

An overview of plant mitochondrial genomes

Structure:

200 - >2500 kbp: wide variation, much larger than mammalian and fungal counterparts (10 -> 75 kbp)

much genome reorganization and/or rearrangement is observed in plant mitochondria

Evolution:

chloroplast sequences have been identified in mitochondrial genomes (and nuclear sequences in the mtDNA of one plant)

mitochondrial sequences have been identified in the nuclear genome as well; these include fragments of genes and entire genes as well

coxII in legumes: pea has a functional mitochondrial coxII, other legumes (soybean, cowpea) have partial or complete inactive coxII genes, and coxII is provided by a nuclear gene

ramifications: DNA can migrate between organellar compartments during evolution (mechanisms??); this may be accompanied by "activation" of genes in the recipient compartment

Coding capacity:

3 rRNAs (23S, 16S, 5S -> procaryotic)

ribosomal proteins (10)

at least 16 tRNAs (not enough for recognition of all codons -> tRNAs must be imported from the cytoplasm)

roughly 20 additional proteins of known function:

ATP synthase (3 subunits), cytochrome bp, NADH dehydrogenase (9 subunits), cytochrome c oxidase (3 subunits), genes involved in cytochrome c biogenesis (at least four genes); note that nuclear-encoded subunits are also needed for mitochondrial complexes)

Several as yet unassigned open reading frames

Gene structure:

poly- and mono- cistronic

procaryotic promoters

procaryotic translation initiation (SD sequences, etc.)

introns - Group I, Group II, nested, protein coding by introns

trans-splicing

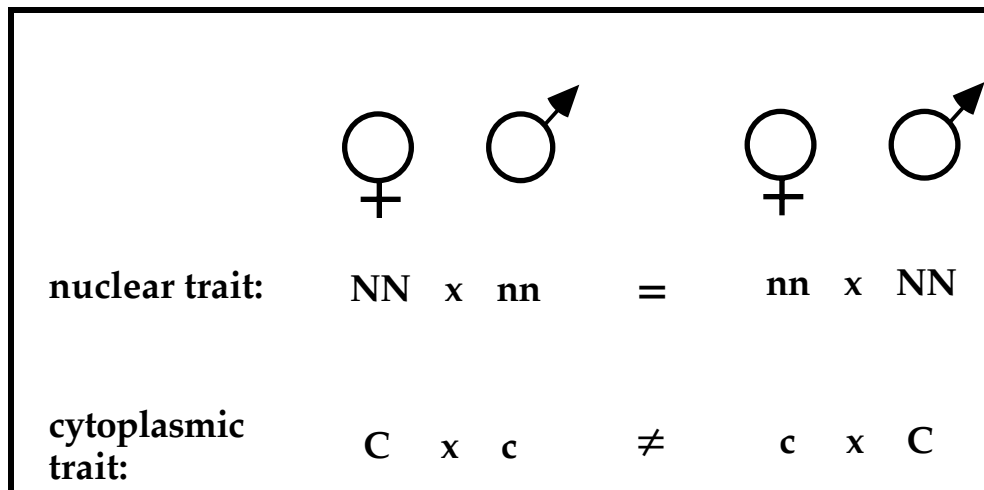
RNAs may be edited - C -> U, U -> C; editing is observed in protein-coding regions and in tRNAs and introns

Cytoplasmic male sterility and the interrelationship between nuclear and organelle genomes

