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Cotton cultivar UA 107

Fred M. Bourland
University of Arkansas, Fayetteville

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Bourland

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(54) **COTTON CULTIVAR UA 107**

(71) Applicant: **BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS**, Little Rock, AR (US)

(72) Inventor: **Freddie M. Bourland**, Blytheville, AR (US)

(73) Assignee: **BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS**, Little Rock, AR (US)

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Primary Examiner — Mykola V. Kovalenko
(74) *Attorney, Agent, or Firm* — Jondie & Associates, P.C.

(57) **ABSTRACT**

A novel cotton cultivar, designated UA 107, is disclosed. The invention relates to the seeds of cotton cultivar UA 107, to the plants and plant parts of cotton UA 107 and to methods for producing a cotton plant produced by crossing the cultivar UA 107 with itself or another cotton variety. The invention also relates to methods of using cotton cultivar UA 107 and products derived therefrom. The invention also relates to methods for producing a cotton plant containing in its genetic material one or more transgenes and to the transgenic cotton plants and plant parts produced by those methods. The invention further relates to hybrid cotton seeds, plants and plant parts produced by crossing the cultivar UA 107 with another cotton cultivar.

23 Claims, No Drawings

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COTTON CULTIVAR UA 107

BACKGROUND OF THE INVENTION

The present invention relates to a new and distinctive cotton cultivar (*Gossypium*), designated UA 107. This invention further relates to a method for producing cotton seed, cotton plants, and cotton hybrids. All publications cited in this application are herein incorporated by reference.

Cotton is a soft, fluffy staple fiber that grows in a boll, or protective capsule, around the seeds of cotton plants of the genus *Gossypium*. The fiber is almost pure cellulose. The botanical purpose of cotton fiber is to aid in seed dispersal.

Cotton fiber most often is spun into yarn or thread and used to make a soft, breathable textile. The use of cotton for fabric is known to date to prehistoric times; fragments of cotton fabric dated from 5000 BC have been excavated in Mexico and Pakistan. Although cultivated since antiquity, it was the invention of the cotton gin that so lowered the cost of production that led to its widespread use, and it is the most widely used natural fiber cloth in clothing today.

There are four commercially-grown species of cotton, including *Gossypium hirsutum*, also known as upland cotton, which makes up 90% of the world production of cotton. Current estimates for world production are about 25 million tons annually, accounting for 2.5% of the world's arable land. China is the world's largest producer of cotton, but most of this is used domestically. The United States has been the largest exporter for many years.

There are numerous steps in the development of any novel, desirable plant germplasm. Plant breeding begins with the analysis and definition of problems and weaknesses of the current germplasm, the establishment of program goals, and the definition of specific breeding objectives. The next step is selection of germplasm that possess the traits to meet the program goals. The goal is to combine in a single cultivar an improved combination of desirable traits from the parental germplasm. In cotton, the important traits include higher fiber (lint) yield, earlier maturity, improved fiber quality, resistance to diseases and insects, resistance to drought and heat, and improved agronomic traits.

Cotton is an important and valuable field crop. Thus, a continuing goal of cotton plant breeders is to develop stable, high yielding cotton cultivars that are agronomically sound and have resistance to diseases. The reasons for this goal are obviously to maximize the amount and quality of the fiber produced on the land used and to supply fiber, oil, and food for animals and humans. To accomplish this goal, the cotton breeder must select and develop plants that have the traits that result in superior cultivars.

The foregoing examples of the related art and limitations related therewith are intended to be illustrative and not exclusive. Other limitations of the related art will become apparent to those of skill in the art upon a reading of the specification.

SUMMARY OF THE INVENTION

The following embodiments and aspects thereof are described in conjunction with systems, tools, and methods which are meant to be exemplary and illustrative, not limiting in scope. In various embodiments, one or more of the above-described problems have been reduced or eliminated, while other embodiments are directed to other improvements.

The present invention relates to a cotton seed, a cotton plant and plant parts thereof, a cotton cultivar, and a method for producing a cotton plant.

The present invention further relates to a method of producing cotton seeds and plants by crossing a plant of the instant invention with another cotton plant. The invention also relates to the plants or plant part(s) thereof having all of the phenotypic and morphological characteristics of cotton cultivar UA 107, and to methods for producing a cotton plant produced by crossing cotton variety UA 107 with itself or with another cotton line, and the creation of variants by mutagenesis, genetic modification or transformation of cotton cultivar UA 107.

One aspect of the present invention relates to seed of the cotton cultivar UA 107. The invention also relates to plants produced by growing the seed of the cotton variety UA 107, as well as the derivatives of such plants. As used herein, the term "plant" includes plant cells, plant protoplasts, plant cells of a tissue culture from which cotton plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants, such as pollen, flowers, seeds, bolls, leaves, stems, and the like.

Another aspect of the invention relates to a tissue culture of regenerable cells of the cotton cultivar UA 107, as well as plants regenerated therefrom, wherein the regenerated cotton plant expresses all the physiological and morphological characteristics of a plant grown from the cotton seed designated UA 107.

Yet another aspect of the current invention is a cotton plant of the cotton cultivar UA 107 further comprising a single locus conversion. In one embodiment, the cotton plant is defined as comprising the single locus conversion and otherwise capable of expressing all the physiological and morphological characteristics of the cotton variety UA 107. In particular embodiments of the invention, the single locus conversion may comprise a transgenic gene which has been introduced by genetic transformation into the cotton variety UA 107 or a progenitor thereof. A transgenic or non-transgenic single locus conversion can also be introduced by backcrossing, as is well known in the art. In certain embodiments of the invention, the single locus conversion may comprise a dominant or recessive allele. The locus conversion may confer potentially any desired trait upon the plant as described herein.

The invention further relates to methods for genetically modifying a cotton plant of the cotton cultivar UA 107 and to the modified cotton plant produced by those methods. The genetic modification methods may include, but are not limited to mutation breeding, genome editing, gene silencing, backcross conversion, genetic transformation, single and multiple gene conversion, and/or direct gene transfer.

The invention also relates to methods for producing a cotton plant containing in its genetic material one or more transgenes and to the transgenic cotton plant produced by those methods.

Still yet another aspect of the invention relates to a first generation (F_1) hybrid cotton seed produced by crossing a plant of the cotton cultivar UA 107 to a second cotton plant. Also included in the invention are the F_1 hybrid cotton plants grown from the hybrid seed produced by crossing the cotton variety UA 107 to a second cotton plant. Still further included in the invention are the seeds of an F_1 hybrid plant produced with the cotton variety UA 107 as one parent, the second generation (F_2) hybrid cotton plant grown from the seed of the F_1 hybrid plant, and the seeds of the F_2 hybrid plant.

In a further aspect of the invention, a composition is provided comprising a seed of cotton cultivar UA 107 comprised in plant seed growth media. In certain embodiments, the plant seed growth media is a soil or synthetic cultivation medium. In specific embodiments, the growth medium may be comprised in a container or may, for example, be soil in a field. Plant seed growth media are well known to those of skill in the art and include, but are in no way limited to, soil or synthetic cultivation medium. Advantageously, plant seed growth media can provide adequate physical support for seeds and can retain moisture and/or nutritional components. Examples of characteristics for soils that may be desirable in certain embodiments can be found, for instance, in U.S. Pat. Nos. 3,932,166 and 4,707,176. Synthetic plant cultivation media are also well known in the art and may, in certain embodiments, comprise polymers or hydrogels. Examples of such compositions are described, for example, in U.S. Pat. No. 4,241,537.

Still yet another aspect of the invention is a method of producing cotton seeds comprising crossing a plant of the cotton variety UA 107 to any second cotton plant, including itself or another plant of the variety UA 107. In particular embodiments of the invention, the method of crossing comprises the steps of: (a) planting seeds of the cotton cultivar UA 107; (b) cultivating cotton plants resulting from said seeds until said plants bear flowers; (c) allowing fertilization of the flowers of said plants; and (d) harvesting seeds produced from said plants.

Still yet another aspect of the invention is a method of producing hybrid cotton seeds comprising crossing the cotton cultivar UA 107 to a second, distinct cotton plant which is nonisogenic to the cotton variety UA 107. In particular embodiments of the invention, the crossing comprises the steps of: (a) planting seeds of cotton variety UA 107 and a second, distinct cotton plant; (b) cultivating the cotton plants grown from the seeds until the plants bear flowers; (c) cross pollinating a flower on one of the two plants with the pollen of the other plant; and (d) harvesting the seeds resulting from the cross pollinating.

Still yet another aspect of the invention is a method for developing a cotton plant in a cotton breeding program comprising: (a) obtaining a cotton plant, or its parts, of the cultivar UA 107; and (b) employing said plant or parts as a source of breeding material using plant breeding techniques. In the method, the plant breeding techniques may be selected from the group consisting of recurrent selection, mass selection, bulk selection, backcrossing, pedigree breeding, genetic marker-assisted selection, and genetic transformation. In certain embodiments of the invention, the cotton plant of variety UA 107 is used as the male or female parent.

Still yet another aspect of the invention is a method of producing a cotton plant derived from the cotton cultivar UA 107, the method comprising the steps of: (a) preparing a progeny plant derived from cotton variety UA 107 by crossing a plant of the cotton variety UA 107 with a second cotton plant; and (b) crossing the progeny plant with itself or a second plant to produce a progeny plant of a subsequent generation which is derived from a plant of the cotton variety UA 107. In one embodiment of the invention, the method further comprises: (c) crossing the progeny plant of a subsequent generation with itself or a second plant; and (d) repeating steps (b) and (c) for at least 2-10 additional generations to produce an inbred cotton plant derived from the cotton variety UA 107. Also provided by the invention is a plant produced by this and the other methods of the invention. Cotton variety UA 107-derived plants produced by this and the other methods of the invention described herein may, in certain embodiments of the invention, be further defined as comprising the traits of cotton variety UA 107 listed in Table 1.

The invention further relates to a method of producing a commodity plant product from cotton cultivar UA 107, such as lint, seed oil, or seed, and to the commodity plant product produced by the method.

The use of the word "a" or "an" when used in conjunction with the term "comprising" in the claims and/or the specification may mean "one," but it is also consistent with the meaning of "one or more," "at least one," and "one or more than one."

Other objects, features, and advantages of the present invention will become apparent from the following detailed description. It should be understood, however, that the detailed description and the specific examples, while indicating specific embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

In addition to the exemplary aspects and embodiments described above, further aspects and embodiments will become apparent by study of the following descriptions.

DETAILED DESCRIPTION OF THE INVENTION

In the description and tables which follow, a number of terms are used. In order to provide a clear and consistent understanding of the specification and claims, including the scope to be given such terms, the following definitions are provided:

Allele. Allele is any of one or more alternative forms of a gene locus, all of which relate to one trait or characteristic. In a diploid cell or organism, the two alleles of a given gene occupy corresponding loci on a pair of homologous chromosomes.

Backcrossing. Backcrossing is a process in which a breeder repeatedly crosses hybrid progeny back to one of the parents, for example, a first generation hybrid F_1 with one of the parental genotypes of the F_1 hybrid. Backcrossing can be used to introduce one or more single locus conversions from one genetic background into another.

Boll. The seed-bearing capsule of certain plants, especially cotton and flax.

Crossing. The mating of two parent plants.

Cross-pollination. Fertilization by the union of two gametes from different plants.

Desired Agronomic Characteristics. Agronomic characteristics (which will vary from crop to crop and plant to plant) such as yield, maturity, pest resistance and lint percent which are desired in a commercially acceptable crop or plant. For example, improved agronomic characteristics for cotton include yield, maturity, fiber content and fiber qualities.

Diploid. A cell or organism having two sets of chromosomes.

Disease Resistance. As used herein, the term "disease resistance" is defined as the ability of plants to restrict the activities of a specified pest, such as an insect, fungus, virus, or bacteria.

Disease Tolerance. As used herein, the term "disease tolerance" is defined as the ability of plants to endure a specified pest (such as an insect, fungus, virus or bacteria) or an adverse environmental condition and still perform and produce in spite of this disorder.

Donor Parent. The parent of a variety which contains the gene or trait of interest which is desired to be introduced into a second variety.

Emasculate. The removal of plant male sex organs or the inactivation of the organs with a cytoplasmic or nuclear genetic factor conferring male sterility or a chemical agent.

Essentially all of the physiological and morphological characteristics. A plant having essentially all of the physiological and morphological characteristics of a designated plant has all of the characteristics of the plant that are otherwise present when compared in the same environment, other than an occasional variant trait that might arise during backcrossing or direct introduction of a transgene.

Elongation (E1). As used herein, the term "elongation" is defined as the measure of elasticity of a bundle of fibers as measured by HVI.

F_1 Hybrid. The first generation progeny of the cross of two nonisogenic plants.

Fiber Characteristics. Refers to fiber qualities such as strength, fiber length, micronaire, fiber elongation, uniformity of fiber and amount of fiber.

Fiber Strength (T1). As used herein, the term "strength" is defined as the force required to break a bundle of fibers as measured in grams per millitex on the HVI.

Fruiting Nodes. As used herein, the term "fruiting nodes" is defined as the number of nodes on the main stem from which arise branches which bear fruit or bolls.

Genetically modified. Describes an organism that has received genetic material from another organism, or had its genetic material modified, resulting in a change in one or more of its phenotypic characteristics. Methods used to modify, introduce or delete the genetic material may include mutation breeding, genome editing, RNA interference, gene silencing, backcross conversion, genetic transformation, single and multiple gene conversion, and/or direct gene transfer.

Genome editing. A type of genetic engineering in which DNA is inserted, replaced, modified or removed from a genome using artificially engineered nucleases or other targeted changes using homologous recombination. Examples include but are not limited to use of zinc finger nucleases (ZFNs), TAL effector nucleases (TALENs) and CRISPR/Cas9. (Ma et. al., *Molecular Plant,* 9:961-974 (2016); Belhaj et. al., *Current Opinion in Biotechnology,* 32:76-84 (2015)).

Genotype. The genetic constitution of a cell or organism.

Gin Turnout. As used herein, the term "gin turnout" is defined as a fraction of lint in a machine harvested sample of seed cotton (lint, seed, and trash).

Haploid. A cell or organism having one set of the two sets of chromosomes in a diploid.

HVI. High Volume Instrumentation is a quality determination system used for cotton. Considered the standard USDA classing system.

Length. As used herein, the term "length" is defined as 2.5% span length in inches of fiber as measured by High Volume Instrumentation (HVI).

Linkage. A phenomenon wherein alleles on the same chromosome tend to segregate together more often than expected by chance if their transmission was independent.

Lint/Boll. As used herein, the term "lint/boll" is the weight of lint per boll.

