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RESEARCH PAPER

Field evaluation and inheritance of leafhopper resistance in segregating generations of Cotton

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Abstract: Cotton (*Gossypium hirsutum* L.) is a globally important fiber crop whose productivity is increasingly threatened by sucking pests, with leafhopper (*Amrasca biguttula biguttula*) infestation emerging as a major concern. The present study aimed to elucidate the inheritance of leafhopper resistance in cotton using F_2 populations derived from four crosses between exotic susceptible and indigenous resistant genotypes. Field evaluations were conducted under unprotected conditions during *kharif* 2023-24 at the Agricultural Research Station, Dharwad. Inheritance analysis revealed variable genetic control of resistance across the crosses. The F_2 population of 0774-3-3 × 1-2-1 exhibited a 13:3 ratio, indicating inhibitory epistasis, whereas the populations of Raider 276 × 8-1-2 and 0774-3-3 × MCU-12 followed a 9:7 ratio, consistent with complementary gene action. In contrast, the F_2 population of Raider 276 × MCU-13 segregated in a 3:1 ratio, confirming control by a single dominant gene. These results demonstrate that leafhopper resistance in cotton is governed by either monogenic or digenic interactions, depending on the parental genetic background. These findings provide valuable insights for cotton breeding programs focused on developing high-yielding, leafhopper-resistant cultivars with improved agronomic performance and fibre quality under unprotected conditions.

Key words: Cotton, F_2 population, Inheritance, Leafhopper

Introduction

Cotton (*Gossypium* spp.), known as the "King of Fibre Crops" or "White Gold," is a major global fibre and commercial crop of immense economic and social importance (Sowmya and Patil, 2021). India, one of the earliest centers of cotton domestication, remains the largest cultivator with over 11.23 million hectares under cultivation and ranks second in production and consumption (Indiastat, 2024-25). The crop supports about 6 million farmers and 50 million people in processing and trade. It provides 59% of raw material to the textile industry, contributes 29.1% to textile exports, and adds 4.9% to the agricultural output (ICAR-AICRP, 2024-25). India ranks first globally in cotton cultivation area but second in production, with productivity at 465 kg/ha, much lower than the global average of 855 kg/ha (ICAR-AICRP, 2024-25; Indiastat, 2024-25). The low yield is attributed to the use of susceptible hybrids, rainfed cultivation, and heavy pest and disease incidence. Cotton is attacked by about 162 insect species, of which 15 are major pests (Rajendran *et al*., 2018). These include sucking pests such as leafhoppers (*Amrasca biguttula biguttula*), whiteflies (*Bemisia tabaci*), aphids (*Aphis gossypii*) and thrips (*Thrips tabaci*), which alone can cause up to 26% yield loss (Makwana *et al*., 2018).

Among the various production challenges affecting cotton, the infestation of the sucking pest *Amrasca biguttula biguttula* (commonly known as jassid or Indian cotton leafhopper) has become a major threat to cotton production across India and other Southeast Asian countries (Teli *et al*., 2021). Infestation occurs from the vegetative to reproductive stages, as nymphs and adults suck sap, causing leaf yellowing, reddening, and drying symptoms known as "hopperburn" (Painter, 1951; Uthamasamy, 1985). Yield losses range from 330-390 kg/ha and may reach up to 50% (Kalkal *et al*., 2009). The pest has a wide host range, including okra, brinjal and jute, and can transmit plant viruses. Its infestation reduces plant vigor, growth, and fibre quality, making it one of the most destructive cotton pests. The present investigation was undertaken to study the nature of inheritance of resistance to leafhoppers in cotton.

