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This article has been cited by other articles in PMC. Abstract We evaluated the influence of mitochondrial haplotype on growth of the common button mushroom *Agaricus bisporus*. Ten pairs of heterokaryon strains, each pair having the same nuclear genome but different mitochondrial genomes, were produced by controlled crosses among a group of homokaryons of both wild and commercial origins. The growth of heterokaryon pairs differing only in their mtDNA haplotypes was compared by measuring mycelial radial growth rate on solid complete yeast medium CYM and compost extract medium and by measuring mycelial dry weight accumulation in liquid CYM. Statistically significant differences were detected in 8 of the 10 heterokaryon pairs evaluated for one or two of the three growth parameters measured. Some heterokaryon pairs showed differences in a single growth parameter at all three temperatures of incubation, suggesting a temperature-independent difference. Others showed differences at only a single temperature, suggesting a temperature-dependent difference. The influence of some mtDNA haplotypes on growth was dependent on the nuclear genetic background. Our results show that mtDNA haplotype can influence growth of *A.* These observations demonstrate the importance of including a number of mitochondrial genotypes and evaluating different nuclear-mitochondrial combinations of *A.*

Selected References These references are in PubMed. This may not be the complete list of references from this article. Attardi G, Schatz G. Annu Rev Cell Biol. Unraveling selection in the mitochondrial genome of *Drosophila*. Natural selection with nuclear and cytoplasmic transmission. Joint analysis of segregation and mtDNA in *Drosophila melanogaster*. Control of mitochondrial gene expression in *Saccharomyces cerevisiae*. Isolation of DNA from filamentous fungi and separation into nuclear, mitochondrial, ribosomal, and plasmid components. Nucleo-mitochondrial interactions in mitochondrial gene expression. Crit Rev Biochem Mol Biol. Nuclear migration and mitochondrial inheritance in the mushroom *agaricus bitorquis*. Junior Hospital Staff Contract. Rapid purification of yeast mitochondrial DNA in high yield. Competition between mitochondrial haplotypes in distinct nuclear genetic environments: Conditional hitchhiking of mitochondrial DNA: Human cells lacking mtDNA: Nonneutral evolution at the mitochondrial NADH dehydrogenase subunit 3 gene in mice. Neutral and non-neutral evolution of *Drosophila* mitochondrial DNA. Nuclear genes associated with a single *Brassica* CMS restorer locus influence transcripts of three different mitochondrial gene regions. Mitochondrial DNA sequence variation in human evolution and disease. Inheritance of DNA methylation in *Coprinus cinereus*.

2: Maize mitochondrial genes | Virginia K Eckenrode - www.enganchecubano.com

Volume , number 1 FEBS LETTERS December competition and is weakest in the breadth of subject matter covered. There is, for example, no.