Lint Index. As used herein, the term "lint index" refers to the weight of lint per seed in milligrams.

Lint Percent. As used herein, the term "lint percent" is defined as the lint (fiber) fraction of seed cotton (lint and seed). Also known as lint turnout.

Lint Yield. As used herein, the term "lint yield" is defined as the measure of the quantity of fiber produced on a given unit of land. Presented below in pounds of lint per acre.

Maturity. As used herein, the term "maturity" is defined as the HVI machine rating which refers to the degree of development of thickening of the fiber cell wall relative to the perimeter or effective diameter of the fiber.

Maturity Rating. As used herein, the term "maturity rating" is defined as a visual rating near harvest on the amount of opened bolls on the plant.

Micronaire. As used herein, the term "micronaire" is defined as a measure of the fineness of the fiber. Within a cotton cultivar, micronaire is also a measure of maturity. Micronaire differences are governed by changes in perimeter or in cell wall thickness, or by changes in both. Within a cultivar, cotton perimeter is fairly constant and maturity will cause a change in micronaire. Consequently, micronaire has a high correlation with maturity within a variety of cotton. Maturity is the degree of development of cell wall thickness. Micronaire may not have a good correlation with maturity between varieties of cotton having different fiber perimeter. Micronaire values range from about 2.0 to 6.0:

TABLE A

Below 2.9	Very fine	Possible small perimeter but mature (good fiber), or large perimeter but immature (bad fiber).
2.9 to 3.7	Fine	Various degrees of maturity and/or perimeter.
3.8 to 4.6	Average	Average degree of maturity and/or perimeter.
4.7 to 5.5	Coarse	Usually fully-developed (mature), but larger perimeter.
5.6+	Very coarse	Fully-developed, large-perimeter fiber.

Phenotype. The detectable characteristics of a cell or organism, which characteristics are the manifestation of gene expression.

Plant Height. As used herein, the term "plant height" is defined as the average height in inches or centimeters of a group of plants.

Quantitative Trait Loci (QTL). Quantitative trait loci (QTL) refer to genetic loci that control to some degree numerically representable traits that are usually continuously distributed.

Recurrent Parent. The repeating parent (variety) in a backcross breeding program. The recurrent parent is the variety into which a gene or trait is desired to be introduced.

Regeneration. The development of a plant from tissue culture.

Seed/boll. As used herein, the term "seed/boll" refers to the number of seeds per boll.

Seedcotton/boll. As used herein, the term "seedcotton/boll" refers to the weight of seedcotton per boll.

Self-pollination. The transfer of pollen from the anther to the stigma of the same plant or a plant of the same genotype.

Single Locus Converted (Conversion) Plant. Plants which are developed by a plant breeding technique called backcrossing or via genetic engineering wherein essentially all of the morphological and physiological characteristics of a variety are recovered in addition to the characteristics conferred by the single locus transferred into the variety via the backcrossing technique or via genetic engineering. A single locus may comprise one gene, or in the case of transgenic plants, one or more transgenes integrated into the host genome at a single site (locus).

Tissue Culture. A composition comprising isolated cells of the same or a different type or a collection of such cells organized into parts of a plant.

Transgene. A nucleic acid of interest that can be introduced into the genome of a plant by genetic engineering techniques (e.g., transformation) or breeding.

Vegetative Nodes. As used herein, the term "vegetative nodes" is defined as the number of nodes from the cotyledonary node to the first fruiting branch on the main stem of the plant.

Cotton cultivar UA 107 is an upland cotton, *Gossypium hirsutum* variety. UA 107 is an open-canopy (okra leaf) variety with glabrous leaves and low trichome density on the stems and bract margins. Cotton cultivar UA 107 is earlier maturing than most cultivars adapted to the Mississippi River Delta, and has fiber quality equal to cotton UA 222 (U.S. Pat. No. 8,859,862) and is superior to most varieties. In addition, cotton cultivar UA 107 has high resistance to bacterial blight.

Cotton cultivar UA 107 was derived from a cross between cotton lines UA103 (U.S. Pat. No. 8,552,274) and Arkot 9704 (Bourland and Jones, 2009) made at the Northeast Research and Extension Center (Keiser, AR) in 2007, and was developed as part of an ongoing effort to develop improved cotton lines having enhanced yield, yield components, earliness, host plant resistance, and fiber properties. The F_1 population was increased at the USDA/ARS Tecomán Cotton Winter Breeding Nursery (Tecomán, Mexico). The F_2 and F_3 populations were seeded and thinned to uniform plant densities (approximately 6 plants$^{-row\ m}$) at Keiser in 2008 and 2009, respectively. In each year, bulk selections of bolls were made from visually superior individual plants after bacterial blight susceptible and morphological off-type plants were removed. Individual plants were selected from the F_4 generation, which was grown at Keiser in 2010. Seed from these selections were evaluated as progeny rows at Keiser and Judd Hill in 2011 and as advanced progenies at Keiser, Marianna, and Rohwer in 2012. UA 107 derived its okra-leaf trait from its UA 103 parent.

During selection, nurseries and seed increases of UA 107 plants were inoculated with multiple races (including race 18) of *Xanthomonas citri* ssp. *malvacearum* (ex Smith 1901) Schaad et al. 2007, the causal agent of bacterial blight using field inoculation procedures described by Bird and Blank (1951). Susceptible plants were rogued from the early-generation populations and subsequent seed increases.

In most tests, cotton cultivar UA 107 produced lint yields greater than two well-adapted conventional cotton varieties, DP 393 (U.S. Pat. No. 6,930,228 and U.S. PVP 200400266) and UA 48 (U.S. Pat. No. 8,492,618 and U.S. PVP 201100041). Cotton cultivar UA 107 produces it high yields by a favorable combination of basic yield components, which should provide high yield stability. UA 107 displays high resistance to bacterial blight and is similar to DP 393 in its response to most other diseases and to tarnished plant bug. The okra-leaf trait of UA 107 helps to reduce effects of boll rots and permits better penetration of pesticides and crop termination chemicals into the plant canopy. The fiber quality of cotton variety UA 107 is very good, and in most tests it produced longer fiber length and lower micronaire (finer fibers) than DP 393. Surprisingly, cotton cultivar UA 107 displays an unusual combination of high yielding ability, favorable yield components, host plant resistance, early maturity and high fiber quality.

The cultivar has shown uniformity and stability, as described in the following Variety Description Information. It has been self-pollinated a sufficient number of generations with careful attention to uniformity of plant type. The cultivar has been increased with continued observation to uniformity. Variety UA 107 shows no variants other than what would normally be expected due to environment or that would occur for almost any characteristic during the course of repeated sexual reproduction. The results of an objective description of the variety are presented below, in Table 1. Those of skill in the art will recognize that these are typical values that may vary due to environment and that other values that are substantially equivalent are within the scope of the invention.

Cotton cultivar UA 107 has the following morphologic and other characteristics from data taken primarily in Arkansas.

TABLE 1

VARIETY DESCRIPTION INFORMATION

Species: *Gossypium hirsutum* L.
General:
- Plant Habit: Open-canopy (okra-leaf)
- Stem Lodging: None observed
- Fruiting Branch: Normal
- Growth: Erect, taller than DP 393 and UA 48
- Leaf Color: Green
- Boll Shape: Not determined
- Boll Breadth: Not determined

Maturity (Date of 50 % open bolls): Approximately 132 days after planting
Plant:
- Cm to 1st Fruiting Branch (from cotyledonary node): Not determined
- No. of Nodes to 1st Fruiting Branch (excluding cotyledonary node): Not determined
- Mature Plant Height (from cotyledonary node to terminal): 103.0 cm

Leaf (Upper-most, fully expanded leaf):
- Type: Smooth
- Pubescence: Smooth (1.3 rating on scale of 1 (smooth) to 9 (pilose))
- Stem Pubescence: Smooth (2.6 rating on scale of 1 (smooth) to 9 (pilose))

Glands:
- Leaf: Present
- Stem: Present
- Calyx Lobe: Absent

Flower:
- Petals (color): White
- Pollen (color): Cream
- Petal Spot: None

Seed:
- Seed Index: 12.1 g
- Lint Index: 8.3 g

Boll:
- Lint Percent (picked): 40.3
- Number of Seeds per Boll: 23.6
- Grams Seed Cotton per Boll: 4.9
- Number of Locules per Boll: Not determined
- Boll Type: Normal

Fiber Properties:
- Method (HVI or other): HVI
- Length (inches, 2.5% SL): 1.22
- Uniformity (%): 85.8
- Strength, T1 (g/tex): 32.4
- Elongation, E1 (%): 6.3
- Micronaire: 4.55

Nematodes, Insects, and Pests:
- Bacterial Blight (Race 1): Resistant
- Bacterial Blight (Race 2): Resistant
- Bacterial Blight (Race 18): Resistant
- *Fusarium* Wilt: Resistant
- *Verticillium* Wilt: Moderately tolerant
- Root-Knot Nematode: Not tested
- Tarnished Plant Bug (*Lygus lineolaris*): Moderately resistant

This invention is also directed to methods for producing a cotton plant by crossing a first parent cotton plant with a second parent cotton plant, wherein the first or second cotton plant is the cotton plant from the cultivar UA 107. Further,

both the first and second parent cotton plants may be the cultivar UA 107 (e.g., self-pollination). Therefore, any methods using the cultivar UA 107 are part of this invention: selfing, backcrosses, hybrid breeding, and crosses to populations. Any plants produced using cultivar UA 107 as parents are within the scope of this invention. As used herein, the term "plant" includes plant cells, plant protoplasts, plant cells of tissue culture from which cotton plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants, such as pollen, flowers, embryos, ovules, seeds, leaves, stems, roots, anthers, pistils, and the like. Thus, another aspect of this invention is to provide for cells which upon growth and differentiation produce a cultivar having essentially all of the physiological and morphological characteristics of UA 107.

The present invention contemplates a cotton plant regenerated from a tissue culture of a cultivar (e.g., UA 107) or hybrid plant of the present invention. As is well known in the art, tissue culture of cotton can be used for the in vitro regeneration of a cotton plant. Tissue culture of various tissues of cotton and regeneration of plants there from is well known and widely published.

Further Embodiments of the Invention

The development of new cotton cultivars requires the evaluation and selection of parents and the crossing of these parents. The lack of predictable success of a given cross requires that a breeder, in any given year, make several crosses with the same or different breeding objectives.

One aspect of the current invention concerns methods for crossing the cotton cultivar UA 107 with itself or a second plant and the seeds and plants produced by such methods. These methods can be used for propagation of the cotton variety UA 107, or can be used to produce hybrid cotton seeds and the plants grown therefrom. A hybrid plant can be used as a recurrent parent at any given stage in a backcrossing protocol during the production of a single locus conversion of the cotton variety UA 107.

The variety of the present invention is well suited to the development of new varieties based on the elite nature of the genetic background of the variety. In selecting a second plant to cross with UA 107 for the purpose of developing novel cotton varieties, it will typically be desired to choose those plants which themselves exhibit one or more selected desirable characteristics. Examples of potentially desired characteristics include higher fiber (lint) yield, earlier maturity, improved fiber quality, resistance to diseases and insects, tolerance to drought and heat, and improved agronomic traits.

Any time the cotton cultivar UA 107 is crossed with another, different, variety, first generation (F_1) cotton progeny are produced. The hybrid progeny are produced regardless of characteristics of the two varieties produced. As such, an F_1 hybrid cotton plant may be produced by crossing UA 107 with any second cotton plant. The second cotton plant may be genetically homogeneous (e.g., inbred) or may itself be a hybrid. Therefore, any F_1 hybrid cotton plant produced by crossing cotton cultivar UA 107 with a second cotton plant is a part of the present invention.

Cotton Breeding Techniques

Cotton plants can be crossed by either natural or mechanical techniques. Natural pollination occurs in cotton either by self pollination or natural cross pollination, which typically is aided by pollinating organisms. In either natural or artificial crosses, flowering and flowering time are important considerations. The cotton flower is monoecious in that the male and female structures are in the same flower. The crossed or hybrid seed can be produced by manual crosses between selected parents. Floral buds of the parent that is to be the female are emasculated prior to the opening of the flower by manual removal of the male anthers. At flowering, the pollen from flowers of the parent plants designated as male, are manually placed on the stigma of the previous emasculated flower. Seed developed from the cross is known as first generation (F_1) hybrid seed. Planting of this seed produces F_1 hybrid plants of which half their genetic component is from the female parent and half from the male parent. Segregation of genes begins at meiosis thus producing second generation (F_2) seed. Assuming multiple genetic differences between the original parents, each F_2 seed has a unique combination of genes.

Self-pollination occurs naturally in cotton with no manipulation of the flowers. For the crossing of two cotton plants, it may be beneficial to use artificial hybridization. In artificial hybridization, the flower used as a female in a cross is manually cross pollinated prior to maturation of pollen from the flower, thereby preventing self fertilization, or alternatively, the male parts of the flower are emasculated using a technique known in the art. Techniques for emasculating the male parts of a cotton flower include, for example, physical removal of the male parts, use of a genetic factor conferring male sterility, and application of a chemical gametocide to the male parts.

For artificial hybridization employing emasculation, flowers that are expected to open the following day are selected on the female parent. The buds are swollen and the corolla is just visible through the calyx or has begun to emerge. Usually no more than two buds on a parent plant are prepared, and all self-pollinated flowers or immature buds are removed with forceps. Special care is required to remove immature buds that are hidden under the stipules at the leaf axil, and could develop into flowers at a later date. The flower is grasped between the thumb and index finger and the location of the stigma determined by examining the sepals. The calyx is removed by grasping a sepal with the forceps, pulling it down and around the flower, and repeating the procedure until the five sepals are removed. The exposed corolla is removed with care to avoid injuring the stigma. Cross-pollination can then be carried out using, for example, petri dishes or envelopes in which male flowers have been collected. Desiccators containing calcium chloride crystals can be used in some environments to dry male flowers to obtain adequate pollen shed.

Either with or without emasculation of the female flower, hand pollination can be carried out by removing the stamens and pistil with a forceps from a flower of the male parent and gently brushing the anthers against the stigma of the female flower. Access to the stamens can be achieved by removing the front sepal and keel petals, or piercing the keel with closed forceps and allowing them to open to push the petals away. Brushing the anthers on the stigma causes them to rupture, and the highest percentage of successful crosses is obtained when pollen is clearly visible on the stigma. Pollen shed can be checked by tapping the anthers before brushing the stigma. Several male flowers may have to be used to obtain suitable pollen shed when conditions are unfavorable, or the same male may be used to pollinate several flowers with good pollen shed.

