

## **CONVENTIONAL COTTON BREEDING IN A TRANSGENIC WORLD**

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### **Abstract**

Cotton improvement activities in most public breeding programs are limited to the use of conventional or non-transgenic germplasm. However, public cotton breeders are often responsible for evaluating transgenic varieties and work in an environment surrounded by agronomic research trials and production fields which often include transgenic varieties. With the introduction of transgenic varieties, private seed companies were required to implement strategies to ensure that conventional varieties remained free of genetically modified organisms (GMO). Limited to the development of conventional breeding lines and varieties, many public breeders have not seen a need to evaluate conventional breeding material for the presence of GMO's. However, in an environment where transgenic varieties are now more common than conventional varieties, numerous sources of potential GMO contamination exist in a conventional breeding program. Parental material, outcrossing, and mechanical mixing, which may occur during ginning, delinting, packaging of seed, planting, and harvest, are all potential sources for GMO contamination of conventional breeding material. Publicly developed conventional varieties destined for the commercial market may be rejected if GMO contamination exceeds a specific threshold. The USA and European Union are in support of standardizing a limit of one percent GMO contamination for classification as a non-GMO or conventional variety. Public and private advanced breeding lines from the 2002 Regional Breeder's Testing Network (RBTN), as well as selected conventional commercial varieties from the 1999, 2001, and 2002 Mississippi Official Variety Trials, were evaluated for presence of the Roundup Ready® (RR) trait. Frequency of RR plants in each entry was determined by two applications of Roundup® (glyphosate) herbicide in field trials conducted over a two year period. Frequency of RR plants was determined after trait confirmation with a lateral flow immunoassay test strip. Commercial conventional varieties tested exhibited a very low frequency of RR plants. Several advanced breeding lines, however, exhibited frequencies of RR plants greater than one percent. Considering that the RR trait is just one of several possible transgenes, actual levels of GMO contamination in breeding lines is likely much higher than estimated. Results suggests a need for public cotton breeders to implement additional strategies to reduce GMO contamination of conventional breeding lines. Several tests are commercially available for detecting gene products of commercial transgenic varieties. Screening in the early stage of development and prior to seed increase would greatly reduce GMO contamination of public breeding material.