INVESTIGATIONS INTO THE CAUSE OF POLLEN ABORTION IN MAIZE CMS-C

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ABSTRACT

Cytoplasmic male sterility type C (CMS-C) is atypical compared to other CMS types as no novel chimeric transcript or protein has been found correlating with the phenotype. However, a tassel-specific decrease for both ATP6 and ATP9, which are mitochondrially encoded components of the ATP synthase F_0 subunit, was discovered in CMS-C. This decrease in levels was not observed when the *restorer of fertility gene* (*Rf*) was present. Other components of the ATP synthase complex analyzed did not appear to be altered in CMS-C, indicating that the cause of pollen abortion in CMS-C is affecting the stability or formation of F_0.

The CMS-C genome has two copies of the *atp9* gene. One is the normal copy of *atp9* (*atp9-1*), which is present in other maize cytotypes but is transcribed ~20 fold less in CMS-C. The other copy of *atp9* (*atp9-2*) is the predominant *atp9* transcript in CMS-C and has a chimeric 5'UTR resulting in the use of a different promoter and a larger transcript (4kb instead of 1kb).

We propose that the *atp9-2* transcript is inefficiently translated. When synthesis demand is high, as in the tapetum layer of an anther, the mitochondria are unable to compensate and ATP9 levels decrease. This results in the formation of fewer F_0 subunits and ATP synthase complexes, ultimately causing a reduction in ATP levels and abortion of the developing pollen.