Cross-pollination is more common within rows than between adjacent rows; therefore, it may be beneficial to grow populations with genetic male sterility on a square grid to create rows in all directions. For example, single plant hills on 50-cm centers may be used, with subdivision of the

area into blocks of an equal number of hills for harvest from bulks of an equal amount of seed from male-sterile plants in each block to enhance random pollination.

Choice of breeding or selection methods depends on the mode of plant reproduction, the heritability of the trait(s) being improved, and the type of cultivar used commercially (e.g., F_1 hybrid cultivar, pureline cultivar, etc.). For highly heritable traits, a choice of superior individual plants evaluated at a single location will be effective, whereas for traits with low heritability, selection should be based on mean values obtained from replicated evaluations of families of related plants. Popular selection methods commonly include pedigree selection, modified pedigree selection, mass selection, recurrent selection, and backcrossing.

The complexity of inheritance influences choice of the breeding method. Backcross breeding is used to transfer one or a few favorable genes for a highly heritable trait into a desirable cultivar. This approach has been used extensively for breeding disease-resistant plant cultivars. Various recurrent selection techniques are used to improve quantitatively inherited traits controlled by numerous genes. The use of recurrent selection in self-pollinating crops depends on the ease of pollination, the frequency of successful hybrids from each pollination, and the number of hybrid offspring from each successful cross.

Each breeding program should include a periodic, objective evaluation of the efficiency of the breeding procedure. Evaluation criteria vary depending on the goal and objectives, but should include gain from selection per year based on comparisons to an appropriate standard, overall value of the advanced breeding lines, and number of successful cultivars produced per unit of input (e.g., per year, per dollar expended, etc.).

Promising advanced breeding lines are thoroughly tested and compared to appropriate standards in environments representative of the commercial target area(s) for generally three or more years. The best lines are candidates to become new commercial cultivars. Those lines still deficient in a few traits are discarded or may be utilized as parents to produce new populations for further selection.

These processes, which lead to the final step of marketing and distribution, may take as much as eight to twelve years from the time the first cross is made. Therefore, development of new cultivars is a time-consuming process that requires precise forward planning, efficient use of resources, and a minimum of changes in direction.

A most difficult task is the identification of individuals that are genetically superior because for most traits the true genotypic value is masked by other confounding plant traits or environmental factors. One method of identifying a superior plant is to observe its performance relative to other experimental lines and widely grown standard cultivars. For many traits a single observation is inconclusive, and replicated observations over time and space are required to provide a good estimate of a line's genetic worth.

The goal of a commercial cotton breeding program is to develop new, unique, and superior cotton cultivars. The breeder initially selects and crosses two or more parental lines, followed by repeated selfing and selection, thus producing many new genetic combinations. The breeder can theoretically generate billions of different genetic combinations via this procedure. The breeder has no direct control over which genetic combinations will arise in the limited population size which is grown. Therefore, two breeders will never develop the same line having the same traits.

Each year, the plant breeder selects the germplasm to advance to the next generation. This germplasm is grown under unique and different geographical, climatic, and soil conditions, and further selections are then made, during and at the end of the growing season. The lines which are developed are unpredictable. This unpredictability is because the breeder's selection occurs in unique environments, with no control at the DNA level (using conventional breeding procedures), and with millions of different possible genetic combinations being generated. A breeder of ordinary skill in the art cannot predict the final resulting lines he develops, except possibly in a very gross and general fashion. The same breeder cannot produce, with any reasonable likelihood, the same cultivar twice by using the exact same original parents and the same selection techniques. This unpredictability results in the expenditure of large amounts of research moneys to develop superior new cotton cultivars.

This invention also is directed to methods for producing a cotton plant by crossing a first parent cotton plant with a second parent cotton plant wherein the first or second parent cotton plant is a cotton plant of the cultivar UA 107. Further, both first and second parent cotton plants can come from the cotton cultivar UA 107. Additionally, the first or second parent cotton plants can be either *Gossypium hirsutum* or *Gossypium barbadense*, or any other cotton plant. Thus, any such methods using the cotton cultivar UA 107 are part of this invention: selfing, backcrosses, hybrid production, crosses to populations, and the like. All plants produced using cotton cultivar UA 107 as a parent are within the scope of this invention, including those developed from varieties derived from cotton cultivar UA 107. Advantageously, the cotton cultivar could be used in crosses with other, different, cotton plants to produce first generation (F_1) cotton hybrid seeds and plants with superior characteristics. The other, different, cotton plants may be *Gossypium hirsutum* or *Gossypium barbadense* or another cotton cultivar. The cultivar of the invention can also be used for transformation where exogenous genes are introduced and expressed by the cultivar of the invention. Genetic variants created either through traditional breeding methods using cultivar UA 107 or through transformation of UA 107 by any of a number of protocols known to those of skill in the art are intended to be within the scope of this invention.

The following describes breeding methods that may be used with cultivar UA 107 in the development of further cotton plants. One such embodiment is a method for developing a UA 107 progeny cotton plant in a cotton plant breeding program comprising: obtaining the cotton plant, or a part thereof, of cultivar UA 107, utilizing said plant or plant part as a source of breeding material, and selecting a UA 107 progeny plant with molecular markers in common with UA 107 and/or with morphological and/or physiological characteristics selected from the characteristics listed in Table 1. Breeding steps that may be used in the cotton plant breeding program include pedigree breeding, backcrossing, mutation breeding, and recurrent selection. In conjunction with these steps, techniques such as RFLP-enhanced selection, genetic marker enhanced selection (for example, SSR markers), and the making of double haploids may be utilized.

Another method involves producing a population of cultivar UA 107 progeny cotton plants, comprising crossing cultivar UA 107 with another cotton plant, thereby producing a population of cotton plants, which, on average, derive 50% of their alleles from cultivar UA 107. The other cotton plant may be *Gossypium hirsutum* or *Gossypium barbadense* or any other cotton plant. A plant of this population may be selected and repeatedly selfed or sibbed with a

cotton cultivar resulting from these successive filial generations. One embodiment of this invention is the cotton cultivar produced by this method and that has obtained at least 50% of its alleles from cultivar UA 107.

One of ordinary skill in the art of plant breeding would know how to evaluate the traits of two plant varieties to determine if there is no significant difference between the two traits expressed by those varieties. For example, see Fehr and Walt, *Principles of Cultivar Development*, pp. 261-286 (1987). Thus the invention includes cotton cultivar UA 107 progeny cotton plants comprising a combination of at least two UA 107 traits selected from the group consisting of those listed in Table 1 or the UA 107 combination of traits listed in the Detailed Description of the Invention, so that said progeny cotton plant is not significantly different for said traits than cotton cultivar UA 107 as determined at the 5% significance level when grown in the same environment. Using techniques described herein, molecular markers may be used to identify said progeny plant as a UA 107 progeny plant. Mean trait values may be used to determine whether trait differences are significant, and preferably the traits are measured on plants grown under the same environmental conditions. Once such a variety is developed its value is substantial since it is important to advance the germplasm base as a whole in order to maintain or improve traits such as yield, disease resistance, pest resistance, and plant performance in extreme environmental conditions.

Progeny of cultivar UA 107 may also be characterized through their filial relationship with cotton cultivar UA 107, as for example, being within a certain number of breeding crosses of cotton cultivar UA 107. A breeding cross is a cross made to introduce new genetics into the progeny, and is distinguished from a cross, such as a self or a sib cross, made to select among existing genetic alleles. The lower the number of breeding crosses in the pedigree, the closer the relationship between cotton cultivar UA 107 and its progeny. For example, progeny produced by the methods described herein may be within 1, 2, 3, 4 or 5 breeding crosses of cotton cultivar UA 107.

Additional Breeding Techniques

Pureline cultivars of cotton are commonly bred by hybridization of two or more parents followed by selection. The complexity of inheritance, the breeding objectives, and the available resources influence the breeding method. The development of new varieties requires development and selection, the crossing of varieties and selection of progeny from superior crosses.

Pedigree breeding and recurrent selection breeding methods are used to develop varieties from breeding populations. Breeding programs combine desirable traits from two or more varieties or various broad-based sources into breeding pools from which varieties are developed by selfing and selection of desired phenotypes. The new varieties are evaluated to determine which have commercial potential.

Pedigree breeding is primarily used to combine favorable genes into a totally new cultivar that is different in many traits than either parent used in the original cross. It is commonly used for the improvement of self-pollinating crops. Two parents which possess favorable, complementary traits are crossed to produce an F_1 (filial generation 1). An F_2 population is produced by selfing one or several F_1 plants. Selection of desirable individual plants may begin as early as the F_2 generation wherein maximum gene segregation occurs or later depending upon the objectives of the breeder. Individual plant selection can occur for one or more generations. Successively, seed from each selected plant can be planted in individual, identified rows or hills, known as progeny rows or progeny hills, to evaluate the line and to increase the seed quantity, or to further select individual plants. Once a progeny row or progeny hill is selected as having desirable traits, it becomes what is known as a breeding line that is specifically identifiable from other breeding lines that were derived from the same original population. At an advanced generation (i.e., F_5 or higher) seed of individual lines are evaluated in replicated testing. At an advanced stage the best lines or a mixture of phenotypically similar lines from the same original cross are tested for potential release as new cultivars.

Mass and recurrent selections can be used to improve populations of either self- or cross-pollinating crops. A genetically variable population of heterozygous individuals is either identified or created by intercrossing several different parents. The best plants are selected based on individual superiority, outstanding progeny, or excellent combining ability. The selected plants are intercrossed to produce a new population in which further cycles of selection are continued.

The single seed descent procedure in the strict sense refers to planting a segregating population, harvesting one seed from every plant, and using the one-seed sample to plant the next generation. When the population has been advanced to the desired level of inbreeding, the plants from which lines are derived will each trace to different F_2 individuals. Primary advantages of the seed descent procedures are to delay selection until a high level of homozygosity (e.g., lack of gene segregation) is achieved in individual plants, and to move through these early generations quickly, usually through using winter nurseries.

The modified single seed descent procedures involve harvesting multiple seed (i.e., a single lock or a simple boll) from each plant in a population and combining them to form a bulk. Part of the bulk is used to plant the next generation and part is put in reserve. This procedure has been used to save labor at harvest and to maintain adequate seed quantities of the population. The multiple-seed procedure may be used to save labor. It is considerably faster to gin bolls with a machine than to remove one seed by hand for the single-seed procedure. The multiple-seed procedure also makes it possible to plant the same number of seeds of a population each generation of inbreeding. Enough seeds are harvested to make up for those plants that did not germinate or produce seed.

Selection for desirable traits can occur at any segregating generation (F_2 and above). Selection pressure is exerted on a population by growing the population in an environment where the desired trait is maximally expressed and the individuals or lines possessing the trait can be identified. For instance, selection can occur for disease resistance when the plants or lines are grown in natural or artificially-induced disease environments, and the breeder selects only those individuals having little or no disease and are thus assumed to be resistant.

Mutation breeding is another method of introducing new traits into cotton varieties. Mutations that occur spontaneously or are artificially induced can be useful sources of variability for a plant breeder. The goal of artificial mutagenesis is to increase the rate of mutation for a desired characteristic. Mutation rates can be increased by many different means including temperature, long-term seed storage, tissue culture conditions, radiation (such as X-rays, Gamma rays, neutrons, Beta radiation, or ultraviolet radiation), chemical mutagens (such as base analogues like 5-bromo-uracil), antibiotics, alkylating agents (such as sulfur mustards, nitrogen mustards, epoxides, ethyleneamines,

sulfates, sulfonates, sulfones, or lactones), azide, hydroxylamine, nitrous acid, or acridines. Once a desired trait is observed through mutagenesis the trait may then be incorporated into existing germplasm by traditional breeding techniques. Details of mutation breeding can be found in Principles of Cultivar Development by Fehr, Macmillan Publishing Company (1993).

The production of double haploids can also be used for the development of homozygous varieties in a breeding program. Double haploids are produced by the doubling of a set of chromosomes from a heterozygous plant to produce a completely homozygous individual. For example, see Wan, et al., Theor. Appl. Genet., 77:889-892 (1989).

Descriptions of other breeding methods that are commonly used for different traits and crops can be found in one of several reference books (e.g., Allard, In: *Principles of plant breeding*, John Wiley & Sons, NY University of California, Davis, Calif., 50-98, 1960; Simmonds, In: *Principles of crop improvement*, Longman, Inc., NY 369-399, 1979; Sneep and Hendriksen, In: *Plant breeding perspectives*, Wageningen (Ed), Center for Agricultural Publishing and Documentation, 1979; Fehr, In: *Principles of variety development*, Theory and Technique (Vol 1) and Crop Species Soybean (Vol 2), Iowa State Univ., Macmillian Pub. Co., NY 360-376, 1987; Fehr, In: *Soybeans: Improvement, Production and Uses,* 2d Ed., Manograph 16:249, 1987). Additionally, with any of the methods disclosed above, mutagenesis can be utilized to increase the diversity of the gene pool that is available in the breeding program.

Proper testing should detect any major faults and establish the level of superiority or improvement over current cultivars. In addition to showing superior performance, there must be a demand for a new cultivar that is compatible with industry standards or which creates a new market. The introduction of a new cultivar will incur additional costs to the seed producer, and to the grower, processor, and consumer, for special advertising, marketing and commercial production practices, and new product utilization. The testing preceding the release of a new cultivar should take into consideration research and development costs as well as technical superiority of the final cultivar. For seed-propagated cultivars, it must be feasible to produce seed easily and economically.

Genetic Analysis

In addition to phenotypic observations, a plant can also be characterized by its genotype. The genotype of a plant can be determined by a molecular marker profiling, which can be applied to plants of the same variety or a related variety, can reveal genetic difference of plants and plant parts which are genetically superior as a result of an event comprising a backcross conversion, transgene, or genetic sterility factor, and can be used to reveal or validate a pedigree or genetic relationship among test materials. Such molecular marker profiling can be accomplished by using a variety of techniques including, but not limited to, restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism (AFLP), sequence-tagged sites (STS), randomly amplified polymorphic DNA (RAPD), arbitrarily primed polymerase chain reaction (AP-PCR), DNA amplification fingerprinting (DAF), sequence characterized amplified regions (SCARs), variable number tandem repeat (VNTR), short tandem repeat (STR), single feature polymorphism (SFP), simple sequence length polymorphism (SSLP), restriction site associated DNA, allozymes, isozyme markers, single nucleotide polymorphisms (SNPs), or simple sequence repeat (SSR) markers, also known as microsatellites (Gupta et al., 1999; Korzun et al., 2001). Various types of these marker platforms, for example, can be used to identify individual varieties developed from specific parent varieties, as well as cells, or other plant parts thereof. See, for example, Tyagi et al. (2014) "Genetic diversity and population structure in the US Upland cotton (*Gossypium hirsutum* L.)," *Theoretical and Applied Genetics* 127(2): 283-295; Tatineni et al. (1996) "Genetic diversity in elite cotton germplasm determined by morphological characteristics and RAPDs," *Crop Science* 36(1):186-192; and Cho et al. (2014) "Genome-wide SNP marker panel applicable to Cotton Genetic diversity test," Proceedings of the International Cotton Genome Initiative Conference 2(1):11, each of which are incorporated by reference herein in their entirety.