cytoplasmic male sterility - cms: an important tool for plant breeders

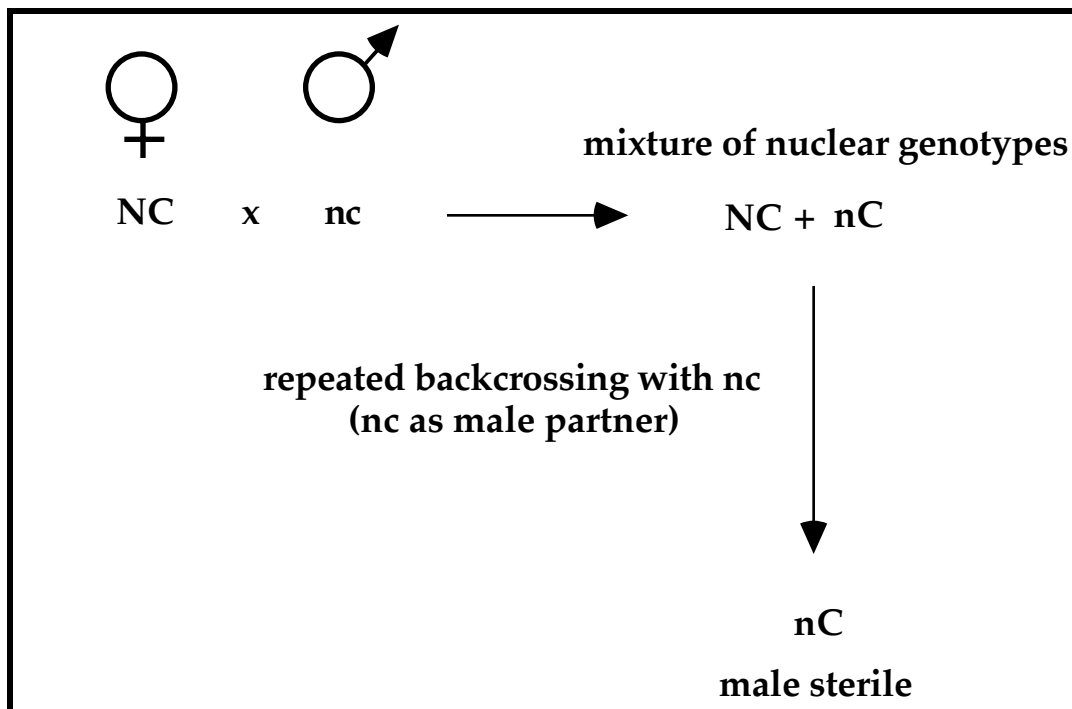
a mitochondria-associated trait

maternally-inherited (a cytoplasmic trait)



can be reversed by nuclear restored mutations

origin of cms traits - "engineer" distantly-related nuclear and cytoplasmic backgrounds:



cmsT - maize trait

cmsT maize are susceptible to race T of Cochliobolus heterotrophus

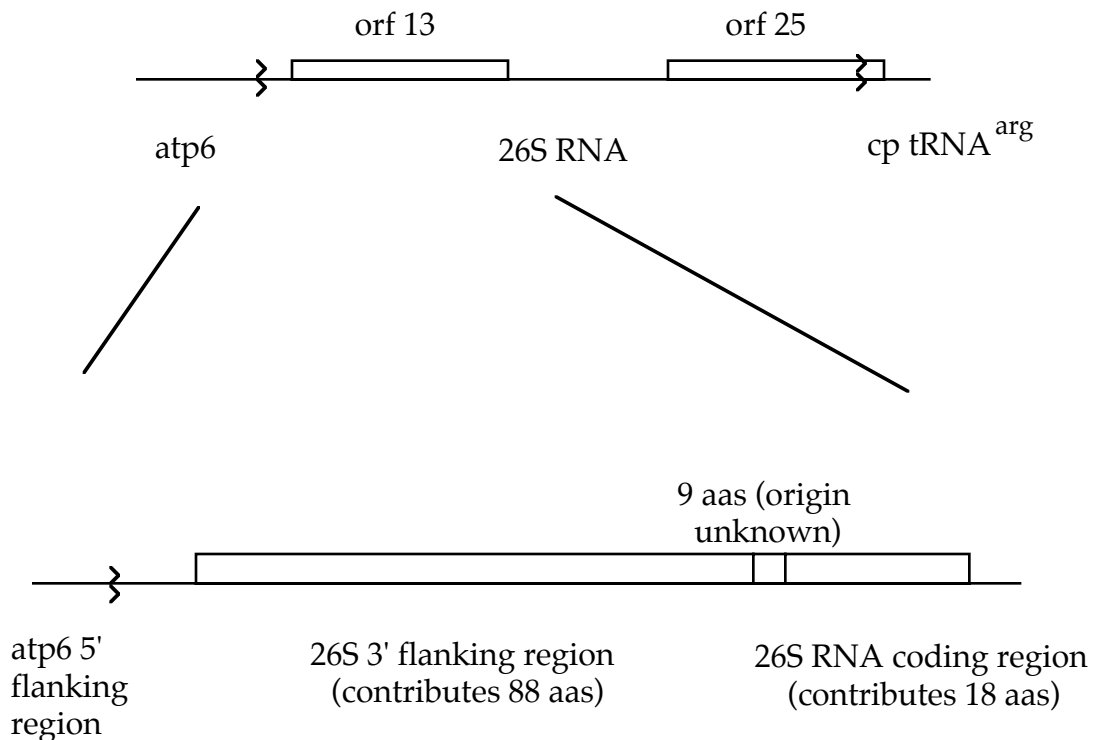
race T of C. heterotrophus produces a toxin that permeabilizes the mitochondrial inner membrane of cmsT maize

cmsT mitochondrial DNA has a different restriction enzyme profile than does wild-type maize mitochondrial DNA

one specific region is associated with cmsT, and its RNAs are specifically altered by nuclear restorers of cmsT

cmsT mitochondria possess a novel gene, capable of encoding a ca. 110 amino acid polypeptide (the so-called orf13 polypeptide, or P-orf13)

at least seven different recombination events are needed to yield orf13:



expression of orf 13 as protein is necessary and sufficient for cms trait:

nuclear restorers reduce P-orf13 (at the level of RNA)

mitochondrial revertants (to fertility and HmT resistance) specifically alter P-orf13 (frameshifts, deletions, etc)

P-orf13 causes respiratory dysfunction and uncoupling in yeast mitochondria in presence of HmT (the race T toxin)

P-orf13 confers HmT sensitivity upon E. coli