

Chapter

Using Host Resistance to Control Cotton Parasitic Reniform Nematode

Chunda Feng, Salliana R. Stetina and John E. Erpelding

Abstract

Cotton (*Gossypium hirsutum*) is the primary source of natural fiber for the textile industry worldwide. The US is a leading cotton producer and the largest exporter for the international cotton market, representing about US\$7 billion annually. Reniform nematode (RN, *Rotylenchulus reniformis*) is a major pest for US cotton production. Annual seedcotton yield losses associated with RN are estimated at 1% representing approximately US\$100 M loss in production. In the major cotton-producing states of Alabama, Louisiana, and Mississippi, RN has become the most important pest problem. Several approaches are required for RN management. Nematicides are effective in providing protection for cotton seedling development to enhance plant vigor and reduce yield losses, but the RN population will dramatically rebound during the cotton growing season. Rotation with non-host crops will reduce RN populations, but long rotational cycles are required to suppress the rapid recovery of the population. Growing resistant cultivars would be the most effective and sustainable strategy for long-term RN management. However, RN resistance was not found in the widely grown tetraploid upland cotton, thus hindering the rapid development of resistance cultivars. Several Sea Island cottons (*G. barbadense*) highly resistant to RN have been used to develop resistant upland cotton varieties. RN resistance was frequently observed in diploid *Gossypium* species. Our research focuses on introgression of RN resistance from diploid *Gossypium* species to upland cotton, understanding the genetics of resistance to enhance genetic diversity and developing genomic tools that can be applied for studying the genetics of resistance and for marker-assisted breeding.

Keywords: cotton, germplasm, reniform nematode, resistance, pest management, wide hybridization

1. Introduction

The plant-parasitic reniform nematode (RN, *Rotylenchulus reniformis* Linford and Oliveira) is a yield-limiting factor for upland cotton (*Gossypium hirsutum*) production in the US [1]. RN has been found in 13 states (from the East Coast to Texas) representing the upland cotton growing belt of the US, and the number of counties where RN is present has rapidly increased [2]. According to the Cotton Disease Loss Estimate

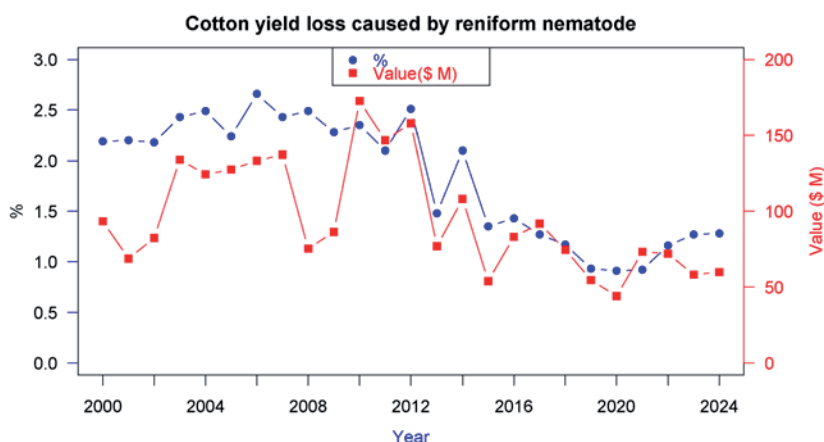


Figure 1.

Estimated percentages and values of annual US cotton production losses attributed to reniform nematode from 2000 to 2024.

Committee reports (<https://www.cotton.org/beltwide/proceedings> and <https://cropprotectionnetwork.org/>), annual seedcotton yield losses caused by reniform nematode ranged from 0.91 to 2.66% from 2000 to 2024, equivalent to values of \$43.94–\$172.65 M (**Figure 1**), with an average loss of \$95.60 million per year, and a total of \$2.39 billion in the past 25 years, excluding additional costs related to RN management. In the states of Alabama, Louisiana, and Mississippi, RN has replaced root-knot nematode (*Meloidogyne incognita*) as the major nematode pest of cotton [1], and yield losses were estimated from 5 to 9% in these states [3], which were much higher than the nationwide average. In some RN infested fields, yield losses were considerably higher. For example, the average yield loss of seven cultivars was 50% compared to the same cultivars grown in an adjacent non-infested field [4].