In some examples, one or more markers may be used to examine and/or evaluate genetic characteristics of a cotton variety. Particular markers used for these purposes are not limited to any particular set of markers and diagnostic platforms, but are envisioned to include any type of markers and diagnostic platforms that can provide means for distinguishing varieties. One method of genetic characterization may to use only homozygous loci for cotton variety UA 107.

Primers and PCR protocols for assaying these and other markers are disclosed in, for example, CottonGen located on the World Wide Web at cottongen.org. In addition to being used for identification of cotton variety UA 107, as well as plant parts and plant cells of cotton variety UA 107, a genetic profile may be used to identify a cotton plant produced through the use of cotton variety UA 107 or to verify a pedigree for progeny plants produced through the use of cotton variety UA 107. A genetic marker profile may also be useful in breeding and developing backcross conversions.

In an embodiment, the present invention provides a cotton plant characterized by molecular and physiological data obtained from a representative sample of said variety deposited with the American Type Culture Collection (ATCC). Thus, plants, seeds, or parts thereof, having all or essentially all of the morphological and physiological characteristics of cotton variety UA 107 are provided. Further provided is a cotton plant formed by the combination of the disclosed cotton plant or plant cell with another cotton plant or cell and comprising the homozygous alleles of the variety.

In some examples, a plant, a plant part, or a seed of cotton cultivar UA 107 may be characterized by producing a molecular profile. A molecular profile may include, but is not limited to, one or more genotypic and/or phenotypic profile(s). A genotypic profile may include, but is not limited to, a marker profile, such as a genetic map, a linkage map, a trait maker profile, a SNP profile, an SSR profile, a genome-wide marker profile, a haplotype, and the like. A molecular profile may also be a nucleic acid sequence profile, and/or a physical map. A phenotypic profile may include, but is not limited to, a protein expression profile, a metabolic profile, an mRNA expression profile, and the like.

One means of performing genetic marker profiling is using SSR polymorphisms that are well known in the art. A marker system based on SSRs can be highly informative in linkage analysis relative to other marker systems, in that multiple alleles for a given locus may be present. Another advantage of this type of marker is that through use of flanking primers, collecting more informative SSR data can be relatively easily achieved, for example, by using the polymerase chain reaction (PCR), thereby eliminating the need for labor-intensive Southern hybridization. PCR detection may be performed using two oligonucleotide primers flanking the polymorphic segment of repetitive DNA to amplify the SSR region.

Following amplification, genotype of test material revealed by each marker can be scored by electrophoresis of the amplification products. Scoring of marker genotype is based on the size of the amplified fragment, which correlates to the number of base pairs of the fragment. While variation in the primer used or in the laboratory procedures can affect the reported fragment size, relative values should remain constant regardless of specific primer or laboratory used. When comparing varieties, it may be beneficial to have all profiles performed in the same lab. Primers that can be used are publically available and may be found in, for example, CottonGen (Yu et al., CottonGen: a genomics, genetics and breeding database for cotton research," *Nucleic Acids Research* 42 (D1):D1229-D1236,2013).

A genotypic profile of cotton cultivar UA 107 can be used to identify a plant comprising variety UA 107 as a parent, since such plants will comprise the same homozygous alleles as variety UA 107. Because the cotton variety at inbred stage is essentially homozygous at all relevant loci, most loci should have only one type of allele present. In contrast, a genetic marker profile of an F_1 progeny should be the sum of those parents, e.g., if one parent was homozygous for allele X at a particular locus, and the other parent homozygous for allele Y at that locus, then the F_1 progeny will be XY (heterozygous) at that locus. Subsequent generations of progeny produced by selection and breeding are expected to be of genotype XX (homozygous), YY (homozygous), or XY (heterozygous) for that locus position. When the F_1 plant is selfed or sibbed for successive filial generations, the locus should be either X or Y for that position.

In addition, plants and plant parts substantially benefiting from the use of variety UA 107 in their development, such as cotton cultivar UA 107 comprising a backcross conversion, transgene, or genetic sterility factor, may be identified by having a molecular marker profile with a high percent identity to cotton variety UA 107. Such a percent identity might be 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or 99.9% identical to cotton variety UA 107.

A genotypic profile of cultivar UA 107 also can be used to identify essentially derived varieties and other progeny varieties developed from the use of cultivar UA 107, as well as cells and other plant parts thereof. Plants of the invention include any plant having at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% of the markers in the genotypic profile, and that retain 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 99.9% of the morphological and physiological characteristics of cultivar UA 107 when grown under the same conditions. Such plants may be developed using markers well known in the art. Progeny plants and plant parts produced using variety UA 107 may be identified, for example, by having a molecular marker profile of at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96% 97%, 98%, 99%, or 99.5% genetic contribution from cotton variety UA 107, as measured by either percent identity or percent similarity. Such progeny may be further characterized as being within a pedigree distance of variety UA 107, such as within 1, 2, 3, 4, or 5 or less cross pollinations to a cotton plant other than variety UA 107, or a plant that has variety UA 107 as a progenitor. Unique molecular profiles may be identified with other molecular tools, such as SNPs and RFLPs.

Methods for Genetic Engineering of Cotton

With the advent of molecular biological techniques that have allowed the isolation and characterization of genes that encode specific protein products, scientists in the field of plant biology developed a strong interest in engineering the genome of plants (genetic engineering) to contain and express foreign genes, or additional, or modified versions of native, or endogenous, genes (perhaps driven by different promoters) in order to alter the traits of a plant in a specific manner. Plants altered by genetic engineering are often referred to as 'genetically modified'. Such foreign additional and/or modified genes are referred to herein collectively as "transgenes." Over the last fifteen to twenty years several methods for producing transgenic plants have been developed, and the present invention, in particular embodiments, also relates to transformed versions of the claimed cultivar.

Plant transformation involves the construction of an expression vector which will function in plant cells. Such a vector comprises DNA comprising a gene under control of or operatively linked to a regulatory element (for example, a promoter). The expression vector may contain one or more such operably linked gene/regulatory element combinations. The vector(s) may be in the form of a plasmid, and can be used alone or in combination with other plasmids, to provide transformed cotton plants, using transformation methods as described below to incorporate transgenes into the genetic material of the cotton plant(s).

Numerous methods for plant transformation have been developed, including biological and physical, plant transformation protocols. See, for example, Miki, et al., "Procedures for Introducing Foreign DNA into Plants" in *Methods in Plant Molecular Biology and Biotechnology*, Glick and Thompson (Eds.), CRC Press, Inc., Boca Raton, pp. 67-88 (1993). In addition, expression vectors and in vitro culture methods for plant cell or tissue transformation and regeneration of plants are available. See, for example, Gruber, et al., "Vectors for Plant Transformation" in *Methods in Plant Molecular Biology and Biotechnology*, Glick and Thompson (Eds.), CRC Press, Inc., Boca Raton, pp. 89-119 (1993).

A. *Agrobacterium*-Mediated Transformation:

One method for introducing an expression vector into plants is based on the natural transformation system of *Agrobacterium*. See, for example, Horsch, et al., *Science,* 227:1229 (1985). *A. tumefaciens* and *A. rhizogenes* are plant pathogenic soil bacteria which genetically transform plant cells. The Ti and Ri plasmids of *A. tumefaciens* and *A. rhizogenes*, respectively, carry genes responsible for genetic transformation of the plant. See, for example, Kado, C. I., *Crit. Rev. Plant Sci.,* 10:1 (1991). Descriptions of *Agrobacterium* vector systems and methods for *Agrobacterium*-mediated gene transfer are provided by Gruber, et al., supra, Miki, et al., supra, and Moloney, et al., *Plant Cell Rep.,* 8:238 (1989). See also, U.S. Pat. No. 5,563,055 (Townsend and Thomas), issued Oct. 8, 1996.

Agrobacterium-mediated transfer is a widely applicable system for introducing gene loci into plant cells, including cotton. An advantage of the technique is that DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations (Klee et al., Bio. Tech., 3(7): 637-642, 1985). Moreover, recent technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate the construction of vectors capable of expressing various polypeptide coding genes. The vectors

described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes. Additionally, *Agrobacterium* containing both armed and disarmed Ti genes can be used for transformation.

In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene locus transfer. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art (Fraley et al., *Bio. Tech.,* 3(7):629-635, 1985; U.S. Pat. No. 5,563,055). One efficient means for transformation of cotton in particular is transformation and regeneration of cotton hypocotyl explants following inoculation with *Agrobacterium tumefaciens* from primary callus development, embryogenesis, embryogenic callus identification, transgenic cotton shoot production and the development of transgenic plants, as is known in the art.

B. Direct Gene Transfer:

Several methods of plant transformation, collectively referred to as direct gene transfer, have been developed as an alternative to *Agrobacterium*-mediated transformation. A generally applicable method of plant transformation is microprojectile-mediated transformation wherein DNA is carried on the surface of microprojectiles measuring 1 μm to 4 μm. The expression vector is introduced into plant tissues with a biolistic device that accelerates the microprojectiles to speeds of 300 m/s to 600 m/s which is sufficient to penetrate plant cell walls and membranes. Sanford, et al., *Part. Sci. Technol.,* 5:27 (1987); Sanford, J. C., *Trends Biotech.,* 6:299 (1988); Klein, et al., *Bio/technology,* 6:559-563 (1988); Sanford, J. C., *Physiol Plant,* 7:206 (1990); Klein, et al., *Bio/technology,* 10:268 (1992). See also, U.S. Pat. No. 5,015,580 (Christou, et al.), issued May 14, 1991; U.S. Pat. No. 5,322,783 (Tomes, et al.), issued Jun. 21, 1994.

Another method for physical delivery of DNA to plants is sonication of target cells. Zhang, et al., *Bio/technology,* 9:996 (1991). Alternatively, liposome and spheroplast fusion have been used to introduce expression vectors into plants. Deshayes, et al., *EMBO* 1, 4:2731 (1985); Christou, et al., *PNAS,* 84:3962 (1987). Direct uptake of DNA into protoplasts using $CaCl_2$ precipitation, polyvinyl alcohol, or poly-L-ornithine has also been reported. Hain, et al., *Mol. Gen. Genet.,* 199:161 (1985) and Draper, et al., *Plant Cell Physiol.* 23:451 (1982). Electroporation of protoplasts and whole cells and tissues has also been described. Donn, et al., In Abstracts of VIIth International Congress on Plant Cell and Tissue Culture IAPTC, A2-38, p. 53 (1990); D'Halluin, et al., Plant Cell, 4:1495-1505 (1992); and Spencer, et al., *Plant Mol. Biol.,* 24:51-61 (1994).

Following transformation of cotton target tissues, expression of selectable marker genes allows for preferential selection of transformed cells, tissues, and/or plants, using regeneration and selection methods now well known in the art.

The methods described herein for transformation would typically be used for producing a transgenic variety. The transgenic variety could then be crossed, with another (non-transformed or transformed) variety, in order to produce a new transgenic variety. Alternatively, a genetic trait which has been engineered into a particular cotton cultivar using the transformation techniques described could be moved into another cultivar using traditional backcrossing techniques that are well known in the plant breeding arts. For example, a backcrossing approach could be used to move an engineered trait from a public, non-elite variety into an elite variety, or from a variety containing a foreign gene in its genome into a variety or varieties which do not contain that gene. As used herein, "crossing" can refer to a simple X by Y cross, or the process of backcrossing, depending on the context.

Expression Vectors for Cotton Transformation: Marker Genes

Expression vectors include at least one genetic marker operably linked to a regulatory element (for example, a promoter) that allows transformed cells containing the marker to be either recovered by negative selection (i.e., inhibiting growth of cells that do not contain the selectable marker gene), or by positive selection (i.e., screening for the product encoded by the genetic marker). Many commonly used selectable marker genes for plant transformation are well known in the transformation arts, and include, for example, genes that code for enzymes that metabolically detoxify a selective chemical agent which may be an antibiotic or an herbicide, or genes that encode an altered target which is insensitive to the inhibitor. A few positive selection methods are also known in the art.

One commonly used selectable marker gene for plant transformation is the neomycin phosphotransferase II (nptII), which, when under the control of plant regulatory signals, confers resistance to kanamycin. Fraley, et al., *PNAS,* 80:4803 (1983). Another commonly used selectable marker gene is the hygromycin phosphotransferase gene which confers resistance to the antibiotic hygromycin. Vanden Elzen, et al., *Plant Mol. Biol.,* 5:299 (1985).

Additional selectable marker genes of bacterial origin that confer resistance to antibiotics include gentamycin acetyl transferase, streptomycin phosphotransferase, and aminoglycoside-3'-adenyl transferase, the bleomycin resistance determinant. Hayford, et al., *Plant Physiol.,* 86:1216 (1988); Jones, et al., *Mol. Gen. Genet.,* 210:86 (1987); Svab, et al., *Plant Mol. Biol.,* 14:197 (1990); Hille, et al., *Plant Mol. Biol.,* 7:171 (1986). Other selectable marker genes confer resistance to herbicides such as glyphosate, glufosinate, or bromoxynil. Comai, et al., *Nature,* 317:741-744 (1985); Gordon-Kamm, et al., *Plant Cell,* 2:603-618 (1990); and Stalker, et al., *Science,* 242:419-423 (1988).

Other selectable marker genes for plant transformation that are not of bacterial origin include, for example, mouse dihydrofolate reductase, plant 5-enolpyruvyl-shikimate-3-phosphate synthase and plant acetolactate synthase. Eichholtz, et al., *Somatic Cell Mol. Genet.,* 13:67 (1987); Shah, et al., *Science,* 233:478 (1986); Charest, et al., *Plant Cell Rep.,* 8:643 (1990).

