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Circular and linear mitochondrial genomes in cytoplasmic male sterile maize

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Cytoplasmic male sterility (CMS) is a maternally inherited condition in which a plant has an inability to produce viable pollen. It is usually due to the production of a toxic chimeric protein within the mitochondria during the maturation of pollen grains. In maize (*Zea mays*), there are three types of CMS: CMS-T, CMS-C and CMS-S. The S-type of cytoplasmic male sterility (CMS-S) in maize is associated with the expression of a rearranged mitochondrial DNA region. This CMS-S-specific region includes two co-transcribed chimeric open reading frames, orf355 and orf77. The nuclear restorer-of-fertility gene, Rf3, cleaves all transcripts containing both orfs, including the CMS-S-specific linear 1.6 kb mRNA; this results in male fertility. The Lancaster Surecrop-derived inbred line A619 carries a different and weaker restorer called Rf9. Fertility restoration by Rf3 and Rf9 was compared for their effects upon the CMS-associated region of mitochondrial DNA. Unlike Rf3, Rf9 affects the organization of the CMS-S-specific region. It appears to do this by affecting recombination between linear "S" plasmids and the CMS-S-specific region of the main mitochondrial genome, which produces a linear end from which transcripts for the 1.6 kb mRNA are initiated. By reducing the amount of recombination, Rf9 reduces the amount of linear template available for transcribing the S-associated 1.6 kb RNA. A reduction in this transcript is associated with an increase in pollen survival. We have studied the effects of the two restorer-of-fertility genes from several different inbred lines on the amounts of integrated and linearized orf355/orf77 genes within CMS-S mtDNA.

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