

Public Abstract

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Title:Localization of the *Rf3* Restorer-of-Fertility Gene for Maize S-Type Cytoplasmic Male Sterility

The goals of this project were to fine-map and to identify the *Rf3* restorer gene of maize. *Rf3* restores pollen shedding to plants that have cytoplasmic male sterility (CMS-S). Because CMS-S plants are male sterile, they can be used by breeders to generate high-yielding hybrid corn without having to detassel plants. If *Rf3* is present in the plants used as males in the breeder's crosses, all the hybrid plants will have fertile tassels in farmers' fields. In this project, four lines were used that were nearly identical to a "non-restoring" inbred (NILs) except that they had *Rf3* introduced from different sources. Molecular mapping techniques, including single nucleotide polymorphism genotyping, localized *Rf3* to a 1.98 Mb region on the long arm of chromosome 2. Candidate genes for *Rf3* were selected from this region based upon the known characteristics of restorer genes. Six candidates, all predicted to code for mitochondrially targeted pentatricopeptide (PPR) proteins, were PCR-amplified, sequenced, and compared from four *Rf3* NILs and two non-restoring lines. One candidate had two sites that were consistently different between the fertile and sterile lines. Gene expression was analyzed in the 3 Mb region surrounding *Rf3* from the pre-emergent tassels. Only 9 genes were expressed differentially between fertility-restored and sterile lines, including genes that could code for an ATP-binding protein, an ATPase, and four PPR proteins. Even though *Rf3* was not identified, several possible candidates were found.