

Mapping an opaque-2 Modifier Gene by RFLP and Bulked Segregant Analysis.**Mauricio Antonio Lopes¹** and Brian A. Larkins²;**1 - CNPMS/EMBRAPA, CP 151 35701-970 Sete Lagoas, MG 2 University of Arizona - Tucson AZ - USA.**

We describe the use of bulked segregant analysis (BSA) in conjunction with restriction fragment length polymorphism (RFLP) analysis to map endosperm modifier genes in the maize genome. The results indicated that a modifier gene maps to the same chromosomal region where the storage protein genes known as gamma-zein are located. Also, PCR-based analysis indicated that variation in allelic composition at the gamma-zein locus correlates with variation in endosperm modification. In order to verify if specific cis-acting modifications are associated with gamma-zein gene sequences in modified *o2* genotypes, the cloning, sequencing, and comparison of these genes with other characterized alleles was also carried out. The results presented represent the first important steps toward the dissection of a complex modifier system. The understanding of *o2* modifier gene action promises to shed light on important aspects of seed development, seed physical structure and nutritional quality. In addition, knowledge of the genomic location of modifier genes will greatly facilitate the use of marker-assisted selection for their rapid transfer to elite inbred lines, thus facilitating the development of high yielding hybrids with superior nutritional quality.

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