Material and methods

The study was conducted under unprotected field conditions during *kharif* 2023-24 at the Agricultural Research Station, Dharwad, University of Agricultural Sciences, Dharwad. The experimental material included six genotypes, two susceptible (0774-3-3 and Raider 276 from the USA) and four resistant (1-2-1, 8-1-2 from Raichur, and MCU-12, MCU-13 from Coimbatore). Four F_2 populations were developed from the crosses 0774-3-3 × 1-2-1, Raider 276 × 8-1-2, 0774-3-3 × MCU-12 and Raider 276 × MCU-13, and screened for leafhopper resistance. Seeds were sown without pesticide treatment to allow natural infestation, and bhendi was planted after every six rows as a trap crop to enhance pest load. All recommended agronomic practices for rainfed cotton were followed, excluding plant protection measures.

Inheritance studies

Each F_2 plant was graded twice, in mid-August and mid-October, during peak leafhopper incidence ($\geq$ 2 nymphs per leaf). Grading was based on injury symptoms observed on three leaves per plant (top, middle, and bottom), following the criteria of the Indian Central Cotton Committee (Sikka *et al*., 1966; Rao, 1973). For inheritance studies, plants were classified as resistant or susceptible based on leafhopper injury grades, and segregation in the F_2 populations was tested for Mendelian ratios using the Chi-square (χ^2) test:

$$`\chi_i^2 = \frac{(Oi-Ei)^2}{Ei} \quad \text{for i=1, 2…., k classes}$$

where O_i and E_i are observed and expected frequencies. The calculated χ^2 was compared with the tabulated value at 0.05 significance to assess goodness of fit.

Results and discussion

A total of 308 plants from the cross 0774-3-3 × 1-2-1, 354 from cross Raider 276 × 8-1-2, 400 in cross 0774-3-3 × MCU-12, and 326 F_2 from cross and Raider 276 × MCU-13 were evaluated for resistance to leafhopper under unprotected field conditions (Fig. 1). A standardized I-IV grading scale was used, where plants with a grade of ≤ II were considered resistant and those with a grade > II were categorized as susceptible. The parental genotypes exhibited significant differences in their response to leafhopper infestation. The exotic lines 0774-3-3 and Raider 276 were highly susceptible (injury grade IV) but possessed desirable agronomic traits, including large bolls with hard rind and superior fibre quality. In contrast, the resistant genotypes 1-2-1, 8-1-2, MCU-12, and MCU-13 showed high resistance to leafhopper (injury grade I) and produced medium-sized bolls. All selected parents were true breeding for leafhopper reaction.

In the F_2 population derived from the cross 0774-3-3 × 1-2-1, 68 out of 308 plants were resistant, while the remaining were susceptible (Table 1). This segregation fit a 13:3 ratio (susceptible: resistant), suggesting the involvement of inhibitory epistasis in controlling leafhopper resistance. The 13:3 ratio indicates that a dominant gene inhibits the expression of resistance contributed by another gene, leading to a modified Mendelian pattern rather than simple dominance.

The F_2 population of Raider 276 × 8-1-2 showed 140 resistant plants out of 354, following a 9:7 segregation ratio for susceptible to resistant phenotypes. Similarly, in 0774-3-3 × MCU-12, 176 out of 400 plants were resistant, also fitting a 9:7 ratio (Table 1). This pattern is indicative of complementary gene action, where the presence of dominant alleles at both loci is required for the resistant phenotype. Complementary epistasis suggests that the expression of resistance depends on the interaction of two genes, rather than being governed by a single locus.

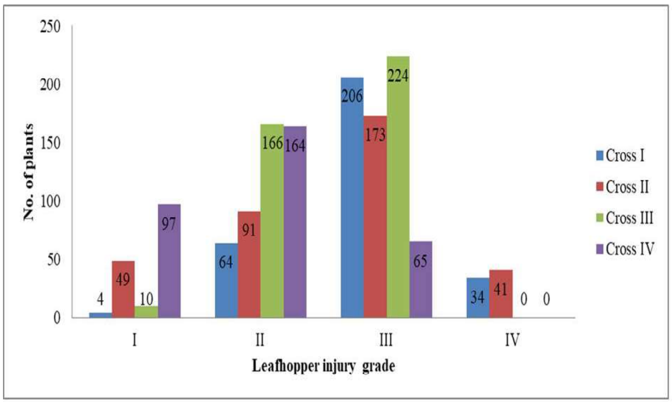

Fig 1. Histogram showing distribution of leafhopper injury grade in F_2 population across the four crosses in cotton