2. *Rotylenchulus reniformis*: host range, biology and distribution in soil

2.1 Host plants

RN was first reported infecting roots of cowpea plants grown in pineapple fields in Hawaii during 1940 [5]. In the same year, RN was observed from cotton plants grown in Georgia [6]. RN can infect roots of 314 plant species distributed in 77 families, including some important crops, such as cotton, soybean, cowpea, sweet potato, tomato, and numerous vegetables [7]. Many weed species commonly found in fields of these crops can also be infected [8] and can influence RN management. The feeding of nematodes on the cotton plant will damage the root system, interfering with the uptake of water and nutrients from the soil, which will result in plant stunting, fruit abortion, delayed maturity, and reductions in seedcotton yield, boll size, and lint percentage [9–11]. Seedling death is common under high infestation levels, and these poor stands can result in greater weed competition. Nematode-disease complex is another concern. The wounds resulting from RN feeding increase the plant's vulnerability to soilborne diseases, such as Fusarium wilt and Verticillium wilt. The incidences of Fusarium wilt in wilt-susceptible varieties were 81.4% when RN was present, but only 10% when the nematode was absent [12].

2.2 RN life cycle

The short life cycle of *R. reniformis* makes it difficult to manage the RN population. The egg-to-egg life cycle is about 17–29 days under favorable environmental conditions, and five to seven generations can be produced during a single cotton growing season [1]. Eggs start to hatch about 8 days after deposition. The first-stage juveniles (J1) molt inside the eggs to produce the second-stage juveniles (J2). After three molts, the juveniles develop into young adults with about equal numbers of males and females after 10–14 days (**Figure 2a**). The male nematodes do not infect roots of the host plant and remain in soil. Female vermiform nematodes penetrate the root cortex of the host plant, and the anterior part of the body reaches the endodermal and pericycle cells, whereas the posterior part remains outside the root (**Figure 2b**). The female nematode modifies the host cells at the feeding site to form a syncytium, which is the permanent and sole nutrient source for development and reproduction [13, 14]. The posterior portion of the body swells and forms a characteristic kidney shape (**Figure 2c**). When the gonads reach maturity, the female nematodes lay eggs in a gelatinous matrix (**Figure 2c**) with about 60 but could be up to 200 eggs, approximately 7 days after infection. This high reproduction rate will also influence pest management.

2.3 RN spatial distribution in soil

RN has been observed in many soil types [1, 15]. It is not clear if soil texture has an impact on the distribution of RN. In Texas, RN was frequently found in finely textured soils but was less common in soils with greater than 40% sand content [16]. The population densities of RN in South Carolina soils were correlated to the percentages of sand and silt in the soil until the observed sand content was greater than 60%, resulting in a greater decline in the population density [17]. In contrast, no correlation was observed between RN population densities and soil texture for evaluations conducted in Arkansas, Louisiana, and Texas [18].

Different tillage and crop sequence systems may impact RN population densities and distribution in the soil profile [19]. Holguin et al. reported that the highest population densities occurred at 15–30 cm deep after a cotton crop, but after a non-host crop, higher population densities were recorded deeper in the soil profile [17]. Robinson et al. reported that nematodes were found below 100 cm in about half of the fields investigated, and often more than half the populations were below 30 cm in the soil profile; while in other fields, nematodes were found only in the top 45 cm with the greatest densities occurring in the top 15 cm of the soil profile [18]. The ability of this nematode to survive deep in the soil profile is another factor hindering pest management strategies.

