48
Generalized selection response (pgR, rgR)	116.00	-1.65	-0.81	0.68	0.28	-3.33	-0.03	0.47	-1.07	0.36
Selection differential response (Ps, rs)	0.75	0.42	-0.33	-0.02	0.53	0.35	-0.11	-0.06	0.40	0.62
Heritability narrow sense (ph^2_{ns})	56.31	-80.18	0.14	0.95	0.14	-161.55	0.00	0.02	-52.07	17.42
Mean	4.64	4.17	4.43	4.29	4.43	4.43				
Mean C1	4.3	4.2	4.4	4.2	4.3	4.4				

The predicted and realized response to selection means for fiber strength (PI) in three cycles of selection presented in Table (7). The results showed that the selected families from F_2 to F_3 and F_4 had desirable higher means (9.7, 9.8 and 10.1), respectively in (pop.1). The predicted response to selection (pR) in F_2 of the (pop.1) and F_4 generations in two populations were higher than realized response (rR) in F_3 generation. The (pR) in F_5 generation were higher than (rR) n F_4. The results of percentage predicted (pR%), generalized selection response (pgR) and selection differential response (ps) reveled higher values in F_2 generation pop.1 and F_4 generation of two populations compared with populations in F_3 generation, similar results were obtained in F_5 generation which recorded higher values of (pR) than (rR), (pgR) and (ps) means improving fiber strength (PI) through recurrent selection cycles. Predicted narrow sense heritability (ph^2_{ns}) were decreased in as generation proceeded except for (pop2) in F_4 generation it's may due to the dominance gene effects is appearance in the inheritance of fiber strength (PI), Table (7).

Table7. Predicated and realized response to selection in F_2, F_3 and F_4 generations through populations for fiber strength (PI).

Selection Parameters	Predicted response in F_2		Realized response F_3		Predicted response in F_4		Realized response in F_4		Predicted response in F_5	
	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2	Pop.1	Pop.2
Selection response ((G.A),PR, rR)	18.41	-0.03	0.18	-0.32	1.47	0.55	0.25	-0.01	0.29	0.74
Percentage proportion (Pr%, rR%)	189.28	-0.32	1.82	-3.41	15.07	5.88	2.47	-0.09	2.87	8.20
Generalized selection response (pgR, rgR)	35.36	-0.10	0.19	-0.67	1.55	1.16	0.45	-0.02	0.53	1.50
Selection differential response (Ps, rs)	1.07	0.63	0.18	0.03	1.96	0.98	0.12	-0.26	1.13	1.02
Heritability narrow sense (ph^2_{ns})	17.16	-4.95	0.75	-7.32	0.75	56.34	0.07	0.00	25.56	72.77
Mean	9.55	9.62	9.72	9.30	9.97	9.29				
Mean C1	9.7	9.7	9.8	9.4	10.1	9.0				

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Producing Bioplastic from Cotton and Textile Waste: A Sustainable Solution

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The global rise in plastic waste has become a pressing environmental concern. Conventional petroleum-based plastics, despite their versatility, are non-biodegradable and contribute significantly to pollution. As a result, researchers and industries are exploring sustainable alternatives, including bioplastics derived from renewable resources. One promising source of bioplastics is cotton and textile waste, which makes up a significant portion of municipal solid waste. This article delves into the process of producing bioplastics from cotton and textile waste, highlighting its environmental benefits and potential applications.

Environmental Impact of Conventional Plastics

Conventional plastics, derived primarily from fossil fuels, have had a significant negative impact on the environment such as:

1. Pollution and Waste:

- Landfilling: Conventional plastics are often non-biodegradable, causing them to accumulate in landfills and contribute to long-term environmental problems.
- Marine Pollution: Plastic waste can end up in the oceans, harming marine life through ingestion, entanglement, and habitat destruction.
- Microplastics: Conventional plastics can break down into microplastics, which can enter the food chain and have harmful effects on ecosystems and human health.

2. Greenhouse Gas Emissions:

- Production and Manufacturing: The production of conventional plastics requires large amounts of fossil fuels, which contribute to greenhouse gas emissions, such as carbon dioxide and methane.
- Incineration: When conventional plastics are burned, they release harmful gases and contribute to air pollution.

