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Opinion Article

Origin and Evolutionary Mechanism of Plant Mitochondrial Genome

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DECSRIPTION

The intergenic portions of the angiosperm mitochondrial genome have been extended, making it the largest and least gene-dense of the eukaryotes. The size of the intergenic sections does not appear to be functionally constrained, and angiosperms continue to have enormous mitochondrial genomes for reasons that are now unknown. Sequence data has shed light on the reasons behind the genetic expansion in the mitochondria of angiosperms. The intergenic areas appear to be larger than those of other creatures, as was already mentioned. It seems that at least two pathways contributed to the creation of intergenic areas. One is the exchange of sequences from different cellular compartments or even from other organisms, such as species that are not able to reproduce together. The evolution of the mitochondrial genome in angiosperms is probably influenced by both of these methods.

1.6% to 8.8% of the mitochondrial genomes of seed plants include plastid-like sequences. The majority of these sequences are found in the intergenic areas, but it has been noted that a plastid atpA sequence has taken the role of an internal mitochondrial atp1 gene segment. The plastid-like sequences play a number of functions, one of which is to supply tRNA genes for mitochondrial translation. As demonstrated by the rice nad9 gene, plastid-like regions can also serve as promoters for mitochondrial genes. The intergenic sections of the mitochondria of angiosperms also contain nuclear-derived sequences, which make up 0.1% to 13.4% of the mitochondrial genome. Rarely, the angiosperm species share these nuclear-like sequences, and no known function has been identified as of yet. It should be highlighted that since more than 60% of the intergenic regions exhibit no similarity with any other sequences, the known amounts of DNA that are known to be derived from external sources, such as plastids and the nucleus, are insufficient to explain the origin of the entire intergenic sections. Since the public database does not currently contain all of the extant sequences on Earth, this does not imply that the remaining intergenic regions are unique.

In other words, it's probable that some of the intergenic areas of the mitochondria of angiosperms have been horizontally transferred from species, such as non-plant creatures, that are sexually incompatible. There is growing proof of horizontal translocation into angiosperm mitochondria. From one plant to another is another source of horizontal transmission. Based on phylogenetic anomalies, certain research teams assert that mitochondrial genes in various plants, including the Amborella nad5 and Actinidia rps11 genes, appear to have been horizontally transported across plant species. The intergenic sections of angiosperm mitochondria may have undergone significant sequence modifications as a result of duplications, inversions, insertions, and deletions, to the point where homology searches are unable to pinpoint the original sources of some sequences. The evolution of angiosperm mitochondria has been characterized by many instances of homologous recombination. Short (less than 25 bp) sections of mitochondrial genes or other recognized sequences are occasionally discovered when the intergenic regions are thoroughly examined. These could be the remains of significant rearrangements.

Cucumber has the second-largest mitochondrial genome to date, of which 136 kb have been sequenced, making its mitochondrial genome as a good case study of genome expansion. A study of the acquired sequences showed that 15% of the region is made up of repetitive sequences that can be classified into seven families. This finding suggests that duplication can, at least in part, account for the genome's expansion. Although certain sequence similarities have been discovered within 100 bp upstream of several angiosperm mitochondrial genes, overall sequence conservation among the intergenic regions of angiosperm mitochondrial genomes is too low to establish any major functional constraints on these regions. Furthermore, intergenic regions could have sequences that are unique to a particular mitotype and not found in other mitochondrial genomes. Although the rate is occasionally accelerated in some particular plant lineages, it is well known that the rate of nucleotide substitution in angiosperm mitochondrial genomes is quite low when compared to that of other organisms.

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On the other hand, even within closely related species, one may easily detect variations in the organization of mitochondrial genes. As a result, angiosperm mitochondria rarely include a gene cluster that is conserved in the mitochondrial genomes of algae or mosses.

Homologous recombination between repetitive sequences appears to be the main mechanism of genome rearrangement. Recombination would be unchecked in mitochondria, which would degrade genomic performance. In fact, deletions and losses of mitochondrial genes due to homologous recombination at short repetitive sequences have resulted in mitochondrial mutants with respiratory abnormalities. Over many generations, the mitochondrial genome's structure typically remains unchanged. However, recombination by short repetitions has occurred on an evolutionary scale, and such mtDNA has taken over. The mitochondrial genome is exclusively inherited from the mother in the majority of angiosperm species. Nevertheless, paternal leaking has been observed in a few of cases and could be a factor in heteroplasmy. To become apparent as a genomic mutation, the altered sublimon must be amplified to the level of the main mtDNA molecule. Such increases in the copy numbers of sublimons might originate from physiological stress or mutations in nuclear genes. Substoichiometric Shifting (SSS) is the term for this occurrence and the quick drop in mtDNA copy number to a substoichiometric level.

Even in the absence of any mutations, the SSS-like behaviour can be seen. One well-known illustration is tissue culture, which can alter the quantity of copies of particular mtDNA molecules. This shows that developmental stimuli may be the cause of SSS.

The meristem and the egg, where the "transmitted form" of the mtDNA, having all components of the genome including sublimons is predicted, are the tissues or organs where SSS might occur.