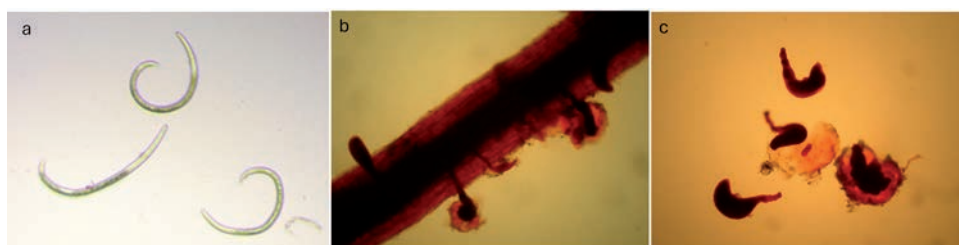


Figure 2. Immature and mature *Rotylenchulus reniformis*. a. vermiform nematodes; b. *R. reniformis* feeding on cotton roots; c. Four mature *R. reniformis* and one egg.

3. Pest management strategies for RN

3.1 Nematicides

Application of chemical nematicides is the most widely used control strategy. Soil fumigation, in-furrow application, and seed treatment are common methods for the application of nematicides. Nematicide applications have been shown to reduce RN populations and increase seedcotton yields [20]. However, the efficacy of the nematicide may vary due to soil type and environmental conditions during the growing season. Nematicides used for soil fumigation or application in plant furrow could control nematodes in the upper 30–45 cm of soil, but nematodes below this depth can escape the chemical treatment, and the nematode population can dramatically rebound during the growing season, resulting in yield losses [18, 19]. A limited number of nematicides are available for cotton production and the applications may not be profitable [21, 22]. There are also human health and environmental concerns with the use of chemical nematicides.

Sustainable nematicides are alternatives for chemical nematicides that can reduce the environmental impact. Plant essential oils can be used as nematicides for various plant-parasitic nematodes, and the essential oils from *Majorana hortensis*, *M. spicata*, and *Thymus vulgaris* have shown 100% mortality for *R. reniformis* [23]. The antimicrobial and insecticidal functions of chemicals 1,3,4-oxadiazoles have been studied for medical and agricultural uses [24]. Cyprocide (1,3,4-oxadiazole thioether) is bioactivated into a lethal reactive electrophilic metabolite by specific nematode cytochrome P450 enzymes, and thus can selectively kill nematodes, including diverse species of plant-parasitic nematodes [25]. Although these sustainable nematicides have a minimum environmental impact, the costs could limit their use for RN management in cotton.

3.2 Biological control

Two fungal strains (ARF and *Pochonia chlamydosporia*) recovered from RN infested soils in Arkansas were found to be nematophagous [26, 27]. The ARF strain was similar to a previously reported ARF 18 isolate that parasitized soybean cyst nematode (*Heterodera glycines*) [28]. Several isolates of *Pochonia chlamydosporia* could significantly reduce RN numbers on cotton roots and in the soil [27]. *Bacillus firmus* GB-126 and *Paecilomyces lilacinus* 251, applied separately or concomitantly, were shown to reduce the number of eggs and vermiform female nematodes in the soil with seedcotton yields for these treatments similar to the chemical nematicide aldicarb treatment [29]. The infectious bacteria in the genus *Pasteuria* can be used for cotton seed treatment with an efficacy comparable to chemical nematicides [30]. These biological control agents are currently not commercially available as a practical means for controlling *R. reniformis*.

3.3 Crop rotation

Crop rotation with non-host crops, such as corn and peanuts, or with resistant host cultivars, was reported to reduce RN populations [31]; however, long rotational cycles were required to significantly reduce the population to have an economic benefit. RN can survive for at least 2 years in dry soil in an anhydrobiosis manner without a host plant [32], and the RN population could recover in one cotton growing season [19]. Moreover, crop rotation is not always feasible due to economic and resource constraints.

