

Selection of initial samples resistant to spider mite from F2 hybrids using the marker-based selection method

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Abstract.

This article describes the use and effectiveness of marker-based selection (MAS) in creating new varieties of cotton resistant to spider mite. Based on the experiments conducted using the MAS method, it is based on the creation of new spider mite-resistant cotton raw materials.

Key words. Selection, selection based on spider mites, cotton, markers.

Marker-based selection (MAS) is an efficient method to create the best cotton sample [1]. The planting of resistant varieties leads to an increase in the yield of cotton and a sharp decrease in the cost [2]. Through MAS, it is possible to dramatically increase seed efficiency [3]. With the help of specific markers, it is possible to distinguish resistant genotypes of cotton even during the germination period [4]. Due to the multidimensional Quantitative Trait Locus (QTL) polymorphism, the selection efficiency with the help of markers increases dramatically [5], [6]. The discovery of alleles associated with valuable economic traits of cotton allows these alleles to be used directly in MAS [6]. F2 plants are selected by 3 methods: phenotype (1), combined marker-genotype and phenotype (MAS) (2), genotype (3) [7]. MAS and backcross breeding can be an effective way to increase the breeding value of lines with a relatively small number of genes by selecting specific combinations of beneficial QTL alleles from several excellent parental lines [3], [8].

The use of MAS in breeding and seed production has grown rapidly over the past two decades [9]. Several scientists have conducted many studies using this method [10]–[14], Maheswari et al. al. [15]. The MAS method is an important tool for repeated selection and improvement of seed yield in any type of crop. [3]. Based on Nayak's research, the most effective marker-assisted selection (MAS) in plant breeding is a method of selecting attractive individuals for seed production using molecular markers, with or without considering the relative importance of traits. [16]. This method works particularly well for generating resistant species [17].

During the research conducted using the selection method based on markers, samples resistant to spider mite were selected from F2 hybrid combinations in cotton.

First, the level of spider mite infestation of varieties and hybrids from the collection was studied, and then polymorphism between resistant and non-resistant samples was determined. Using molecular markers, PCR screening was performed and mutual polymorphism between these varieties and samples was determined.

When tested with molecular markers, samples showing mutual polymorphism, resistant and resistant to spider mite were selected, and monohybrid hybridization was carried out between them. Spider web resistance of F1 hybrids obtained by crossing was studied. F1 hybrids were screened by PCR using molecular markers.

F2 hybrids were also planted in field and phytotron boxes, and the degree of spider mite infestation was studied in natural and artificial environments. Genomic DNA was isolated from F2 hybrids and PCR screening was carried out with specific primers attached to the marker of resistance to sucking pests. Among the F2 hybrids that are phenotypically resistant to spider mite and have resistance alleles in their genome, the initial sources of spider mite resistance were selected (look Figure 1).