Another class of marker genes for plant transformation requires screening of presumptively transformed plant cells rather than direct genetic selection of transformed cells for resistance to a toxic substance such as an antibiotic. These genes are particularly useful to quantify or visualize the spatial pattern of expression of a gene in specific tissues and are frequently referred to as reporter genes because they can be fused to a gene or gene regulatory sequence for the investigation of gene expression. Commonly used genes for screening presumptively transformed cells include 0-glucuronidase (GUS), 0-galactosidase, luciferase, and chloramphenicol acetyltransferase. Jefferson, R. A., *Plant Mol. Biol.* Rep., 5:387 (1987); Teeri, et al., *EMBO J.,* 8:343 (1989); Koncz, et al., *PNAS,* 84:131 (1987); DeBlock, et al., *EMBO* 1, 3:1681 (1984).

In vivo methods for visualizing GUS activity that do not require destruction of plant tissue are available. Molecular Probes Publication 2908, IMAGENE GREEN, pp. 1-4 (1993) and Naleway, et al., *J. Cell Biol.,* 115:151a (1991). However, these in vivo methods for visualizing GUS activ-

ity have not proven useful for recovery of transformed cells because of low sensitivity, high fluorescent backgrounds, and limitations associated with the use of luciferase genes as selectable markers.

More recently, a gene encoding Green Fluorescent Protein (GFP) has been utilized as a marker for gene expression in prokaryotic and eukaryotic cells. Chalfie, et al., *Science,* 263:802 (1994). GFP and mutants of GFP may be used as screenable markers.

Expression Vectors for Cotton Transformation: Promoters

Genes included in expression vectors must be driven by a nucleotide sequence comprising a regulatory element (for example, a promoter). Several types of promoters are now well known in the transformation arts, as are other regulatory elements that can be used alone or in combination with promoters.

As used herein, "promoter" includes reference to a region of DNA upstream from the start of transcription and involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells. Examples of promoters under developmental control include promoters that preferentially initiate transcription in certain tissues, such as leaves, roots, seeds, fibers, xylem vessels, tracheids, or sclerenchyma. Such promoters are referred to as "tissue-preferred." Promoters which initiate transcription only in certain tissue are referred to as "tissue-specific." A "cell type" specific promoter primarily drives expression in certain cell types in one or more organs, for example, vascular cells in roots or leaves. An "inducible" promoter is a promoter which is under environmental control. Examples of environmental conditions that may effect transcription by inducible promoters include anaerobic conditions or the presence of light. Tissue-specific, tissue-preferred, cell type specific, and inducible promoters constitute the class of "non-constitutive" promoters. A "constitutive" promoter is a promoter which is active under most environmental conditions.

A. Inducible Promoters:

An inducible promoter is operably linked to a gene for expression in cotton. Optionally, the inducible promoter is operably linked to a nucleotide sequence encoding a signal sequence which is operably linked to a gene for expression in cotton. With an inducible promoter the rate of transcription increases in response to an inducing agent.

Any inducible promoter can be used in the instant invention. See Ward, et al., *Plant Mol. Biol.,* 22:361-366 (1993). Exemplary inducible promoters include, but are not limited to, that from the ACEI system which responds to copper (Mett, et al., *PNAS,* 90:4567-4571 (1993)); In2 gene from maize which responds to benzenesulfonamide herbicide safeners (Hershey, et al., *Mol. Gen. Genet.,* 227:229-237 (1991) and Gatz, et al., *Mol. Gen. Genet.,* 243:32-38 (1994)); or Tet repressor from Tn10 (Gatz, et al., *Mol. Gen. Genet.,* 227:229-237 (1991)). A particularly preferred inducible promoter is a promoter that responds to an inducing agent to which plants do not normally respond. An exemplary inducible promoter is the inducible promoter from a steroid hormone gene, the transcriptional activity of which is induced by a glucocorticosteroid hormone (Schena, et al., *PNAS,* 88:0421 (1991)).

B. Constitutive Promoters:

A constitutive promoter is operably linked to a gene for expression in cotton or the constitutive promoter is operably linked to a nucleotide sequence encoding a signal sequence which is operably linked to a gene for expression in cotton.

Many different constitutive promoters can be utilized in the instant invention. Exemplary constitutive promoters include, but are not limited to, the promoters from plant viruses such as the 35S promoter from CaMV (Odell, et al., *Nature,* 313:810-812 (1985)) and the promoters from such genes as rice actin (McElroy, et al., *Plant Cell,* 2:163-171 (1990)); ubiquitin (Christensen, et al., *Plant Mol. Biol.,* 12:619-632 (1989) and Christensen, et al., *Plant Mol. Biol.,* 18:675-689 (1992)); pEMU (Last, et al., *Theor. Appl. Genet.,* 81:581-588 (1991)); MAS (Velten, et al., *EMBO J.,* 3:2723-2730 (1984)); and maize H3 histone (Lepetit, et al., *Mol. Gen. Genet.,* 231:276-285 (1992) and Atanassova, et al., *Plant Journal,* 2 (3): 291-300 (1992)).

The ALS promoter, Xbal/Ncol fragment 5' to the *Brassica napus* ALS3 structural gene (or a nucleotide sequence similarity to said Xbal/Ncol fragment), represents a particularly useful constitutive promoter. See PCT Application No. WO 96/30530.

C. Tissue-Specific or Tissue-Preferred Promoters:

A tissue-specific promoter is operably linked to a gene for expression in cotton. Optionally, the tissue-specific promoter is operably linked to a nucleotide sequence encoding a signal sequence which is operably linked to a gene for expression in cotton. Plants transformed with a gene of interest operably linked to a tissue-specific promoter produce the protein product of the transgene exclusively, or preferentially, in a specific tissue.

Any tissue-specific or tissue-preferred promoter can be utilized in the instant invention. Exemplary tissue-specific or tissue-preferred promoters include, but are not limited to, a root-preferred promoter, such as that from the phaseolin gene (Murai, et al., *Science,* 23:476-482 (1983) and Sengupta-Gopalan, et al., *PNAS,* 82:3320-3324 (1985)); a leaf-specific and light-induced promoter, such as that from cab or rubisco (Simpson, et al., *EMBO J.,* 4(11):2723-2729 (1985) and Timko, et al., *Nature,* 318:579-582 (1985)); an anther-specific promoter, such as that from LAT52 (Twell, et al., *Mol. Gen. Genet.,* 217:240-245 (1989)); a pollen-specific promoter, such as that from Zm13 (Guerrero, et al., *Mol. Gen. Genet.,* 244:161-168 (1993)); or a microspore-preferred promoter, such as that from apg (Twell, et al., *Sex. Plant Reprod.,* 6:217-224 (1993)).

Signal Sequences for Targeting Proteins to Subcellular Compartments

Transport of protein produced by transgenes to a subcellular compartment, such as the chloroplast, vacuole, peroxisome, glyoxysome, cell wall, or mitochondrion, or for secretion into the apoplast, is accomplished by means of operably linking the nucleotide sequence encoding a signal sequence to the 5' and/or 3' region of a gene encoding the protein of interest. Targeting sequences at the 5' and/or 3' end of the structural gene may determine, during protein synthesis and processing, where the encoded protein is ultimately compartmentalized.

The presence of a signal sequence directs a polypeptide to either an intracellular organelle or subcellular compartment or for secretion to the apoplast. Many signal sequences are known in the art. See, for example, Becker, et al., *Plant Mol. Biol.,* 20:49 (1992); Close, P. S., Master's Thesis, Iowa State University (1993); Knox, C., et al., *Plant Mol. Biol.,* 9:3-17 (1987); Lerner, et al., *Plant Physiol.,* 91:124-129 (1989); Fontes, et al., *Plant Cell,* 3:483-496 (1991); Matsuoka, et al., *PNAS,* 88:834 (1991); Gould, et al., *J. Cell. Biol.,* 108:1657 (1989); Creissen, et al., *Plant J.,* 2:129 (1991); Kalderon, et al., *Cell,* 39:499-509 (1984); Steifel, et al., *Plant Cell,* 2:785-793 (1990).

Cotton Cultivar UA 107 Further Comprising a Transgene

Transgenes and transformation methods provide means to engineer the genome of plants to contain and express heterologous genetic elements, including but not limited to foreign genetic elements, additional copies of endogenous elements, and/or modified versions of native or endogenous genetic elements, in order to alter at least one trait of a plant in a specific manner. Any heterologous DNA sequence(s), whether from a different species or from the same species, which are inserted into the genome using transformation, backcrossing, or other methods known to one of skill in the art are referred to herein collectively as transgenes. The sequences are heterologous based on sequence source, location of integration, operably linked elements, or any combination thereof. One or more transgenes of interest can be introduced into cotton cultivar UA 107. Transgenic variants of cotton cultivar UA 107 plants, seeds, cells, and parts thereof or derived therefrom are provided. Transgenic variants of UA 107 comprise the physiological and morphological characteristics of cotton cultivar UA 107, such as listed in Table 1 as determined at the 5% significance level when grown in the same environmental conditions, and/or may be characterized or identified by percent similarity or identity to UA 107 as determined by SSR or other molecular markers. In some examples, transgenic variants of cotton cultivar UA 107 are produced by introducing at least one transgene of interest into cotton cultivar UA 107 by transforming UA 107 with a polynucleotide comprising the transgene of interest. In other examples, transgenic variants of cotton cultivar UA 107 are produced by introducing at least one transgene by introgressing the transgene into cotton cultivar UA 107 by crossing.

In one example, a process for modifying cotton cultivar UA 107 with the addition of a desired trait, said process comprising transforming a cotton plant of cultivar UA 107 with a transgene that confers a desired trait is provided. Therefore, transgenic UA 107 cotton cells, plants, plant parts, and seeds produced from this process are provided. In some examples one more desired traits may include traits such as herbicide resistance, insect resistance, disease resistance, modified fatty acid metabolism, abiotic stress resistance, site-specific genetic recombination, modified carbohydrate metabolism or modified cotton fiber characteristics. The specific gene may be any known in the art or listed herein, including but not limited to a polynucleotide conferring tolerance or resistance to an ALS-inhibitor herbicide, imidazolinone, sulfonylurea, protoporphyrinogen oxidase (PPO) inhibitors, hydroxyphenyl pyruvate dioxygenase (HPPD) inhibitors, glyphosate, glufosinate, triazine, 2,4-dichlorophenoxyacetic acid (2,4-D), dicamba, broxynil, metribuzin, or benzonitrile herbicides; a polynucleotide encoding a *Bacillus thuringiensis* polypeptide, a polynucleotide encoding a phytase, a fatty acid desaturase (e.g., FAD-2, FAD-3), galactinol synthase, a raffinose synthetic enzyme, a sucrose phosphate synthase nucleic acid; or a polynucleotide conferring resistance to plant pathogens.

Foreign Protein Genes and Agronomic Genes

With transgenic plants according to the present invention, a foreign protein can be produced in commercial quantities. Thus, techniques for the selection and propagation of transformed plants, which are well understood in the art, yield a plurality of transgenic plants which are harvested in a conventional manner, and a foreign protein then can be extracted from a tissue of interest or from total biomass. Protein extraction from plant biomass can be accomplished by known methods which are discussed, for example, by Heney and Orr, *Anal. Biochem.,* 114:92-6 (1981).

According to an embodiment, the transgenic plant provided for commercial production of foreign protein is a cotton plant. In another embodiment, the biomass of interest is lint or seed. For the relatively small number of transgenic plants that show higher levels of expression, a genetic map can be generated, primarily via conventional RFLP, PCR, and SSR analysis, which identifies the approximate chromosomal location of the integrated DNA molecule. For exemplary methodologies in this regard, see Glick and Thompson, *Methods in Plant Molecular Biology and Biotechnology*, CRC Press, Boca Raton, 269:284 (1993). Map information concerning chromosomal location is useful for proprietary protection of a subject transgenic plant. If unauthorized propagation is undertaken and crosses made with other germplasm, the map of the integration region can be compared to similar maps for suspect plants, to determine if the latter have a common parentage with the subject plant. Map comparisons would involve hybridizations, RFLP, PCR, SSR and sequencing, all of which are conventional techniques.

Likewise, by means of the present invention, agronomic genes can be expressed in transformed plants. More particularly, plants can be genetically engineered to express various phenotypes of agronomic interest. Exemplary genes and methods implicated in this regard include, but are not limited to, those categorized below:

A. Genes that Confer Resistance to Pests or Disease and that Encode:

1. Plant disease resistance genes. Plant defenses are often activated by specific interaction between the product of a disease resistance gene (R) in the plant and the product of a corresponding avirulence (Avr) gene in the pathogen. A plant variety can be transformed with cloned resistance gene to engineer plants that are resistant to specific pathogen strains. See, for example, Jones, et al., *Science,* 266:789 (1994) (cloning of the tomato Cf-9 gene for resistance to *Cladosporium fulvum*); Martin, et al., *Science,* 262:1432 (1993) (tomato Pto gene for resistance to *Pseudomonas syringae* pv. tomato encodes a protein kinase); Mindrinos, et al., *Cell,* 78:1089 (1994) (*Arabidopsis* RSP2 gene for resistance to *Pseudomonas syringae*).

2. A gene conferring resistance to a pest, such as nematodes. See, e.g., PCT Application No. WO 96/30517; PCT Application No. WO 93/19181.

3. A *Bacillus thuringiensis* protein, a derivative thereof or a synthetic polypeptide modeled thereon. See, for example, Geiser, et al., *Gene,* 48:109 (1986), who disclose the cloning and nucleotide sequence of a Bt δ-endotoxin gene. Moreover, DNA molecules encoding δ-endotoxin genes can be purchased from American Type Culture Collection, Manassas, Va., for example, under ATCC Accession Nos. 40098, 67136, 31995, and 31998.

4. A lectin. See, for example, the disclosure by Van Damme, et al., *Plant Molec. Biol.,* 24:25 (1994), who disclose the nucleotide sequences of several *Clivia miniata* mannose-binding lectin genes.

5. A vitamin-binding protein such as avidin. See PCT Application No. US 93/06487. The application teaches the use of avidin and avidin homologues as larvicides against insect pests.

6. An enzyme inhibitor, for example, a protease or proteinase inhibitor or an amylase inhibitor. See, for example, Abe, et al., *J. Biol. Chem.,* 262:16793 (1987) (nucleotide sequence of rice cysteine proteinase inhibitor); Huub, et al., *Plant Molec. Biol.,* 21:985 (1993) (nucleotide sequence of cDNA encoding tobacco proteinase inhibitor I); Sumitani, et al., *Biosci. Biotech. Biochem.,* 57:1243 (1993) (nucleotide

sequence of *Streptomyces nitrosporeus* α-amylase inhibitor); and U.S. Pat. No. 5,494,813 (Hepher and Atkinson, issued Feb. 27, 1996).