3.4 Resistant cotton cultivars

Growing resistant cultivars or combining approaches of resistant cultivars and nematicide application have been shown to be effective for RN management [1, 33, 34]. Growing commercial resistant cotton cultivars could dramatically reduce the RN populations, and achieve higher yield compared to the susceptible cultivar, and the yield could be further increased with the integration of nematicide management [34]. Singh et al. reported that growing resistant cultivars reduced the RN population by 38% [35]. Using resistant cotton cultivars would be the most economical and effective approach for RN management, and developing upland cotton cultivars with RN resistance is a common goal for cotton breeding programs.

4. Breeding RN resistant upland cotton cultivars

The *Gossypium* genus consists of 55 species, including seven tetraploid (genomes AD1 to AD7) and 48 diploid species (genome groups A to G, and K) [36]. Only four species, including two tetraploids, *G. hirsutum* (upland cotton) and *G. barbadense* (sea island cotton), and two diploids, *G. arboreum* and *G. herbaceum*, are cultivated, with *G. hirsutum* and *G. barbadense* accounting for 95 and 3% of the world cotton production and 97 and 3% of the US cotton production. Based on the potential usages for genetic improvement of the two tetraploid cultigens, the exotic cotton genetic resource comprises in primary germplasm pool (all seven tetraploid species that can cross with cultivated tetraploid species and produce fertile progenies), secondary germplasm pool (A, B, D, F genome species whose chromosomes have reasonably high homoeology to either the A subgenome or the D subgenome of the tetraploid AD species), and tertiary germplasm pool (C, E, G, K genome species whose chromosomes have limited homoeology to the two subgenomes of the tetraploid AD species) [37].

4.1 Screening cotton germplasm accessions for RN resistance

Upland cotton accounts for 97% of US cotton production (USDA-ERS, 2024), and more than 7000 accessions are maintained in the USDA-GRIN upland cotton germplasm collection. Identifying sources of resistance from this collection would be highly desirable for the rapid development of resistant cultivars. The collection has been extensively evaluated [9, 38–41]. Yik and Birchfield identified two accessions, Marie Galante 893 (PI 529860) collected from Haiti and Marie Galante 903 (PI 529864) collected from Cuba that showed RN resistance and one moderately resistant accession, Marie Galante 874 (PI 529852), from St. Thomas, the US Virgin Islands, but no resistant cotton cultivars were developed using these accessions [42]. Additionally, these accessions are photoperiod sensitive, limiting their utilization in breeding programs. Robinson et al. evaluated 1866 accessions with six accessions rated as moderately resistant, and three of these accessions were also resistant to root-knot nematode [38]. Weaver et al. screened 1973 accessions of *G. hirsutum* germplasm, none showed high levels of resistance, seven accessions showed lower RN population development than the susceptible control Paymaster ‘PM 1218’, and only two out of the six previous identified moderate resistant accessions were confirmed resistant in this test, the discrepancy may result from different nematode populations and/or controls were used [41]. Several breeding lines have been developed from RN resistant upland cotton germplasm, which reduced the RN population to one-half or reduced yield losses to RN by 33% compared

to a susceptible cultivar [43, 44]. However, because of the lower level of RN resistance associated with upland cotton germplasm, breeding programs have not extensively utilized these resistant sources for the development of commercial cultivars.

G. barbadense is another commercially cultivated cotton species. Cultivars of the species are grown for their high-quality fiber, but cottonseed yields are lower than upland cotton, and fewer acres are planted. More than 1800 accessions are maintained in the USDA-GRIN *G. barbadense* germplasm collection. This species is also a tetraploid and can be crossed with upland cotton to produce fertile hybrids; thus, the collection was evaluated for RN resistance. Yik and Birchfield evaluated six accessions, and TX 110 (PI 163608) was rated as highly resistant, suggesting useful sources of RN resistance are present in the collection [42]. Two accessions, TX-1347 and TX-1348, were rated as moderately resistant [45]. A more extensive evaluation was conducted by Robinson et al. [38]. From the 907 accessions evaluated, five accessions were rated as resistant and 17 accessions rated as moderately resistant. Accession GB 713 (PI 608139) showed the highest level of resistance, but TX 110 was rated as moderately resistant for this study [38]. Photoperiod sensitivity is commonly observed for *G. barbadense* accessions, and hybrid breakdown has been reported for crosses between *G. barbadense* and upland cotton, thus, additional resources would be required to introgress RN resistance from other *G. barbadense* accessions.

