

LOCALIZATION OF THE *Rf3* RESTORER-OF-FERTILITY GENE FOR MAIZE S-TYPE CYTOPLASMIC MALE STERILITY

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ABSTRACT

Maize S-type cytoplasmic male sterility (CMS-S) is a maternally inherited trait that prevents pollen grains from developing to maturity. CMS-S is associated with the high levels of a novel mitochondrial transcript, *orf355/orf77*. Cleavage of this RNA, mediated by the nuclear restorer *Rf3*, reverses the sterility. *Rf3* was previously mapped on the long arm of chromosome 2. The goals of this research were to fine-map the locus and to identify *Rf3* using a candidate gene approach. Genotyping of near-isogenic lines (NILs) mapped *Rf3* to a 1.98 Mb region of 2L. Six candidate genes, all predicted to code for mitochondrially targeted pentatricopeptide repeat proteins (PPR), were PCR-amplified, sequenced, and compared from multiple *Rf3*-containing NILs and non-restoring *rf3* inbreds. One PPR-*Rf3* candidate gene had two consistent differences between multiple restoring and non-restoring lines. Gene expression in pre-emergent tassels from the fertility-restored and non-restored plants was compared. Within the 3 Mb region surrounding *Rf3*, 9 genes were differentially expressed between restoring and non-restoring lines, including genes that could code for an ATP-binding protein, an ATPase, and four PPR proteins. Although *Rf3* has not yet been identified, this study has revealed five promising candidates.