This has been due primarily to the development of rapid and sophisticated molecular techniques. Mitochondria are bounded by an outer membrane that surrounds a highly folded inner membrane. The capacity to isolate genes by inter-molecular cloning and to analyze them at the nucleotide level membrane space separates the two membranes and has been a major contributor to our increased knowledge. The Genes can now be analyzed for their informational content as major structural elements of mitochondria are proteins well as for regulatory elements affecting their expression. There are to different polypeptides in the electron transport is linked to ATP formation. Plant cells are protein component. Chloroplasts convert light energy into chemical energy and use it to reduce carbon dioxide to carbohydrates. Mitochondrial biogenesis is the consequence of coordinated interactions between the nuclear and mitochondrial genetic systems. Thus, plant cells differ from and mitochondrial genetic systems. This interaction is other eukaryotic cells by containing three distinct genomes: The are now analyzing the specific genes and gene products nuclear genome is the largest of the three and is inherited in a non-Mendelian fashion through the maternal parent. In maize, the haploid nuclear genome is approximately 5. In essential polypeptides and structural RNAs. Although contrast, the chloroplast and mitochondrial genomes are much smaller and are generally inherited in a non-Mendelian fashion through the maternal parent. In maize, the chloroplast genome is approximately 120 kb in size, whereas the mtDNA genomes are the smallest and range from 14 to 18 kb in size. The animal mitochondrial genes are very small and are generally inherited in a non-Mendelian fashion through the maternal parent. The animal mitochondrial genomes consist of naked DNA, that is DNA which is not tightly packed on a small circular molecule. Even though tightly complexed with proteins to form chromosomes. Much fungal mtDNAs are organized in circles up to nine times more is known about nuclear genes than organelle genes, larger than mammalian mtDNAs, from 19 to 25 kb in size primarily because Mendelian genes and their mutants are 41, they encode a similar number of genes. The "extra" more abundant and more easily studied. The Plant mtDNAs are much larger and more variable than following sections describe our current knowledge of the those of other organisms. Plant mitochondrial genomes mitochondrial genes in maize and some other higher plants. Even within a single family, the cucurbits, there is a dramatic eight fold difference in mtDNA size, with watermelon at 120 kb and muskmelon at 15 kb. Although plant mtDNA contains a variety of ways. Finally, those involved in glycolysis, phospholipid metabolism, and protein import arranged in a single circular molecule, whereas plant are found in the outer membrane. Restriction ized from the maize mitochondrial genome Table 1. Plant mitoribosomes differ from those of maize 57 have provided insight into their organization. The largest circle is 16S distinctly larger than the animal and fungal counterparts length, and contains the entire sequence complexity of In comparison, animal mitoribosomes contain 16S the Brassica genome. The maize mitochondrial 18S rRNA is the circle, and 83 kb from each other. Recombination even larger than its cytoplasmic counterpart; the between the two repetitive elements produces two circular mitochondrial subunit contains nucleotides nt 17 molecules of and 83 kb. This accounts for the two and the cytoplasmic nt An analogous model has eukaryotic cells All 5S rRNA species are related in been proposed for the organization of the maize primary and secondary structures, but those from plant mitochondrial genome 57, although the maize organiza- mitochondria differ sufficiently from the others to be tion is more complex than Brassica. The maize considered in a group of their own A larger arranged in a way unique to plant mitochondria. Those participating in nucleic acid replication, tran- RNA processing enzymes scription and translation, the tricarboxylic acid cycle, fatty Intron 2 CoB maturase -- ? Sequence analysis indicates maize the universal and the animal and fungal mitochondrial mitochondrial rRNA genes [18S 17, 5S 16, 26S