More than 2200 accessions for 33 cotton diploid species are also maintained in the USDA-GRIN cotton germplasm collection [46]. Yik and Birchfield evaluated 32 accessions representing 19 diploid species. The *G. longicalyx* accessions were rated as immune, whereas resistant or moderately resistant accessions were identified from the *G. somalense*, *G. stocksii*, *G. raimondii*, *G. arboreum*, and *G. herbaceum* species included in this study [42]. The diploid species *G. aridum* may also be a source of RN resistance [47]. The two diploid species *G. arboreum* and *G. herbaceum* were once widely cultivated in Asia, and more extensive evaluations have been conducted for these species. Most of the accessions for the two species are photoperiod-insensitive, which aids in the evaluation and breeding of these accessions in temperate regions. More than 1800 accessions for *G. arboreum* and 160 for *G. herbaceum* are maintained in the germplasm collection [46]. RN resistance was more frequently observed for *G. arboreum* accessions with 26 rated as resistant and 102 as moderately resistant [37, 42, 48]. For *G. herbaceum*, four accessions were rated as resistant and 24 accessions as moderately resistant [42, 49]. Although transferring resistance from these species to upland cotton is more difficult, novel sources of RN resistance may be present in the diploid species.

4.2 Genetics of RN resistance

Understanding the genetic basis of resistance is critical for breeding cotton cultivars and will aid in the introgression of resistance from related cotton species; however, few studies have evaluated the genetics of resistance for tetraploid cotton accessions. The inheritance of RN resistance for upland cotton was evaluated by analyzing the generation means of populations developed by crossing the susceptible cultivar ‘Deltapine 41’ and three cultivars, La RN-910, Auburn (Aub) 612-RNR, M 019-RNR, reported to be resistant, and data suggested complex inheritance of resistance [50]. These findings may have resulted from the low level of resistance associated with the parents; nevertheless, it is likely that the multiple genes with minor effects may be associated with resistance for upland cotton. The RN resistance associated with the *G. barbadense* line GB 713 was controlled by three QTL, two QTL (*Ren*^{barb1} and *Ren*^{barb2}) were mapped to chromosome AD_ch21_Dt.11, and the third

QTL (Ren^{barb3}) was mapped to chromosome AD_ch18_Dt.13 [51]. These QTL were further mapped to a 17.7 MB interval (36.5–54.2 MB) on AD_ch21_Dt.11 and a 1.8 MB interval (5.9–7.7 MB) on AD_ch18_Dt.13 [52]. Most of the resistance was associated with QTL Ren^{barb2} and the presence of QTL Ren^{barb3} was required to recover the high level of resistance characteristic of GB 713.

For the cotton diploid species *G. longicalyx*, RN resistance was controlled by one dominant gene Ren^{lon} , which was mapped on *G. longicalyx* chromosome 11 [53, 54]. The resistance QTL Ren^{ari} from *G. aridum* introgressed into upland cotton (*G. hirsutum* × *G. aridum*) was mapped to the tetraploid chromosome AD_ch21_Dt.11 [47]. For *G. arboreum*, RN resistance was controlled by a single recessive gene for the moderately resistant accession PI 529728 (A2-100) [55], and by two recessive genes for the highly resistant accessions PI 529740 (A2-113) and PI 417895 (A2-87) [56, 57]. The two QTL controlling resistance for PI 417895 have been mapped on chromosomes 10 and 12, and disease resistance genes have been identified in these regions [58]. Using a genome-wide association study approach, 15 significant SNPs associated with RN resistance were identified in a panel of 246 *G. arboreum* accessions, and these SNPs showed additive effects for RN resistance [59]. Eight SNPs identified from a genome-wide association study were linked with resistance in *G. herbaceum* [49]. These studies suggest genetic diversity for RN resistance within the *G. arboreum* and *G. herbaceum* germ-plasm collections. Transcriptome analysis from several *Gossypium* species revealed differentially expressed genes associated with RN resistance, including disease resistance genes [60, 61]. The application of genomic tools will expedite the genetic dissection of RN resistance for *Gossypium* and facilitate introgression of resistance to upland cotton.