3. Resource Depletion:

- Fossil Fuels: Conventional plastic production relies on non-renewable fossil fuels, such as petroleum and natural gas, which contribute to their depletion.

4. Impacts on Wildlife and Ecosystems:

Ingestion and Entanglement: Wildlife can mistake plastic debris for food, leading to ingestion and subsequent health problems or death. Animals can also become entangled in plastic, causing injury or death.

Habitat Destruction: Plastic pollution can disrupt ecosystems and habitats, affecting biodiversity and ecological balance.

5. Chemical Contamination:

- Laxatives and Additives: Many conventional plastics contain harmful chemicals, such as phthalates and bisphenol A (BPA), which can leach into the environment and pose risks to human health.

Cotton and Textile Waste: A Valuable Resource

Cotton is a natural fiber known for its softness, breathability, and durability. However, the textile industry generates a significant amount of waste, including fabric scraps, scraps, and used clothing. Traditionally, these materials have been buried or burned, contributing to environmental pollution. By reusing cotton and textile waste, reducing waste disposal costs, conserve resources, and create valuable products.

Properties and Applications of Bioplastics from Cotton and Textile Waste:

Bioplastics derived from cotton and textile waste offer a range of properties and applications that make them attractive alternatives to conventional plastics.

Properties:

Biodegradability: One of the most important advantages of bioplastics derived from cotton and textile waste is their biodegradability. These materials can naturally decompose under specific environmental conditions, reducing their environmental impact.

Degradability: Many bioplastics derived from cotton and textile waste are also biodegradable, meaning they can be broken down into nutrient-rich compost that can be used to fertilize soil.

Renewable Resources: Bioplastics derived from cotton and textile waste are manufactured from renewable resources, reducing reliance on fossil fuels.

Mechanical Properties: While the mechanical properties of bioplastics can vary depending on the specific composition and production process, they often exhibit similar strength, flexibility, and durability to some conventional plastics.

Thermal Properties: Bioplastics generally have similar thermal properties to conventional plastics, allowing them to be used in a variety of applications that require heat or processing resistance.

Applications:

Packaging: Bioplastics from cotton and textile waste are suitable for a wide range of packaging applications

Textiles: Bioplastics can be used to produce textiles, providing a more sustainable alternative to traditional synthetic fibers.

Agricultural Applications: Bioplastics can be used in agricultural applications, such as biodegradable mulch films and plant pots, ……etc.

Bioplastic Production Process

Producing bioplastic from cotton and textile waste involves several key steps:

Collection and Sorting: Cotton and textile waste is collected from various sources, including clothing manufacturers, retailers, and households. The waste is then sorted to separate different types of fabrics and remove contaminants.

Pretreatment: The sorted waste undergoes pretreatment processes to prepare it for further processing. This may include washing, drying, and shredding the material to increase its surface area and facilitate chemical reactions.

Chemical Treatment: The pretreated waste undergoes chemical treatment to break down the cellulose fibers into smaller molecules. This process typically involves the use of strong acids or alkalis to break down the cellulose.

Polymerization: The resulting cellulose-derived molecules are polymerized to form bioplastics.

Polymerization is a chemical reaction that combines molecules into long chains, creating a plastic-like material.

Forming and casting: Bioplastics can be formed and cast into various products, such as packaging materials, disposable items, and even automotive components.

Biodegradability: Bioplastics derived from cotton and textile waste are biodegradable, meaning they can naturally decompose under specific environmental conditions. This property helps reduce environmental impact and reduce landfill waste.

Environmental benefits of bioplastics

Producing and using bioplastics from cotton and textile waste offers several environmental benefits:

- Reduced dependence on fossil fuels: Bioplastics are extracted from renewable resources, reducing our dependence on fossil fuels and reducing greenhouse gas emissions.
- Waste reduction: By reusing cotton and textile waste, we can divert these materials from landfills and reduce the overall volume of waste.
- Biodegradability: Bioplastics can naturally decompose, reducing the accumulation of plastic waste in the environment and reducing pollution.
- Carbon sequestration: Cotton plants absorb carbon dioxide as they grow, contributing to carbon sequestration and mitigating the effects of climate change.