7. An insect-specific hormone or pheromone, such as an ecdysteroid and juvenile hormone, a variant thereof, a mimetic based thereon, or an antagonist or agonist thereof. See, for example, the disclosure by Hammock, et al., *Nature,* 344:458 (1990), of baculovirus expression of cloned juvenile hormone esterase, an inactivator of juvenile hormone, Gade and Goldsworthy (*Eds. Physiological System in Insects*, Elsevier Academic Press, Burlington, Mass., 2007), describing allostatins and their potential use in pest control; and Palli et al. (*Vitam. Horm.,* 73:59-100, 2005), disclosing use of ecdysteroid and ecdysteroid receptor in agriculture. The diuretic hormone receptor (DHR) was identified in Price et al. (*Insect Mol. Biol.,* 13:469-480, 2004) as a candidate target of insecticides.

8. An insect-specific peptide or neuropeptide which, upon expression, disrupts the physiology of the affected pest. For example, see the disclosures of Regan, *J. Biol. Chem.,* 269:9 (1994) (expression cloning yields DNA coding for insect diuretic hormone receptor) and Pratt, et al., *Biochem. Biophys. Res. Comm.,* 163:1243 (1989) (an allostatin is identified in *Diploptera puntata*). See also, U.S. Pat. No. 5,266,317 to Tomalski, et al., who disclose genes encoding insect-specific, paralytic neurotoxins.

9. An insect-specific venom produced in nature by a snake, a wasp, etc. For example, see Pang, et al., *Gene,* 116:165 (1992), for disclosure of heterologous expression in plants of a gene coding for a scorpion insectotoxic peptide.

10. An enzyme responsible for a hyper-accumulation of a monoterpene, a sesquiterpene, a steroid, a hydroxamic acid, a phenylpropanoid derivative, or another non-protein molecule with insecticidal activity.

11. An enzyme involved in the modification, including the post-translational modification, of a biologically active molecule. For example, a glycolytic enzyme, a proteolytic enzyme, a lipolytic enzyme, a nuclease, a cyclase, a transaminase, an esterase, a hydrolase, a phosphatase, a kinase, a phosphorylase, a polymerase, an elastase, a chitinase, and a glucanase, whether natural or synthetic. See PCT Application No. WO 93/02197 in the name of Scott, et al., which discloses the nucleotide sequence of a callase gene. DNA molecules which contain chitinase-encoding sequences can be obtained, for example, from the ATCC under Accession Nos. 39637 and 67152. See also, Kramer, et al., *Insect Biochem. Molec. Biol.,* 23:691 (1993), who teach the nucleotide sequence of a cDNA encoding tobacco hornworm chitinase, and Kawalleck, et al., *Plant Molec. Biol.,* 21:673 (1993), who provide the nucleotide sequence of the parsley ubi4-2 polyubiquitin gene.

12. A molecule that stimulates signal transduction. For example, see the disclosure by Botella, et al., *Plant Molec. Biol.,* 24:757 (1994), of nucleotide sequences for mung bean calmodulin cDNA clones and Griess, et al., *Plant Physiol.,* 104:1467 (1994), who provide the nucleotide sequence of a maize calmodulin cDNA clone.

13. A hydrophobic moment peptide. See PCT Application No. WO 95/16776 (disclosure of peptide derivatives of Tachyplesin which inhibit fungal plant pathogens) and PCT Application No. WO 95/18855 (teaches synthetic antimicrobial peptides that confer disease resistance).

14. A membrane permease, a channel former or a channel blocker. For example, see the disclosure of Jaynes, et al., *Plant Sci.,* 89:43 (1993), of heterologous expression of a cecropin-β lytic peptide analog to render transgenic tobacco plants resistant to *Pseudomonas solanacearum.*

15. A viral-invasive protein or a complex toxin derived therefrom. For example, the accumulation of viral coat proteins in transformed plant cells imparts resistance to viral infection and/or disease development effected by the virus from which the coat protein gene is derived, as well as by related viruses. See, Beachy, et al., *Ann. Rev. Phytopathol.,* 28:451 (1990). Coat protein-mediated resistance has been conferred upon transformed plants against alfalfa mosaic virus, cucumber mosaic virus, tobacco streak virus, potato virus X, potato virus Y, tobacco etch virus, tobacco rattle virus and tobacco mosaic virus. Id.

16. An insect-specific antibody or an immunotoxin derived therefrom. Thus, an antibody targeted to a critical metabolic function in the insect gut would inactivate an affected enzyme, killing the insect. See, Taylor, et al., Abstract #497, Seventh Int'l Symposium on Molecular Plant-Microbe Interactions (Edinburgh, Scotland) (1994) (enzymatic inactivation in transgenic tobacco via production of single-chain antibody fragments).

17. A virus-specific antibody. See, for example, Tavladoraki, et al., *Nature,* 366:469 (1993), who show that transgenic plants expressing recombinant antibody genes are protected from virus attack. Additional means of inducing whole-plant resistance to a pathogen include modulation of the systemic acquired resistance (SAR) or pathogenesis related (PR) genes, for example genes homologous to the *Arabidopsis thaliana* NIM1/NPR1/SAI1, and/or increasing salicylic acid production (Ryals et al., *Plant Cell,* 8:1809-1819, 1996).

18. A developmental-arrestive protein produced in nature by a pathogen or a parasite. Thus, fungal endo-α-1, 4-D-polygalacturonases facilitate fungal colonization and plant nutrient release by solubilizing plant cell wall homo-α-1,4-D-galacturonase. See, Lamb, et al., *Bio/technology,* 10:1436 (1992). The cloning and characterization of a gene which encodes a bean endopolygalacturonase-inhibiting protein is described by Toubart, et al., *Plant* 1, 2:367 (1992).

19. A developmental-arrestive protein produced in nature by a plant. For example, Logemann, et al., *Bio/technology,* 10:305 (1992), have shown that transgenic plants expressing the barley ribosome-inactivating gene have an increased resistance to fungal disease.

20. Plant defensins may be used to provide resistance to fungal pathogens (Thomma et al., *Planta,* 216:193-202, 2002).

B. Genes that Confer Resistance to an Herbicide:

1. An herbicide that inhibits the growing point or meristem, such as an imidazolinone or a sulfonylurea. Exemplary genes in this category code for mutant ALS and AHAS enzyme as described, for example, by Lee et al., *EMBO J.,* 7:1241, 1988; Gleen et al., *Plant Molec. Biology,* 18:1185-1187, 1992; Miki et al., *Theor. App. Genet.,* 80:449, 1990.

2. Glyphosate (resistance conferred by mutant 5-enolpyruvlshikimate-3-phosphate synthase (EPSPS) and aroA genes, respectively) and other phosphono compounds such as glufosinate (phosphinothricin acetyl transferase (PAT) and *Streptomyces hygroscopicus* PAT bar genes), and pyridinoxy or phenoxy proprionic acids and cyclohexones (ACCase inhibitor-encoding genes). See, for example, U.S. Pat. No. 4,940,835 to Shah, et al., which discloses the nucleotide sequence of a form of EPSP which can confer glyphosate resistance. A DNA molecule encoding a mutant aroA gene can be obtained under ATCC Accession No. 39256, and the nucleotide sequence of the mutant gene is disclosed in U.S. Pat. No. 4,769,061 to Comai. European Patent Application No. 0 333 033 to Kumada, et al., and U.S. Pat. No. 4,975,374 to Goodman, et al., disclose nucleotide

sequences of glutamine synthetase genes which confer resistance to herbicides such as L-phosphinothricin. The nucleotide sequence of a PAT gene is provided in European Application No. 0 242 246 to Leemans, et al. DeGreef, et al., *Bio/technology,* 7:61 (1989), describe the production of transgenic plants that express chimeric bar genes coding for PAT activity. Exemplary of genes conferring resistance to phenoxy proprionic acids and cyclohexones, such as sethoxydim and haloxyfop are the Accl-S1, Accl-S2, and Accl-S3 genes described by Marshall, et al., *Theor. Appl. Genet.,* 83:435 (1992). U.S. Patent Application No: 20030135879 describes isolation of a gene for dicamba monooxygenase (DMO) from Psueodmonas *maltophilia* which is involved in the conversion of a herbicidal form of the herbicide dicamba to a non-toxic 3,6-dichlorosalicylic acid and thus may be used for producing plants tolerant to this herbicide.

3. An herbicide that inhibits photosynthesis, such as a triazine (psbA and gs+ genes) or a benzonitrile (nitrilase gene). Przibila, et al., *Plant Cell,* 3:169 (1991), describe the transformation of *Chlamydomonas* with plasmids encoding mutant psbA genes. Nucleotide sequences for nitrilase genes are disclosed in U.S. Pat. No. 4,810,648 to Stalker, and DNA molecules containing these genes are available under ATCC Accession Nos. 53435, 67441, and 67442. Cloning and expression of DNA coding for a glutathione S-transferase is described by Hayes, et al., *Biochem.* 1, 285:173 (1992). Protoporphyrinogen oxidase (PPO) is the target of the PPO-inhibitor class of herbicides; a PPO-inhibitor resistant PPO gene was recently identified in *Amaranthus tuberculatus* (Patzoldt et al., *PNAS,* 103(33):12329-2334, 2006). The herbicide methyl viologen inhibits CO.sub.2 assimilation. Foyer et al. (*Plant Physiol,* 109:1047-1057, 1995) describe a plant overexpressing glutathione reductase (GR) which is resistant to methyl viologen treatment.

4. Siminszky (*Phytochemistry Reviews,* 5:445-458, 2006) describes plant cytochrome P450-mediated detoxification of multiple, chemically unrelated classes of herbicides.

5. Other examples of herbicide resistance have been described, for instance, in U.S. Pat. Nos. 6,803,501; 6,448,476; 6,248,876; 6,225,114; 6,107,549; 5,866,775; 5,804,425; 5,633,435; 5,463,175.

C. Genes that Confer or Contribute to a Value-Added Trait, Such as:

1. Modified fatty acid metabolism, for example, by transforming a plant with an antisense gene of stearyl-ACP desaturase to increase stearic acid content of the plant. See Knultzon, et al., *PNAS,* 89:2624 (1992).

2. Decreased phytate content: (a) Introduction of a phytase-encoding gene would enhance breakdown of phytate, adding more free phosphate to the transformed plant. See, for example, Van Hartingsveldt, et al., *Gene,* 127:87 (1993), for a disclosure of the nucleotide sequence of an *Aspergillus niger* phytase gene; and (b) A gene could be introduced that reduced phytate content. For example, in maize, this could be accomplished by cloning and then reintroducing DNA associated with the single allele which is responsible for maize mutants characterized by low levels of phytic acid. See, Raboy, et al., *Maydica,* 35:383 (1990).

3. Modified carbohydrate composition effected, for example, by transforming plants with a gene coding for an enzyme that alters the branching pattern of starch. See, Shiroza, et al., *J. Bacteol.,* 170:810 (1988) (nucleotide sequence of *Streptococcus* mutants fructosyltransferase gene); Steinmetz, et al., *Mol. Gen. Genet.,* 20:220 (1985) (nucleotide sequence of *Bacillus subtilis* levansucrase gene); Pen, et al., *Bio/technology,* 10:292 (1992) (production of transgenic plants that express *Bacillus* lichenifonnis α-amylase); Elliot, et al., *Plant Molec. Biol.,* 21:515 (1993) (nucleotide sequences of tomato invertase genes); Søgaard, et al., *J. Biol. Chem.,* 268:22480 (1993) (site-directed mutagenesis of barley α-amylase gene); and Fisher, et al., *Plant Physiol.,* 102:1045 (1993) (maize endosperm starch branching enzyme II).

4. Abiotic stress includes dehydration or other osmotic stress, salinity, high or low light intensity, high or low temperatures, submergence, exposure to heavy metals, and oxidative stress. Delta-pyrroline-5-carboxylate synthetase (PSCS) from mothbean has been used to provide protection against general osmotic stress. Mannitol-1-phosphate dehydrogenase (mtlD) from *E. coli* has been used to provide protection against drought and salinity. Choline oxidase (codA from *Arthrobactor globiformis*) can protect against cold and salt. *E. coli* choline dehydrogenase (betA) provides protection against salt. Additional protection from cold can be provided by omega-3-fatty acid desaturase (fad7) from *Arabidopsis thaliana.* Trehalose-6-phosphate synthase and levansucrase (SacB) from yeast and *Bacillus subtilis*, respectively, can provide protection against drought (summarized from Annex II Genetic Engineering for Abiotic Stress Tolerance in Plants, Consultative Group On International *Agricultural Research* Technical Advisory Committee). Overexpression of superoxide dismutase can be used to protect against superoxides, as described in U.S. Pat. No. 5,538,878 to Thomas et al.

D. Genes that Confer Male Sterility:

Male sterility genes can increase the efficiency with which hybrids are made, in that they eliminate the need to physically emasculate the plant used as a female in a given cross. Where one desires to employ male-sterility systems, it may be beneficial to also utilize one or more male-fertility restorer genes. For example, where cytoplasmic male sterility (CMS) is used, hybrid crossing requires three inbred lines: (1) a cytoplasmically male-sterile line having a CMS cytoplasm; (2) a fertile inbred with normal cytoplasm, which is isogenic with the CMS line for nuclear genes ("maintainer line"); and (3) a distinct, fertile inbred with normal cytoplasm, carrying a fertility restoring gene ("restorer" line). The CMS line is propagated by pollination with the maintainer line, with all of the progeny being male sterile, as the CMS cytoplasm is derived from the female parent. These male sterile plants can then be efficiently employed as the female parent in hybrid crosses with the restorer line, without the need for physical emasculation of the male reproductive parts of the female parent.

The presence of a male-fertility restorer gene results in the production of fully fertile F_1 hybrid progeny. If no restorer gene is present in the male parent, male-sterile hybrids are obtained. Examples of male-sterility genes and corresponding restorers which could be employed with the plants of the invention are well known to those of skill in the art of plant breeding. Examples of such genes include CMS-D2-2, CMS-hir, CMS-DS, CMS-D4, and CMS-Cl. Fertility can be restored to CMS-D2-2 by the D2 restorer in which the restorer factor(s) was introduced from the genome of *G. harknessii* Brandegee (D2-2). Microsporogenesis in both CMS systems aborts during the premeiotic stage. One dominant restorer gene from the DS restorer was identified to restore fertility of CMS-DS. The D2 restorer for CMSD2-2 also restores the fertility of CMS-DS, CMS-hir, and CMS-Cl.