4.3 Developing upland cotton varieties using *G. barbadense* resistance

Multiple upland cotton varieties with improved RN resistance have been developed and released using *G. barbadense* resistance. Using TX 110 and a root-knot nematode resistant *G. hirsutum* line M315 RNR (PI 592514) as parents, two upland cotton lines, TAM RKRNR-9 (PI 662039) and TAM RKRNR-12 (PI 662040), were developed that suppress reniform nematode reproduction by 40–70% and reduce root-knot nematode reproduction by more than 90% [62]. Multiple resistant lines were developed using GB 713 as the source of RN resistance. Three lines, M713Ren1 (PI 665928), M713Ren2 (PI 665929), and M713Ren5 (PI 665930), developed in Mississippi, showed approximately 90% suppression in reniform nematode egg production [63]. The lines BARBREN-713 (PI 671965) and BARBREN-713-32 (PI 701076) developed in Texas suppressed nematode egg production by 74–92% [64, 65]. These GB 713 lines have been used to breed commercial cotton cultivars with RN resistance; however, relying on a single source of resistance could contribute to shifts in the nematode population and the loss of resistance.

4.4 Developing upland cotton varieties using resistance from diploid *Gossypium* species

Crossing diploid species with upland cotton to obtain hybrid seeds is rarely successful. Ovule rescue has been used to recover hybrid plants from these wide hybridizations [66, 67]. The triploid plants that are recovered are typically sterile and are treated with colchicine to double the chromosome number to generate hexaploid plants, which can be crossed with upland cotton or serve as bridging lines to cross with diploid *Gossypium* species [68].

Two upland cotton lines LONREN-1 (PI 669509) and LONREN-2 (PI 669510) were developed using bridging lines (*G. hirsutum* x *G. longicalyx*) and (*G. hirsutum* x *G. herbaceum*) to introgress RN resistance from *G. longicalyx* [54, 69, 70]. These lines were incorporated into many breeding programs; however, plant stunting was commonly observed in breeding lines derived from this source of resistance. Resistance was shown to be associated with a hypersensitive reaction under high nematode pressure, and severe root necrosis and plant stunting were reported [71], thus eliminating the use of this resistance source in commercial cotton breeding programs.

G. hirsutum cultivars have been crossed with several diploid species, including *G. herbaceum* (A1), *G. arboreum* (A2), *G. thurberi* (D1), *G. aridum* (D4), *G. raimondii* (D5), and *G. longicalyx* (F1) to generate additional hexaploid breeding lines. Triploid F1 plants have been obtained through ovule culture [66, 67] or from hybrid seeds harvested in vivo. Abnormal growth was commonly observed for seedling generated from ovule culture reducing the success rate, and some plants showed poor root growth that would require grafting to recover healthy plants. Triploid plants were male and female sterile. The meristematic or lateral buds of triploid plants were treated with 0.2% colchicine for 24 h for chromosome doubling to recover fertility. Several hexaploid lines have been obtained (**Figure 3**). These hexaploid plants can be crossed with upland cotton cultivars to recover the upland cotton phenotype or be used as bridging lines in crosses with other diploid cotton accessions. The hexaploid (*G. hirsutum* x *G. aridum*) bridging line was used to introgress RN resistance from *G. arboreum* and *G. aridum* into upland cotton [47, 72]. So far, no resistant upland cotton lines have been developed using this hexaploid, and these bridging lines are no longer available. Newly developed hexaploid lines are crossed with selected diploid genotypes to introduce resistance to upland cotton.

