Sequence of integrated S-1 homologous DNA in the normal maize mitochondrial genome

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Cytoplasmic male sterility (cms) in maize (Zea mays L.) is correlated with alterations in the mitochondrial genome. Four genetically distinct cytoplasms exist: N (normal) in which fertile pollen develops, and S, C and T in which pollen fails to develop [4,5]. Cms-S is characterized [4] by two free replicating elements, S-1 (6.4 kb) and S-2 (5.2 kb), which are not present in N, C or T cytoplasms. Sequences homologous to S-1 and S-2 are present in N mitochondrial DNA, but are essentially absent in T and C [5]. Reintegration of S-1 and S-2 DNA into mitochondrial DNA [1] or into nuclear DNA [2] is correlated with the restoration of fertile pollen development, suggesting that the S-1 and S-2 elements are derived from normal mitochondrial genes which control fertility and that loss or rearrangement of these genes gives rise to sterility. Our DNA sequence and Southern analysis show that the structure of the integrated S-1 homologous sequence in normal mitochondrial DNA shares 4.3 kb (bases 2588-6862) of homology with the free S-1 element (bases 651-4935 of [6]), and that it lacks the repeated termini and the 1.4 kb homology region (bases 4936-6397 of [6]) common to both the free S-1 and S-2 elements. Southern analysis of other normal maize strains [3] indicates that this structure, present in Zea mays Mo17 vg cms mitochondria, is not an aberration but is common to other N mitochondrial genomes. This DNA sequence appears in the EMBL/GenBank/DDBJ nucleotide sequence databases under the accession number X07041.

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