22] are codes. There is a single codon difference between the very similar to other plant mitochondrial rRNA genes universal code and the plant mitochondrial code. Plant mitochondrial mitochondria 4,23,34,45,47,49, The UGA codon, rRNAs show greater primary and secondary structural which specifies tryptophan in other mitochondrial similarities to bacterial and chloroplast rRNAs than to systems, seems to function as a terminator in plant mammalian or fungal mitochondrial or cytoplasmic mitochondria, as with the universal code 9, Two maize methionine tRNA methionine, sometimes as an initiator methionine The fact that two separate methionine mitochondrial genes have been deduced by comparison tRNA genes have been identified in maize mitochondria with mitochondrial polypeptides in other systems. UAG, and UGA, are assumed to function as translational Plant mitochondria probably contain at least as many signals in plant mitochondria. Finally, a strong bias for tRNA genes as the 25 found in yeast mitochondria, where thymine and adenine residues in the third codon position separate methionine initiator and elongator tRNA genes exists in maize mitochondrial genes 9,23,26,27,34, In animals, tRNAs are frequently situated apocytochrome b cob from maize 23 and *Oenothera* 83 , immediately adjacent to protein-coding sequences and Fo-ATPase subunit 6 atp6 from maize 26 , Fo-ATPase are important in processing the mitochondrial polycistron- subunit 9 atp9 from maize 27 , and F,-ATPase alpha ic message Most of the mitochondrial tRNA genes subunit atp-alpha from maize 9. All of these polypeptides of yeast and other fungi are clustered into several groups are associated with the inner mitochondrial membrane and are However, in both *Neurospora crassa* and *Torulopsis* involved in electron transport or phosphorylation events. The three maize mitochondrial general, plant mitochondrial polypeptides show no tRNA genes examined are neither immediately adjacent greater similarity to the animal polypeptides than to to protein-coding genes nor located closely to each other fungal. They are situated on both strands of maize The mitochondrial location d the F,-ATPase alpha mitochondrial DNA, indicating that both strands are gene is unique to plants. In both animals and fungi, this transcribed Bonen and Gray 5 indicate that in subunit is encoded in the nucleus Hack and Leaver wheat most of the mitochondrial tRNA genes are scattered 42 have suggested that the maize atp-alpha gene is throughout the genome, but that some tRNA genes are located in the mitochondria because their studies show clustered, especially in the area of the 18S and 5S rRNA the alpha subunit is the product of mitochondrial protein genes. This has been confirmed by Spencer et al. The characterization of an actively tran- rRNA gene. Whether any tRNA nucleotide and predicted amino acid homologies to the genes or tRNA-like structures are located in close atp-alpha gene from *Escherichia coli* and tobacco proximity to maize mitochondrial genes remains to be chloroplast extends the evidence that the maize polypep- determined. The 44 *Neurospora* largest detected transcripts are huge relative to their atp- protein-coding regions. The nt R N A species alpha tg proposed as the primary transcript for the atp9 gene is almost nine times larger than the nt coding region An analogous situation exists with the Fo-ATPase Little is known about the events responsible for subunit 9 gene; it is a nuclear gene in animals and splicing introns and processing the primary messenger *Neurospora* 84 , but is a mitochondrial gene in yeast 44 R N A in plant mitochondria. DCCD-binding studies with in vitro The complexity of maize mitochondrial transcriptional translational products indicate that the maize mitochon- patterns is partially explained by chimeric genes, where drial atp9 polypeptide is synthesized in mitochondria short regions of D N A homologous to one gene are present Curiously, in addition to the nuclear atp9 gene 84 , within the transcriptional unit of another gene. Although within the protein-coding region of maize atp6 Due to the conservation of the mitochondrial ntp9 gene and the lack of stop codons within its open reading frame, van den Boogaart et al. Interestingly, only one plant mitochondrial gene, Coding Intron Transcript cytochrome oxidase subunit II, contains an intron. Coding regions for c o i l have been described from five plant species, maize 34 , rice 49 , Protein Coding Genes wheat 4 , *Oenothera* 45 and pea Of these, an intron col "7 -- , is found in the c o i l gene of the three monocots, but not in coil s2 ,, , the two dicots. Additional studies indicate that the intron , , is absent in bean and cucumber c o i l genes 4. Interestingly, an insertion sequence Structural RNA Genes is found at the same position in the introns of the rice and wheat genes 4, All three plant mitochondrial introns 5S rRNA "6 There is no indication that the InitiatorPTM 74 --? A similar situation may exist with a maize coil However, Ise et al. Furthermore, Brown et al. These findings conserved sequence thought to be important in transcrip- indicate that genes encoding subunits of the NADH-Q tional initiation in

yeast They note that both transcripts originate from a maize mitochondrial genome. Due to the and it has not been rigorously demonstrated that either prokaryotic nature of the structural RNA molecules, a sequence plays a role in transcription. Transcriptional ter- full set of 32 tRNA genes may be encoded in maize and mination has not been studied in plant mitochondrial genes. Steitz and Jakes 91 been identified As yet a similar gene has not been reported that sequences complementary to the Shine- reported in maize mitochondria. The nucleotide potential ribosome binding sites. It may be that they code for proteins may be a ribosomal binding site. Additional experimental important in the replication and maintenance of the verification is needed to determine whether this sequence plasmid-like molecules, rather than typical mitochondri- functions as an mRNA recognition site. Finally, approximately 30 polypeptides are synthesized by isolated maize mitochondria Some protein-coding genes that have not been identified in the of these may be similar to those already reported in maize mitochondrial genome. These include genes for mitochondria of other organisms. Recently, the products of six human mitochondrial unique genes may be identified. This leaves one expressed open reading frame 62 unassigned Mitochondrial mutants are rare in higher plants, in mammalian mitochondria. Sequence and susceptibility 54 , and nonchromosomal stripe mutants organization of the human mitochondrial genome. Two ncs mutations have been described and 2. Different each correlated with specific changes in their m t D N A pattern of codon recognition by mammalian mitochondrial restriction fragments. Sequence and gene organization of mouse mitochondrial DNA. Cell The cytoplasmic male-sterile trait is encountered in Although the specific 4. The wheat cytochrome mechanisms causing male sterility may differ from oxidase subunit II gene has an intron insert and three radical species to species, the cms trait is characterized by the amino acid changes relative to maize. Organization and expression of the non-Mendelian pattern of inheritance. Abundant evi- mitochondrial genome of plants I. The genes for wheat dence suggests that the cms trait in maize is due to a mitochondrial ribosomal and transfer RNA:

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