Autotetraploid *G. arboreum* lines (AAAA) and synthetic allotetraploid (AADD) lines, which can be crossed with *G. hirsutum*, were also developed for introgression of RN resistance. The *G. arboreum* accessions A2-190 (PI 615699), A2-272 (PI 615766), A2-354 (PI 615848), A2-514 (PI 616008), A2-690 (PI 616184), and A2-737 (PI 616231) were rated as highly resistant to reniform nematode [48] and (R x R) F1 plants were treated with colchicine. The chromosomes of five F1 plants (one each from crosses A2-690 x A2-190, A2-690 x A2-272, A2-737 x A2-190, A2-737 x A2-354, A2-737x A2-514) have been doubled. The derived tetraploid plants have larger and thicker leaves compared to their original diploid counterparts (**Figure 4a**), and flowers are larger and usually sterile (**Figure 4b**), boll shapes are different from



Figure 3.
A hexaploid plant of (*G. hirsutum* x *G. raimondii*). a. plant; b. bud; c. flower and boll.

G. arboreum as well (**Figure 4c**). These plants barely shed pollen but can be crossed with *G. hirsutum* and *G. barbadense* cultivars to produce seeds.

To generate synthetic allotetraploid plants, crosses were made between *G. arboreum* (A2 genome) and the D genome species, *G. aridum* (D4), *G. raimondii* (D5), and *G. trilobum* (D8). A synthetic allotetraploid (A2A2D8D8) plant was obtained through colchicine chromosome doubling (**Figure 5a**). The leaf shape and flowers resemble those of *G. hirsutum*. Flowers are male sterile but can be pollinated with tetraploid cotton cultivars (**Figure 5b**), and the boll shape is different from the parents (**Figure 5c**). Some progenies using this synthetic tetraploid crossed with *G. hirsutum* and *G. barbadense* have been produced for further evaluations.

There are multiple challenges using diploid cotton accessions as a source of RN resistance for the development of upland cotton cultivars. (1) It is difficult to obtain triploid hybrids by crossing tetraploid and diploid cotton species. Triploid plants can be recovered through ovule tissue culture methodology, but the success rate is low, and additional resources and technical expertise are required. (2) The success rate of doubling cotton chromosomes with colchicine was low, which could be as little as 0.1%. (3) Sterility of progenies derived from wide hybridization was highly frequent. Plants of the artificial autotetraploid and allotetraploid, and one hexaploid (AhAhDhDhD5D5) were male sterile. No self-pollinated seeds were obtained from these plants except one boll from an autotetraploid *G. arboreum*. These plants were female fertile and can be pollinated using tetraploid or diploid plants to produce seeds, except for one tetraploid plant of [*G. arboreum* x 2(ADD)], which was male and female sterile. All triploid hybrids showed female and male sterility, requiring chromosome doubling to recover female fertility. Male fertility can be recovered by