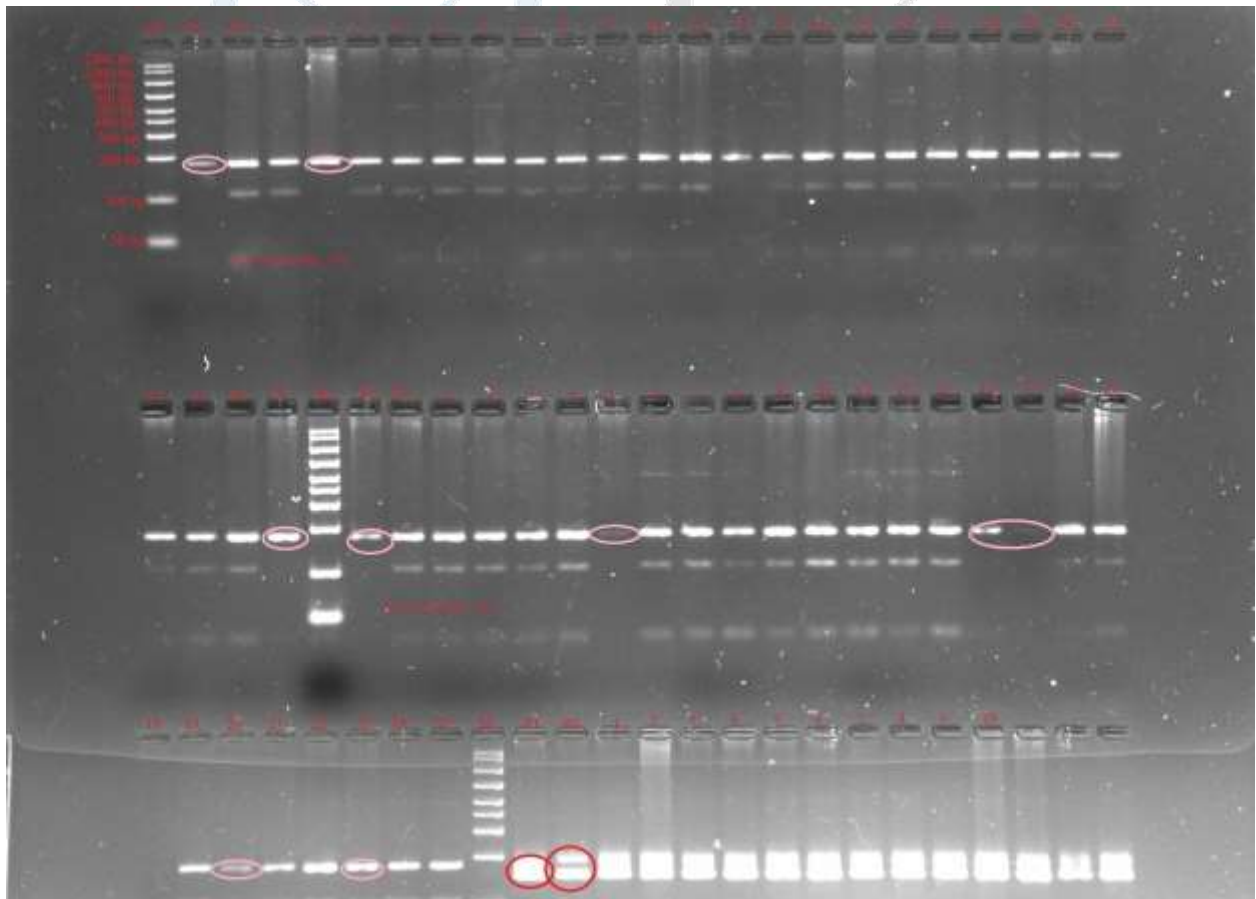


Figure 1. Polymorphism among F2 hybrids of Upland x Omad, New Impr x Namangan 77 hybrid combinations. Image of NAU 922 BNL, 1705 SSR markers on gel electrophoresis. M-molecular weight marker, P1, P2 - parental forms, line 1 1-25 Upland x Omad hybrid combination F2 generation plants. 2nd row 1-25 New Impr x Namangan 77 hybrid combination F2 generation plants. Line 3 1-13 BNL SSR marker Upland x Omad hybrid combination plants.

Selections from the F2 generation of New Impr x Namangan 77 hybrid combination with another SSR marker NAU922 [18, pp. 1–7] was carried out with. Namangan 77 sample has 1 allele at 190 base pairs, New Impr sample has two alleles at 110, 190 base pairs. In New Impr x Namangan 77 hybrid combinations, separations were observed in samples number 5, 14, 15, 20, 23 and gave the same bent as the resistant sample alleles (see Fig. 1). Even in this combination, cases of spider mite damage were observed in plants with the same alleles as the resistant sample alleles.

Conclusion.

Phenotypic and genotypic separation occurred in the second generation of hybrid combinations. Plants with resistance alleles were selected with the help of DNA markers, and starting materials resistant to spider mites were created.

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