E. Genes that Improve Cotton Fiber Characteristics:

Fiber characteristics such as fiber quality of quantity represent another example of a trait that may be modified in

cotton varieties. For example, U.S. Pat. No. 6,472,588 describes transgenic cotton plants transformed with a sucrose phosphate synthase nucleic acid to alter fiber characteristics such as strength, length, fiber fineness, fiber maturity ratio, immature fiber content, fiber uniformity, and micronaire. Cotton plants comprising one or more genes coding for an enzyme selected from the group consisting of endoxyloglucan transferase, catalase and peroxidase for the improvement of cotton fiber characteristics are also described in U.S. Pat. No. 6,563,022. Cotton modification using ovary-tissue transcriptional factors preferentially directing gene expression in ovary tissue, particularly in very early fruit development, utilized to express genes encoding isopentenyl transferase in cotton ovule tissue and modify the characteristics of boll set in cotton plants and alter fiber quality characteristics including fiber dimension and strength is discussed in U.S. Pat. No. 6,329,570. A gene controlling the fiber formation mechanism in cotton plants is described in U.S. Pat. No. 6,169,174.

Genes involved in lignin biosynthesis are described by Dwivedi et al., *Mol. Biol.,* 26:61-71, 1994; Tsai et al., *Physiol.,* 107:1459, 1995; U.S. Pat. No. 5,451,514 (claiming the use of cinnamyl alcohol dehydrogenase gene in an antisense orientation such that the endogenous plant cinnamyl alcohol dehydrogenase gene is inhibited).

F. Additional Traits:

Additional traits can be introduced into the cotton variety of the present invention. A non-limiting example of such a trait is a coding sequence which decreases RNA and/or protein levels. The decreased RNA and/or protein levels may be achieved through RNAi methods, such as those described in U.S. Pat. No. 6,506,559 to Fire and Mellow. Further, reduction of the activity of specific genes (also known as gene silencing, or gene suppression) is desirable for several aspects of genetic engineering in plants.

Many techniques for gene silencing are well known to one of skill in the art, including but not limited to knock-outs (such as by insertion of a transposable element such as mu (Vicki Chandler, The Maize Handbook ch. 118 (Springer-Verlag 1994) or other genetic elements such as the FRT sequence, used with the FLP recombinase (Zhu and Sadowski, *J. Biol. Chem.,* 270:23044-23054, 1995), the LOX sequence, used with CRE recombinase (Sauer, *Mol. Cell. Biol.,* 7:2087-2096, 1987), or other site specific integration sites, antisense technology (see, e.g., Sheehy et al. (1988) *PNAS USA* 85:8805-8809; and U.S. Pat. Nos. 5,107,065; 5,453,566; and 5,759,829); co-suppression (e.g., Taylor (1997) *Plant Cell* 9:1245; Jorgensen (1990) *Trends Biotech.* 8(12):340-344; Flavell (1994) *PNAS USA* 91:3490-3496; Finnegan et al. (1994) *Bio/Technology* 12: 883-888; and Neuhuber et al. (1994) *Mol. Gen. Genet.* 244:230-241); RNA interference (Araji et al. (2014) *Plant Physiology* 164:1191-1203; Napoli et al. (1990) *Plant Cell* 2:279-289; U.S. Pat. No. 5,034,323; Sharp (1999) *Genes Dev.* 13:139-141; Zamore et al. (2000) *Cell* 101:25-33; and Montgomery et al. (1998) *PNAS USA* 95:15502-15507), virus-induced gene silencing (Burton, et al. (2000) *Plant Cell* 12:691-705; and Baulcombe (1999) *Curr. Op. Plant Bio.* 2:109-113); target-RNA-specific ribozymes (Haseloff et al. (1988) *Nature* 334: 585-591); hairpin structures (Smith et al. (2000) *Nature* 407:319-320; WO 99/53050; and WO 98/53083); MicroRNA (Aukerman& Sakai (2003) *Plant Cell* 15:2730-2741); ribozymes (Steinecke et al. (1992) *EMBO J.* 11:1525; and Perriman et al. (1993) *Antisense Res. Dev.* 3:253); oligonucleotide mediated targeted modification (e.g., WO 03/076574 and WO 99/25853); Zn-finger targeted molecules (e.g., WO 01/52620; WO 03/048345; and WO 00/42219); and other methods or combinations of the above methods known to those of skill in the art.

It may also be desirable to make cotton plants more tolerant to or more easily transformed with *Agrobacterium tumefaciens*. Expression of p53 and iap, two baculovirus cell-death suppressor genes, inhibited tissue necrosis and DNA cleavage. Additional targets can include plant-encoded proteins that interact with the *Agrobacterium* Vir genes; enzymes involved in plant cell wall formation; and histones, histone acetyltransferases and histone deacetylases (reviewed in Gelvin, *Microbiology & Mol. Biol. Reviews,* 67: 16-37, 2003).

Single Locus Conversion

When the term "cotton plant" is used in the context of the present invention, this also includes any single locus conversions of that variety. The term "single locus converted plant" or "single gene converted plant" refers to those cotton plants which are developed by a plant breeding technique called backcrossing or via genetic engineering wherein essentially all of the desired morphological and physiological characteristics of a variety are recovered in addition to the single gene transferred into the variety via the backcrossing technique or via genetic engineering. Backcrossing methods can be used with the present invention to improve or introduce a characteristic into the variety. The term "backcrossing" as used herein refers to the repeated crossing of a hybrid progeny back to the recurrent parent, i.e., backcrossing 1, 2, 3, 4, 5, 6, 7, 8, 9, or more times to the recurrent parent. The parental cotton plant which contributes the gene for the desired characteristic is termed the "nonrecurrent" or "donor parent". This terminology refers to the fact that the nonrecurrent parent is used one time in the backcross protocol and therefore does not recur. The parental cotton plant to which the gene or genes from the nonrecurrent parent are transferred is known as the recurrent parent as it is used for several rounds in the backcrossing protocol (Poehlman & Sleper (1994); Fehr (1987)). In a typical backcross protocol, the original variety of interest (recurrent parent) is crossed to a second variety (nonrecurrent parent) that carries the single gene of interest to be transferred. The resulting progeny from this cross are then crossed again to the recurrent parent and the process is repeated until a cotton plant is obtained wherein essentially all of the desired morphological and physiological characteristics of the recurrent parent are recovered in the converted plant, in addition to the single transferred gene from the nonrecurrent parent, as determined at the 5% significance level when grown in the same environmental conditions.

The backcross process may be accelerated by the use of genetic markers, such as Simple Sequence Length Polymorphisms (SSLPs) (Williams et al., *Nucleic Acids Res.,* 18:6531-6535, 1990), Randomly Amplified Polymorphic DNAs (RAPDs), DNA Amplification Fingerprinting (DAF), Sequence Characterized Amplified Regions (SCARs), Arbitrary Primed Polymerase Chain Reaction (AP-PCR), Amplified Fragment Length Polymorphisms (AFLPs) (EP 534 858, specifically incorporated herein by reference in its entirety), and Single Nucleotide Polymorphisms (SNPs) (Wang et al., *Science,* 280:1077-1082, 1998) to identify plants with the greatest genetic complement from the recurrent parent.

The selection of a suitable recurrent parent is an important step for a successful backcrossing procedure. The goal of a backcross protocol is to alter or substitute a single trait or characteristic in the original variety. To accomplish this, a single gene of the recurrent variety is modified or substituted

with the desired gene from the nonrecurrent parent, while retaining essentially all of the rest of the desired genetic, and therefore the desired physiological and morphological, constitution of the original variety. The choice of the particular nonrecurrent parent will depend on the purpose of the backcross. One of the major purposes is to add some commercially desirable, agronomically important trait to the plant. The exact backcrossing protocol will depend on the characteristic or trait being altered to determine an appropriate testing protocol. Although backcrossing methods are simplified when the characteristic being transferred is a dominant allele, a recessive allele may also be transferred. In this instance it may be necessary to introduce a test of the progeny to determine if the desired characteristic has been successfully transferred.

Many single gene traits have been identified that are not regularly selected for in the development of a new variety but that can be improved by backcrossing techniques. A genetic locus conferring the traits may or may not be transgenic. Examples of these traits include but are not limited to, male sterility, waxy starch, herbicide resistance, resistance for bacterial, fungal, or viral disease, insect resistance, male fertility, enhanced nutritional quality, industrial usage, yield stability, and yield enhancement. These genes are generally inherited through the nucleus, but may be inherited through the cytoplasm. Several of these are described in U.S. Pat. Nos. 5,959,185; 5,973,234; and 5,977,445, the disclosures of which are specifically hereby incorporated by reference.

Direct selection may be applied where a genetic locus acts as a dominant trait. An example of a dominant trait is the herbicide tolerance trait. For this selection process, the progeny of the initial cross are sprayed with the herbicide prior to the backcrossing. The spraying eliminates any plants which do not have the desired herbicide tolerance characteristic, and only those plants which have the herbicide tolerance gene are used in the subsequent backcross. This process is then repeated for all additional backcross generations.

Tissue Culture and In Vitro Regeneration of Cotton Plants

Further reproduction of the variety can occur by tissue culture and regeneration. Tissue culture of various tissues of cotton and regeneration of plants therefrom is well known and widely published. For example, reference may be had to Komatsuda, T., et al., *Crop Sci.,* 31:333-337 (1991); Stephens, P. A., et al., *Theor. Appl. Genet.,* 82:633-635 (1991); Komatsuda, T., et al., *Plant Cell, Tissue and Organ Culture,* 28:103-113 (1992); Dhir, S., et al. *Plant Cell Rep.,* 11:285-289 (1992); Pandey, P., et al., *Japan J Breed.,* 42:1-5 (1992); and Shetty, K., et al., *Plant Science,* 81:245-251 (1992); as well as U.S. Pat. No. 5,024,944 issued Jun. 18, 1991 to Collins, et al., and U.S. Pat. No. 5,008,200 issued Apr. 16, 1991 to Ranch, et al. Thus, another aspect of this invention is to provide cells which upon growth and differentiation produce cotton plants having the physiological and morphological characteristics of cotton cultivar UA 107.

As used herein, the term "tissue culture" indicates a composition comprising isolated cells of the same or a different type or a collection of such cells organized into parts of a plant. Exemplary types of tissue cultures are protoplasts, calli, plant clumps, and plant cells that can generate tissue culture that are intact in plants or parts of plants, such as embryos, pollen, flowers, seeds, leaves, stems, roots, root tips, anthers, pistils, and the like. Means for preparing and maintaining plant tissue culture are well known in the art. By way of example, a tissue culture comprising organs has been used to produce regenerated plants. U.S. Pat. Nos. 5,959,185; 5,973,234; and U.S. Pat. No. 5,977,445, described certain techniques.

An important ability of a tissue culture is the capability to regenerate fertile plants. This allows, for example, transformation of the tissue culture cells followed by regeneration of transgenic plants. For transformation to be efficient and successful, DNA must be introduced into cells that give rise to plants or germ-line tissue.

Plants typically are regenerated via two distinct processes; shoot morphogenesis and somatic embryogenesis. Shoot morphogenesis is the process of shoot meristem organization and development. Shoots grow out from a source tissue and are excised and rooted to obtain an intact plant. During somatic embryogenesis, an embryo (similar to the zygotic embryo), containing both shoot and root axes, is formed from somatic plant tissue. An intact plant rather than a rooted shoot results from the germination of the somatic embryo.

Shoot morphogenesis and somatic embryogenesis are different processes and the specific route of regeneration is primarily dependent on the explant source and media used for tissue culture manipulations. While the systems are different, both systems show variety-specific responses where some lines are more responsive to tissue culture manipulations than others. A line that is highly responsive in shoot morphogenesis may not generate many somatic embryos. Lines that produce large numbers of embryos during an induction step may not give rise to rapidly growing proliferative cultures. Therefore, it may be desired to optimize tissue culture conditions for each cotton line. These optimizations may readily be carried out by one of skill in the art of tissue culture through small-scale culture studies. In addition to line-specific responses, proliferative cultures can be observed with both shoot morphogenesis and somatic embryogenesis. Proliferation is beneficial for both systems, as it allows a single, transformed cell to multiply to the point that it will contribute to germ-line tissue.

Embryogenic cultures can also be used successfully for regeneration, including regeneration of transgenic plants, if the origin of the embryos is recognized and the biological limitations of proliferative embryogenic cultures are understood. Biological limitations include the difficulty in developing proliferative embryogenic cultures and reduced fertility problems (culture-induced variation) associated with plants regenerated from long-term proliferative embryogenic cultures. Some of these problems are accentuated in prolonged cultures. The use of more recently cultured cells may decrease or eliminate such problems.

Tables

Cotton cultivar UA 107 was compared to DP 393 and UA 48 in replicated field tests at four Arkansas Agricultural Experiment Station sites in 2013 through 2016, as shown in Tables 2-5, and was tested as 'Ark 0701-17'. The test locations included the Northeast Research and Extension Center at Keiser on Sharkey clay (very-fine, smectitic, thermic Chromic Epiaquerts), the Judd Hill Cooperative Research Site at Judd Hill on Dundee silt loam (fine-silty, mixed, active, thermic Typic Endoaqualfs), the Lon Mann Cotton Research Station at Marianna on Callaway silt loam (fine-silty, mixed, thermic Glossaquic Fragiudalfs), and the Southeast Branch Experiment Station at Rohwer on Hebert silt loam (fine-silty, mixed, active, thermic Aeric Epiaqualfs).

Each field test was arranged in a randomized complete block design with four replications of two-row plots (12-14

m×1 m). Standard production practices with furrow irrigation were followed in each test. Percentage of open bolls was visually rated within 1-3 days before or after first application of defoliants to the plots. Seedcotton yields were determined by machine picking for all plots. Hand-harvested boll samples, collected from two of the four replications, were ginned on a laboratory gin. Variables determined using the gin data and samples included lint fraction, seed index, lint index, fibers per seed, seed per area, fiber density, and HVI (High Volume Instrument) fiber parameters. Fiber density, an estimate of the number of fibers per mm^2 seed surface area, was determined using a regression equation to calculate seed surface area based on fuzzy seed weights (Groves and Bourland, 2010). Procedures for collecting and processing boll samples were the same as described for the Arkansas Cotton Variety Test (Bourland et al., 2017). The average lint percentage for an entry over two replications at each location was used to convert seedcotton yield to lint yield. All data were analyzed by SAS v. 9.1 PROC GLM (SAS Institute, Cary, N.C.). Years and replications were considered to be random, while entry and location were fixed.

Leaves, stems, and bracts were sampled at the Keiser test site in 2013 through 2016. Leaf and stem pubescence were rated using the rating system established by Bourland et al. (2003). Bracts were sampled and marginal trichome density was determined using methods of Bourland and Hornbeck (2007). Leaf and bract data were analyzed by SAS v. 9.1 PROC GLM (SAS Institute, Cary, N.C.) with years and replications being random and entries being fixed.