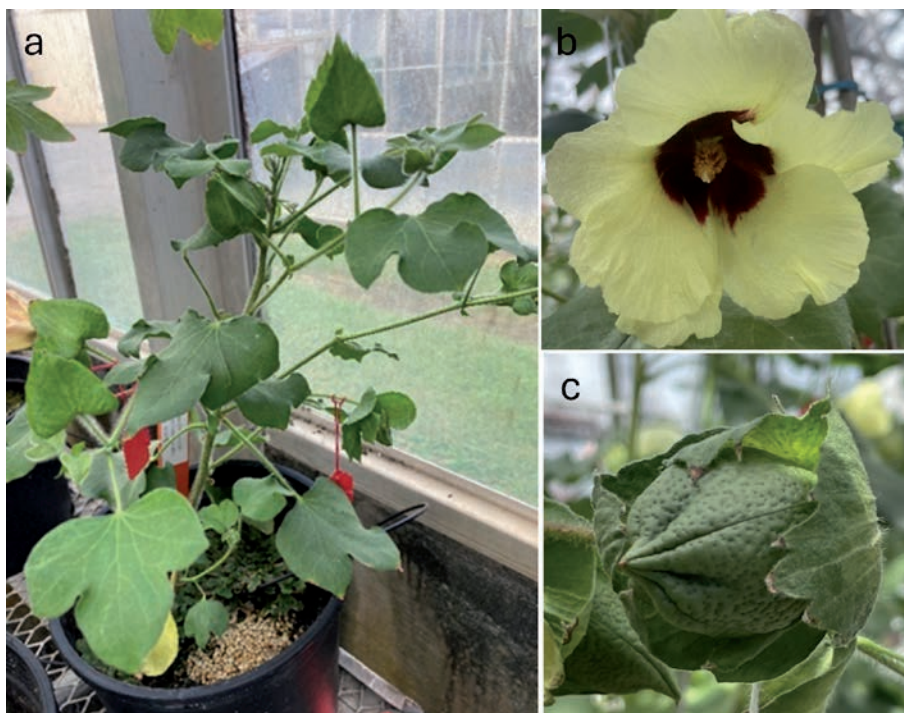


Figure 4.
An autotetraploid plant of (A2-737 x A2-190) F1. a. plant; b. flower; c. boll.



Figure 5.
An allotetraploid plant of (A2A2D8D8). a. plant; b. flower; c. boll.

crossing the hexaploid plants with diploid plants or by backcrossing with *G. hirsutum* cultivars. (4) Dramatic segregation may be observed in the interspecific progenies. RN resistance progeny often showed segregation over multiple generations, even though resistance should have been fixed in previous generations. It is possible that high rates of recombination or chromosomal rearrangements at the site of integration in the *G. hirsutum* genome result in a loss of function for the resistance gene. Alternatively, a lack of recombination between different genomes could result in the elimination of the donor genome. The inherent variability in screening for RN resistance can also impede the recovery of resistant progeny. (5) When RN resistance is controlled by recessive gene(s), as observed for several *G. arboreum* genotypes, large populations are required to recover progenies showing a constant resistant response over multiple generations. Marker-assisted selection will be critical for breeding resistant upland cultivars. However, DNA markers tightly linked to resistance will be essential to recover plants where recombination has occurred between the diploid and tetraploid genomes. Variability in evaluating RN resistance and the ability to evaluate large populations can impact the identification of DNA markers linked to resistance genes.

However, there are many benefits for the utilization of RN resistant diploid germplasm in cotton breeding programs. Narrow genetic diversities among modern upland cotton cultivars have created a bottleneck that has restricted genetic improvement. Introgression of RN resistance from diploid species can capture genetic diversity lacking in upland cultivars. Moreover, resistance to other biotic and abiotic stresses, such as bacterial blight, Fusarium wilt race 4, Verticillium wilt, various viruses, drought, and soil salinity, may be introduced to upland cotton. Moreover, along with increases in fiber yield, fiber quality can be improved as well. Tetraploid progenies derived from *G. arboreum* accessions have premium fiber qualities, especially fiber strength

(data not shown). The autotetraploid, allotetraploid, and hexaploid bridging lines will make it possible to introduce RN resistance into upland cotton to increase cotton productivity and profitability for growers.

5. New technologies for RN management

Genome editing offers a promising approach for controlling plant-parasitic nematodes [73]. The RNA interference (RNAi) strategy, through the expression of a putative double-stranded RNA (dsRNA) in the host plant to silence important genes involved in nematode development or parasitism, could ultimately reduce the nematode's ability to infect the host plant and reproduce [74]. This method has been used to improve tolerance to root-knot nematode for cotton [75]. Some genes may facilitate pathogenesis in plant-nematode interactions. Loss of function of these susceptibility genes through CRISPR gene editing may be an alternative strategy for RN management [73, 76]. A better understanding of the genes involved in RN resistance would be required to successfully use these technologies.

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