

USE OF THE DOMINANT MALE- STERILITY GENE (Ms_4) IN COTTON BREEDING

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Abstract

Typical commercial cotton breeding involves the making of multiple bi-parental crosses and ultimately advancing near-homozygous lines. Use of random inter-mating in cotton has been shown to reduce negative associations of yield and fiber quality. However, the use of multiple parent population breeding with inter-mating has been rare in cotton breeding with a few notable exceptions.

The dominant male-sterility gene (Ms_4) can be a useful tool to facilitate large scale cross pollination in cotton improvement programs. The male-fertile (ms_4ms_4) genotype is ubiquitous in cotton germplasm. Progeny resulting from crossing a male-fertile (ms_4ms_4) plant to a male-sterile (Ms_4ms_4) plant, segregate 50% male-sterile and 50% male-fertile. A primary advantage of utilizing the dominant form of male-sterility is in the immediate derivation of homozygous male-fertile lines upon S_1 selection.

Five populations were developed utilizing the Ms_4 gene. The most advance population was developed to introgress resistance to cotton leaf curl virus (CLCuV) into elite U.S. germplasm. CLCuV is the cause of cotton leaf curl disease. This disease has not yet been found in the U.S, but is on the USDA list of top potential threats to U.S. agriculture. DNA markers to identify the Mac7 source of resistance to the Burewala strain of CLCuV and additional markers that identify the Multan strain of CLCuV were used to screen plants from the population. A total of 79 male-fertile plants and 66 male-sterile plants were identified and inter-mated. The male-fertile plants were self-pollinated and advanced for S_1 progeny rows. It is worth noting that the DNA markers used to identify resistance to the Multan strain of CLCuV are also used to identify resistance to cotton blue disease (CBD), commonly found in Brazil and other countries in South America.

Another population was developed to introgress germplasm from the USDA at Starkville, MS, having resistance to both root knot and reniform nematodes, into elite U.S. germplasm. Plants were screened with markers for nematode resistance, and the resulting crosses were selected to ensure presence of all positive markers in each combination.

A third population was developed to continually introgress elite germplasm into a diverse population. Each crossing cycle included top performing entries from the previous year's Regional Breeders Testing Network (RBTN) trials. Four cycles of crossing have been completed with plans to inter-mate the population in the next cycle.

Two additional Ms_4 populations were initiated involving sources from diverse populations developed by the USDA at Starkville, MS. RMPAP-C4 is a primitive race accession population, and RMBHMTUP-C4 is a tetraploid substitution population.

Plans are to release these populations as germplasm sources for cotton breeders. Each population would be released in two forms: as a segregating Ms_4 population for further development; and as a male-fertile S_1 bulk for line derivation.

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