Cotton cultivar UA 107 was also evaluated in the 2015 Regional Breeders' Testing Network (RBTN; http://rbtn.cottoninc.com/files/), which included agronomic field tests at 12 locations from Suffolk, Va. to West Side, Calif. UA 107 was also compared to other conventional varieties at four locations in the 2016 Arkansas Conventional Cotton Variety Test (Bourland et al., 2017).

Table 2 shows the lint yields in pounds per acre of cotton cultivar UA 107 compared to check cultivars (DP 393 and UA 48) at locations in the Mississippi River Delta region of Arkansas from 2013 through 2016. Locations are arranged from north (left) to south (right) in the table.

TABLE 2

Cultivar	Keiser	Judd Hill	Marianna	Rohwer
UA 107	750	1167	1343	1177
DP 393	786	1078	1236	1092
UA 48	673	1025	1142	959
LSD0.10	81	63	61	84

As shown in Table 2, the lint yields of cotton cultivar UA 107 exceeded those of both check cultivars at all locations except Keiser, where its yield was equal to the higher yielding check. The relatively low yields of all lines at Keiser were primarily due to production problems in 2013 and 2015.

Table 3 shows the yield and lint component-related parameters of cotton cultivar UA 107 compared to two check cultivars over years from 2013 to 2016 at Arkansas test sites. Each parameter was determined in tests at Keiser, Judd Hill, Marianna, and Rohwer. Lint fraction, seed index, lint index and fibers per seed, and fiber density were determined from boll samples taken from two replications per test. Lint yield and seed per acre were determined on four replications per test. Location by line interaction was significant (P=0.10) for lint yield, seed per acre, and lint index.

TABLE 3

Cultivar	Lint yield (lb/acre)	Lint Fraction (%)	Seed/acre (no. × 10^6)	Lint Index (g)	Seed index (g)	Fibers/seed (no.)	Fiber density (no./mm^2)
UA 107	1109	40.3	6.046	8.3	12.1	17692	158
DP 393	1048	39.3	6.375	7.5	11.2	15514	146
UA 48	951	37.7	5.615	7.6	12.4	14013	123
LSD0.10	60	0.5	0.439	0.3	0.4	396	6

As shown in Table 3, the lint yields of cotton cultivar UA 107 exceeded yields of each check cultivar. Together with Table 2, these data suggest that UA 107 is better adapted to silt loam soils than clay soils. Compared to the check cultivars, UA 107 derived its higher yield from an increase in lint per seed (lint index) rather than seed per area. According to Lewis et al. (2000), increased reliance on high lint index relative to seeds produced per area should contribute to more stable yield production. The higher lint index and higher fibers per seed of UA 107 may be partly attributed to its higher seed index. Fiber density of UA 107 was much higher than DP 393 and UA 48. The measurement of fiber density attempts to compensate for variation in seed size by estimating the number of fibers per unit area of seed surface area. Groves et al. (2016) suggested that fiber density could serve as a selection criterion for increasing lint yield and yield stability without negatively affecting fiber quality traits.

Cotton cultivar UA 107 was also evaluated in the 2015 Regional Breeders' Testing Network (RBTN; http://rbtn.cottoninc.com/files/), which included agronomic field tests at 12 different U.S. locations from Suffolk, Va. to West Side, Calif. Among the 28 entries in the 2015 RBTN, cotton cultivar UA 107 produced the second highest lint yield over all 12 locations, and equaled the highest yielding entry at all locations except Suffolk (VA), Tifton (GA), Keiser (AR), and Lubbock (Tex.). These yields indicate that cotton cultivar UA 107 is broadly adapted to contrasting growing conditions.

Table 4 shows the morphological and host plant resistance traits for cotton cultivar UA 107 and check cultivars in 2013-2016. The percentage of open bolls (visually estimated) measurements were taken at the approximate time of defoliation in each test. The location by line interaction was significant (P=0.10). The leaf and stem pubescence was visually rated on 6 plants per plot for 4 repetitions at the Keiser, AR site in 2013-2016 from 1 (smooth) to 9 (pilose) using the rating system developed by Bourland et al. (2003). The number of marginal bract trichomes was determined on 6 plants per plot for 4 repetitions at the Keiser, AR site in 2013-2016 using methods described by Bourland and Hornbeck (2007). The percentages of flowers with discoloured anthers were determined in 8 repetitions of tests at the Keiser, AR site in 2014-2016, with all lines included in the same test each year. Discolored anthers were due to feeding by tarnished plant bugs, *Lygus lineolaris*, for which the susceptible check was a Frego-bract breeding line. The year by line interaction was not significant (P=0.10). The percentage of surviving plants showing *Fusarium* wilt comes from evaluations at the 2015 National Cotton *Fusarium* Wilt Test in Tallassee, Ala.; the susceptible check was 'Rowden' and the resistant check was M315.

Response to tarnished plant bug (*Lygus lineolaris* (Palisot de Beauvois)) was determined in small plot field tests conducted at Keiser, AR, in 2014-2016. Single-row plots, 6 m×1 m, were replicated 8 times in a randomized complete

block (RCB) design, and managed to encourage tarnished plant bug populations. Brown or black discoloured anthers indicate tarnished plant bug feeding (Maredia et al., 1994). Plots were sequentially examined for five to eight days (six flowers per plot per day) over a two-week period in August of each year. Damaged flowers, as indicated by discolored anthers, were enumerated. A collective measure of percentage of damaged flowers over the sequential samples was determined for each plot.

All pest resistance data collected in Arkansas, except bacterial blight data, were analyzed using SAS v. 9.1 PROC GLM (SAS Institute, Cary, N.C.) with years and replications as random and entries being fixed. Cotton cultivar UA 107 was evaluated for responses to *fusarium* wilt (caused by *Fusarium oxysporum* Schlect, F. sp. *vasinfectum* (Atk.) Snyd. & Hans) in the 2015 National Cotton *Fusarium* Wilt Test at Tallassee, Ala. (Glass et al., 2015).

TABLE 4

Cultivar	Plant height (cm)	Open bolls (%)	Leaf pubescence (1-9)	Stem pubescence (1-9)	Bract trichomes (no./cm)	Fusarium wilt (%)	Damaged flowers (%)
UA 107	103	64.4	1.3	2.6	21.3	80	62
DP 393	101	57.1	2.8	5.1	31.6	—	56
UA 48	95	55.6	2.0	4.4	27.8	—	66
Res. check	—	—	—	—	—	81	—
Sus. check	—	—	—	—	—	69	84
LSD0.05	2	1.2	0.5	0.4	1.9	7	5

As shown in Table 4, cotton cultivar UA 107 was earlier maturing (based on percentage of open bolls), but produced taller plants than either DP 393 or UA 48. The taller plants of UA 107 may allow it to be more tolerant to stress than other early maturing lines that produce shorter plant structure. Compared to DP 393 and UA 48, UA 107 had lower trichome density on leaves, stems and bract margins. Based on these data, UA 107 would be classified as a smooth-leaf variety. Lower values for leaf pubescence rating and marginal bract trichomes should contribute to less trash in ginned lint. All other morphological traits of UA 107 were similar to DP 393 and UA 48.

During selection, UA 107 plants were inoculated with multiple races (including race 18) of *Xanthomonas citri* ssp. *malvacearum* (ex Smith 1901) Schaad et al. 2007, the causal agent of bacterial blight. Resistance to the multiple races conveys resistance to all known U.S. races of this pathogen. Cotton cultivar UA 107 exhibited resistance to bacterial blight in annually produced seed increase blocks inoculated with the pathogen. UA 107 produced stands equal to the resistant check in the presence of *fusarium* wilt in the 2015 National Cotton *Fusarium* Wilt Test.

Data from the 2014-2016 tarnished plant bug field test indicated that UA 107 was moderately resistant to this pest. Its response to tarnished plant bug was equal to UA 48, but more susceptible than DP 393 in field tests conducted in 2014 through 2016. All three varieties were more resistant to tarnished plant bug than the susceptible check.

Table 5 shows the fiber traits for cotton cultivar UA 107 compared to two check cultivars in 2013-2016 at the Arkansas test sites. The fiber parameters were determined in tests at Keiser, Judd Hill, Marianna, and Rohwer. Location by line interaction was significant (P=0.10) only for quality score and micronaire. Fiber parameters were determined by HVI on lint from boll samples taken from two replications per test. The quality score (Q-score) is an index based on four fiber parameters (relative weight): fiber length (50%), micronaire (25%), uniformity (15%) and strength (10%).

TABLE 5

Cultivar	Quality score	Micronaire	Fiber length (in.)	Uniformity index (%)	Fiber Strength (g/tex)	Fiber elongation (%)
UA 107	70	4.55	1.22	85.8	32.4	6.3
DP 393	54	4.85	1.17	85.2	33.0	6.8
UA 48	83	4.98	1.27	86.8	36.5	5.7
LSD0.05	6	0.13	0.02	0.7	0.8	0.4

As shown in Table 5, the Q-score of cotton cultivar UA 107 exceeded those of DP 393, but was less than UA 48. Compared to DP 393, the higher Q-scores for UA 107 were primarily associated with longer fiber length and lower micronaire. Both fiber strength and length uniformity index of UA 107 were equal to DP 393, but lower than UA 48. The fiber elongation of UA 107 (not included in the Q-score) was lower than DP 393 but higher than UA 48.

Relative variation among fiber traits for UA 107 and DP 393 across the 12 locations of the 2015 RBTN was similar to that found in the Arkansas tests.

The use of the terms "a," "an," and "the," and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms (i.e., meaning "including, but not limited to,") unless otherwise noted. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. For example, if the range 10-15 is disclosed, then 11, 12, 13, and 14 are also disclosed. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

Deposit Information

A deposit of the Board of Trustees of the University of Arkansas proprietary Cotton Cultivar UA 107 disclosed above and recited in the appended claims has been made with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, Va. 20110 under the terms of the Budapest Treaty. The date of deposit was Feb. 16, 2018. The deposit of 2,500 seeds was taken from the same deposit maintained by Board of Trustees of the University of Arkansas since prior to the filing date of this application. All restrictions will be irrevocably removed upon granting of a patent, and the deposit is intended to meet all of the requirements of 37 C.F.R. §§ 1.801-1.809. The ATCC Accession Number is PTA-124915. The deposit will be maintained in the depository for a period of thirty years, or

five years after the last request, or for the enforceable life of the patent, whichever is longer, and will be replaced as necessary during that period.

While a number of exemplary aspects and embodiments have been discussed above, those of skill in the art will recognize certain modifications, permutations, additions, and sub-combinations thereof. It is therefore intended that the following appended claims and claims hereafter are interpreted to include all such modifications, permutations, additions, and sub-combinations as are within their true spirit and scope.

What is claimed is:

1. A plant of cotton cultivar UA 107, wherein a representative sample of seed of said cultivar was deposited under ATCC Accession No. PTA-124915.

2. A plant part of the plant of claim **1**, wherein the plant part comprises at least one cell of said plant.

3. The plant part of claim **2**, further defined as pollen, a meristem, a cell, or an ovule.

4. A seed of cotton cultivar UA 107, wherein a representative sample of seed of said cultivar was deposited under ATCC Accession No. PTA-124915.

5. A cotton plant that expresses all of the morphological and physiological characteristics of the plant of claim **1**.

6. A method of producing a cotton seed, wherein the method comprises crossing the plant of claim **1** with itself or a second cotton plant.

7. The method of claim **6**, wherein the method comprises crossing the plant of cotton cultivar UA 107 with a second, distinct cotton plant to produce an F_1 hybrid cotton seed.

8. An F_1 cotton seed produced by the method of claim **7**.

9. An F_1 cotton plant produced by growing the seed of claim **8**.

10. A composition comprising the seed of claim **4** comprised in plant seed growth media.

11. The composition of claim **10**, wherein the growth media is soil or a synthetic cultivation medium.

12. A plant of cotton cultivar UA 107 further comprising a single locus conversion, wherein a representative sample of seed of said cultivar was deposited under ATCC Accession No. PTA-124915.

13. The plant of claim **12**, wherein the single locus conversion comprises a transgene.

14. A seed that produces the plant of claim **12**.

15. The seed of claim **14**, wherein the single locus comprises a nucleic acid sequence that enables site-specific genetic recombination or confers a trait selected from the group consisting of male sterility, herbicide tolerance, insect or pest resistance, disease resistance, modified fatty acid metabolism, abiotic stress resistance, modified carbohydrate metabolism, and modified cotton fiber characteristics.

16. The seed of claim **15**, wherein the single locus confers tolerance to an herbicide selected from the group consisting of glyphosate, sulfonylurea, imidazolinone, dicamba, glufosinate, phenoxy propionic acid, L-phosphinothricin, protoporphyrinogen oxidase (PPO) inhibitors, 2,4-dichlorophenoxyacetic acid, hydroxyphenyl-pyruvate dioxygenase (HPPD) inhibitors, cyclohexanedione, triazine, benzonitrile, and bromoxynil.

17. The seed of claim **15**, wherein the trait is insect resistance and said single locus comprises a transgene encoding a *Bacillus thuringiensis* (Bt) endotoxin.

18. The seed of claim **14**, wherein the single locus comprises a transgene.

19. The method of claim **7**, wherein the method further comprises:

(a) crossing a plant grown from said F_1 hybrid cotton seed with itself or a different cotton plant to produce a seed of a progeny plant of a subsequent generation;

(b) growing a progeny plant of a subsequent generation from said seed of a progeny plant of a subsequent generation and crossing the progeny plant of a subsequent generation with itself or a second plant to produce a progeny plant of a further subsequent generation; and

(c) repeating steps (a) and (b) using said progeny plant of a further subsequent generation from step (b) in place of the plant grown from said F_1 hybrid cotton seed in step (a), wherein steps (a) and (b) are repeated with sufficient inbreeding to produce an inbred cotton plant derived from the cotton cultivar UA 107.

20. The method of claim **19**, further comprising crossing said inbred cotton plant derived from the cotton cultivar UA 107 with a plant of a different genotype to produce a seed of a hybrid cotton plant derived from the cotton cultivar UA 107.

21. A method of producing a genetically modified cotton plant, wherein the method comprises mutation, genome editing or gene silencing of the plant of claim **1**.

22. A genetically modified cotton plant produced by the method of claim **21**, wherein said plant comprises said mutation, genome editing or gene silencing and otherwise comprises all of the physiological and morphological characteristics of cotton cultivar UA 107.

23. A method of producing a commodity plant product comprising obtaining the plant of claim **1**, or a plant part thereof, and producing the commodity plant product from said plant or plant part thereof, wherein said commodity plant product is selected from the group consisting of lint, seed oil or seed.

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