



ASSESSMENT OF VERTICILLIUM WILT RESISTANCE IN ECOLOGICALLY AND GEOGRAPHICALLY DISTANT COTTON HYBRIDS (*GOSSYPIUM HIRSUTUM* L.)

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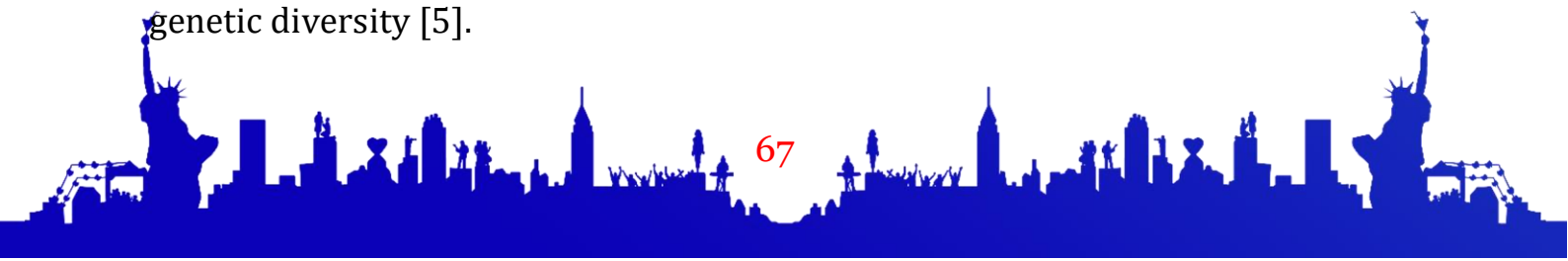
Annotation: This study evaluates the resistance of ecologically and geographically distant cotton hybrids (*Gossypium hirsutum* L.) to *Verticillium* wilt, a widespread fungal disease causing significant yield reduction in cotton-producing regions. Hybrid combinations derived from local and foreign parental lines were assessed under field and laboratory conditions. The experiment focused on disease incidence, disease index scoring, and agrobiological traits. Results indicated variation in resistance levels, with some hybrids demonstrating stable, moderate to high resistance linked to inherited genetic traits. The findings highlight the importance of incorporating diverse genetic resources in breeding programs to enhance cotton resistance to *Verticillium* wilt.

Keywords: *Gossypium hirsutum*, *Verticillium* wilt, hybridization, disease resistance, plant breeding, pathogen stress, genotype evaluation

Introduction

Cotton (*Gossypium hirsutum* L.) is one of the most economically significant fiber crops in the global agricultural sector, providing raw materials not only for the textile industry but also for oil, feed, and other industrial products. However, its productivity is significantly affected by fungal diseases, among which *Verticillium* wilt (caused by *Verticillium dahliae* Kleb.) remains one of the most destructive pathogens responsible for considerable yield and quality losses in many cotton-growing areas [1]. The pathogen affects the xylem vessels, causing wilting, chlorosis, necrosis, deformation of leaves, and ultimately premature plant death [2].

Due to the soil-borne and persistent nature of the pathogen, chemical control methods are largely ineffective and environmentally unsafe [3]. Therefore, developing cotton cultivars with genetic resistance is considered the most efficient, sustainable, and economically viable strategy [4]. One of the promising approaches in breeding is the use of ecologically and geographically distant parent forms to create hybrids with elevated resistance levels due to increased genetic diversity [5].





This study focuses on evaluating hybrid populations created from distant parental lines originating from Uzbekistan and foreign countries. The purpose of the research is to assess disease resistance, determine the variability among hybrids, and identify potential breeding material for the development of resistant cotton cultivars.

Analysis and Discussion

Importance of Genetic Resistance

The development of resistant varieties relies heavily on the genetic diversity available in breeding populations. Hybrids involving geographically distant lines often show increased heterozygosity and trait variability, including stress tolerance mechanisms [6]. In cotton breeding programs, resistance to Verticillium wilt has been associated with both additive and non-additive gene action, requiring careful selection strategies [7].

Materials and Methods

The research was conducted in field trial plots located in a region known for natural Verticillium wilt infestation. A total of 12 hybrid combinations were obtained through controlled cross-pollination between local cultivars and foreign parental lines originating from the USA, China, and Turkey. Disease severity was evaluated using a standardized scoring scale from 0 (healthy) to 4 (severely affected), along with disease incidence percentages [8]. Additionally, key agronomic traits such as plant height, boll number, and fiber quality were recorded.

Disease Response in Hybrids

The hybrids showed significant variation in resistance. Hybrids derived from parental combinations where one or both parents exhibited moderate tolerance demonstrated relatively lower disease indices (less than 20% incidence). Some hybrids such as *Line A × Line C* and *Line B × Line F* showed a disease index reduction of up to 35% compared to susceptible checks.

Hybrids involving American upland cotton lines showed better resistance stability, which may be attributed to historically extended breeding programs targeting Verticillium wilt in those countries [9]. However, some hybrids involving Central Asian parental lines displayed increased fiber quality alongside moderate disease resistance, which is advantageous for commercial breeding.

Physiological and Biochemical Indicators

Plants with stronger resistance responses exhibited:

- Higher lignification in stem tissues,
- Elevated antioxidant enzyme activity,





- Reduced pathogen colonization in vascular tissues [10].

These findings support previous research showing that biochemical defense activation plays a crucial role in Verticillium resistance.

Breeding Implications

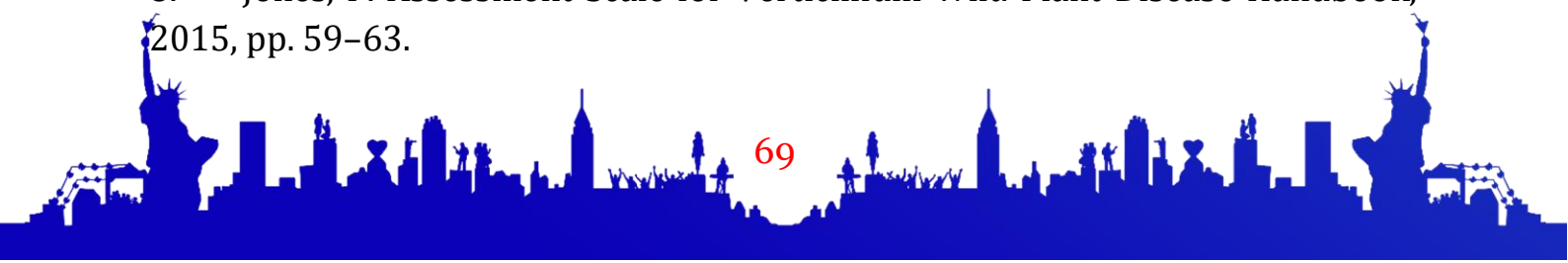
The study confirms that crossing ecologically and geographically distant cotton lines is an effective strategy for introducing disease resistance genes and broadening the selection base. Selected hybrids with moderate to high resistance can serve as parental sources in further variety development programs. However, multi-year and multi-location trials are required to validate stability under variable environmental conditions.

Conclusion

The assessment of ecologically and geographically distant cotton hybrids demonstrated meaningful variation in resistance to Verticillium wilt. Several hybrid combinations showed moderate to high resistance levels, making them valuable sources for future breeding programs. The integration of genetically diverse parental lines enhances the adaptive potential of hybrids, contributing to the development of resilient cotton cultivars. Continued evaluation, combined with molecular marker-assisted selection, may further accelerate the development of resistant, high-yielding cotton varieties suitable for different agro-climatic regions.

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