In contrast, the cross between Raider 276 and MCU-13 exhibited a predominance of resistant plants, with 261 out of 326 categorized as resistant (Table 1). The segregation of the F_2 population followed a classical Mendelian 3:1 ratio for resistant to susceptible plants, indicating that resistance in this cross is controlled by a single dominant gene. Such a simple inheritance pattern contrasts with the epistatic interactions observed in the other crosses, highlighting the influence of genetic background on the expression of leafhopper resistance.

The present results are in agreement with earlier findings on leafhopper resistance in upland cotton. Pushpa and Raveendran (2005) reported segregation ratios of 13:3 and 9:7 in several F_2 crosses, suggesting the involvement of epistatic gene interactions. Similar observations were documented by Sikka and Singh (1953), Sharma and Gill (1984) and Aralikatti *et al*. (2024). The 3:1 Mendelian segregation observed in the cross Raider 276 × MCU-13 aligns with reports by Mahal (1978), Radhika *et al*. (2004), Murugesan and Kavitha (2010), Zhang *et al*. (2013), Venkatesha (2017), and Yaksha *et al*. (2022), confirming that single-gene dominance can also confer leafhopper resistance in certain genetic combinations.

The variation in inheritance patterns observed across the four F_2 populations underscores the complex nature of leafhopper resistance in cotton. While some crosses demonstrate simple Mendelian inheritance controlled by a single dominant gene, others exhibit digenic interactions with

Table 1. Segregation pattern for reaction to jassids in F_2 generation of the four individual crosses of cotton

Cross		Reaction to leafhopper		Total	χ^2 value (test statistic)	χ^2 value (critical value)	Expected ratio	p
		Susceptible (grade III & IV)	Resistant (grade I &II)					
0774-3-3 × 1-2-1	O	240	68	308	2.21	3.841	13:3	0.05
	E	250.25	57.75					
Raider 276 × 8-1-2	O	214	140	354	2.53	3.841	9:7	
	E	199.12	154.87					
0774-3-3 × MCU- 12	O	224	176	400	0.01	3.841	9:7	
	E	225	175					
Raider 276 × MCU-13	O	65	261	326	1.62	3.841	3:1	
	E	81.5	244.5					

Note: O- observed, E-expected

either inhibitory or complementary epistasis. These differences likely reflect the genetic constitution of the parents involved and the specific allelic interactions influencing resistance expression. Such findings are critical for breeding programs, as they indicate that the choice of parental lines can determine the genetic mechanism of resistance in segregating populations.

Furthermore, the study highlights the importance of selecting parents with both resistance and desirable agronomic traits. While exotic susceptible lines contributed favourable fibre qualities, the indigenous resistant lines provided moderate trichome density and strong resistance to leafhopper infestation. The combination of these traits in F_2 populations can facilitate the development of high-yielding, leafhopper-resistant cultivars suitable for cultivation under unprotected conditions. In summary, the present investigation demonstrates that leafhopper resistance in cotton is governed either by a single dominant gene or by the interaction of two genes exhibiting inhibitory or complementary epistatic effects, depending on the genetic background of the cross. Understanding these inheritance patterns provides valuable insights for breeding programs aimed at developing resistant cotton varieties with improved agronomic performance and fibre quality.

Conclusion

The present study reveals that leafhopper resistance in cotton is controlled either by a single dominant gene or through the interaction of two genes exhibiting inhibitory or complementary epistasis, depending on the genetic background of the cross. Resistant parental lines with moderate trichome density effectively limited pest damage, while susceptible exotic lines contributed desirable fibre traits. These findings provide valuable insights for breeding programs, enabling the development of high-yielding, leafhopper-resistant cotton cultivars with improved fibre quality suitable for cultivation under unprotected conditions.

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