Economic Feasibility and Market Potential of Bioplastics from Cotton and Textile Waste:

The economic feasibility and market potential of bioplastics from cotton and textile waste depend on several factors:

1. Economic Feasibility: Raw Material Costs: The cost of cotton and textile waste can vary depending on factors such as supply, demand, and geographic location. However, these materials are often considered relatively low-cost compared to fossil fuel-based plastics.
2. Production Costs: The costs of producing bioplastics can be affected by factors such as the specific production process, energy consumption, and labor costs. While bioplastic production may involve higher initial costs compared to conventional plastics, the long-term economic benefits can be significant.

3. Government Policies and Incentives: Government policies and incentives, such as tax breaks, subsidies, and mandates, can play a critical role in improving the economic feasibility of bioplastic production.
4. Market Potential: Growing Demand for Sustainable Products: There is a growing global demand for sustainable products, including bioplastics. Consumers and businesses are increasingly seeking alternatives to conventional plastics that have a lower environmental impact.
5. Regulatory pressures: Governments and regulatory bodies are implementing stricter regulations to reduce plastic pollution and promote the use of sustainable materials. This could create a favorable market environment for bioplastics.
6. Technological developments: Advances in bioplastic production technology can improve the properties and performance of bioplastics, making them more competitive with conventional plastics.
7. Brand image and differentiation: Companies that adopt bioplastics can enhance their brand image and differentiate themselves from competitors by demonstrating their commitment to sustainability.

Environmental Impact Assessment of Bioplastics from Cotton and Textile Waste:

Environmental impact assessment is a critical tool for assessing the potential environmental impacts of a proposed project, such as the production of bioplastics from cotton and textile waste as follow:

1. Resource Consumption:

- Raw Materials: Assess the consumption of cotton and textile waste, as well as any other resources used in the production process, such as water, energy and chemicals.
- Land Use: Assess the land use requirements for growing cotton, collecting textile waste and establishing bioplastic production facilities.

2. Greenhouse Gas Emissions:

- Production Processes: Assess the greenhouse gas emissions associated with the production process, including those from energy consumption, transportation and waste management.

- Carbon Sequestration: Consider the potential for carbon sequestration through the use of bio-based materials in the production of bioplastics.

3. Water Pollution:

- Wastewater Discharge: Assess the potential for water pollution from wastewater generated by bioplastic production facilities.
- Chemical leakage: Assess the risk of chemical leakage from production facilities, particularly if harmful chemicals are used.

4. Air pollution:

- Emissions from production facilities: Assess emissions of air pollutants, such as particulate matter, volatile organic compounds, and greenhouse gases, from bioplastic production facilities.

5. Waste generation:

- Solid waste: Assess the generation of solid waste, such as packaging materials, process waste, and end-of-life products.
- Waste management: Assess the effectiveness of waste management practices to reduce the environmental impact of waste disposal.

6. Biodiversity impacts:

- Habitat loss: Assess the potential for habitat loss due to land use changes associated with cotton farming or bioplastic production facilities.
- Species impacts: Assess potential impacts on biodiversity, including impacts on wildlife and ecosystems.

7. Social impacts:

- Community health: Assess potential health impacts on communities near bioplastic production facilities, including exposure to air pollution, water pollution, and noise.
- Economic Impacts: Assessing the economic impacts of bioplastic production on local communities, including job creation, income generation and economic development.

Technological Advances and Future Trends in Bioplastic Production from Cotton and Textile Waste:

Technological advances and emerging trends are driving the development and adoption of bioplastics from cotton and textile waste.

1. Improving production processes:

- Enzyme engineering: Advances in enzyme engineering are leading to the development of more efficient and cost-effective enzymes for the breakdown of cellulose and other plant materials.
- Process optimization: Research is underway to improve bioplastic production processes, reduce energy consumption, improve yields, and reduce waste generation.
- Expansion and commercialization: Efforts are underway to expand bioplastic production facilities and improve the commercial viability of bioplastic products.

2. Improved material properties:

- Customized properties: Technological advances are enabling the development of bioplastics with customized properties, such as improved mechanical strength, heat resistance, and barrier properties.
- Composite materials: Combining bioplastics with other materials, such as natural fibers or nanomaterials, can enhance their performance and expand their potential applications.

3. Emerging Technologies:

- 3D Printing: Bioplastics are increasingly being used in 3D printing applications, enabling the production of customized and complex products while reducing waste.
- Biodegradable Electronics: Research is underway into developing biodegradable electronics using bio-based materials, providing sustainable alternatives to traditional electronic components.
- Circular Economy: Bioplastics play a critical role in promoting a circular economy, where materials are recycled and reused to reduce waste and reduce dependence on fossil fuels.

4. Policy and Regulatory Support:

- Government Initiatives: Governments are implementing policies and regulations to promote the adoption of bioplastics and reduce plastic pollution.
- Standards and Certifications: Developing standardized testing methods and certifications for bioplastics

can help ensure their quality and environmental performance.

5. Consumer Awareness and Acceptance:

- Education and Marketing: Increasing consumer awareness of the benefits and environmental advantages of bioplastics is critical to driving market adoption.
- Product Labeling and Transparency: Clear labeling and transparency regarding the bio-based content and sustainability of bioplastic products can help consumers make informed choices.

Life Cycle Assessment of Bioplastics from Cotton and Textile Waste

A life cycle assessment of bioplastics is a comprehensive tool used to assess the environmental impacts of a product throughout its entire life cycle, from raw material extraction to end-of-life disposal. The key aspects to consider in a life cycle assessment of bioplastics from cotton and textile waste:

1. Raw material sourcing:

- Cotton farming: Assess the environmental impacts of cotton farming, including land use, water consumption, pesticide use, and greenhouse gas emissions.
- Textile waste: Assess the environmental impacts of textile waste collection and processing, including transportation, sorting, and cleaning.

2. Production:

- Bioplastics processing: Assess the environmental impacts of the bioplastics production process, including energy consumption, water use, chemical emissions, and waste generation.
- Manufacturing: Assess the environmental impacts of manufacturing products from bioplastics, including energy consumption, transportation, and waste generation.

3. Use and Consumption:

- Product Use: Assess the environmental impacts of using bioplastic products, including energy consumption, transportation and waste generation during use.
- End of Life: Assess the environmental impacts of disposal at the end of life, including landfilling, incineration or composting.

4. Transportation:

- Raw Material Transport: Assess the environmental impacts of transporting cotton, textile waste and bioplastics.
- Product Transport: Assess the environmental impacts of transporting bioplastics to the market and to consumers.

5. Infrastructure:

- Waste Management: Assess the environmental impacts of waste management infrastructure, including landfills, composting facilities and recycling plants.

6. Carbon Footprint:

- Greenhouse Gas Emissions: Quantify the global greenhouse gas emissions associated with each stage of the bioplastic life cycle.
- Carbon Sequestration: Consider the potential for carbon sequestration through the use of bio-based materials in the production of bioplastics.

7. Water Consumption:

- Agricultural Production: Assess the water consumption associated with cotton cultivation.
- Production Processes: Assess the water consumption during the production and manufacturing of bioplastics.

8. Land Use:

- Cotton Farming: Assessing land use requirements for cotton farming.
- Production Facilities: Assessing land use requirements for bioplastic production facilities.

By conducting a comprehensive life cycle analysis, it is possible to identify environmental hotspots and potential benefits of bioplastics from cotton and textile waste. This information can be used to inform decision making and promote the development of more sustainable and environmentally friendly bioplastic products.

Challenges and Future Directions

While the production of bioplastics from cotton and textile waste holds great promise, there are several challenges that need to be addressed:

- Cost competitiveness: The cost of producing bioplastics can be higher than that of conventional petroleum-based plastics, limiting their commercial viability.
- Mechanical properties: Bioplastics may not always have the same mechanical properties as conventional

  plastics, limiting their applications in certain industries.
- Scaling up production: Scaling up bioplastics requires significant investments in infrastructure and technology.
- Market acceptance: Increasing consumer awareness and acceptance of bioplastics is essential to driving market demand.

Despite these challenges, ongoing research and development efforts are focused on improving production processes, enhancing the properties of bioplastics, and expanding their applications. By addressing these challenges, we can unlock the full potential of bioplastics derived from cotton and textile waste and contribute to a more sustainable future. However, the properties and applications of bioplastics from cotton and textile waste are constantly evolving as research and development efforts continue to advance. As the demand for sustainable materials grows, we can expect to see more innovative and diverse applications for these bioplastics in the future.