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Mitochondrial Biogenesis Discharging in *Labyrinthulea*

Siyuan Ding*

Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, USA

***Corresponding author:** Siyuan Ding, Department of Molecular Microbiology, Washington University School of Medicine, St. Louis, USA, E-mail: dings@gmail.com

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Editorial Note

Mitochondrial translation frequently deviates from the usual genetic code, but the full range of these modifications has yet to be identified and the molecular mechanisms behind these alterations in codon meaning are rarely investigated. The mitochondrial genetic coding in the stramenopile group *Labyrinthulea* (Labyrinthulomycetes) and its relatives has been studied in depth. In the genus *Aplanochytrium*, UAG is not a termination codon but rather encodes tyrosine, as opposed to the UAA codon's unaltered meaning. The distribution of sense-to-stop and stop-to-sense reassignments correlates with specific modifications of the mitochondrial release factor mtRF2a in different subsets of labyrinthuleans, as well as the unprecedented loss of mtRF1a in Aplanochytrium and possibly also in the LAB14 clade, suggesting a possible mechanistic basis for the observed code changes.

A sense-to-sense codon reassignment has also been observed in labyrinthulean mitochondria, with AUA encoding methionine rather than isoleucine. Change, along with the reassignment of the AGR codons from arginine to serine, developed separately in the uncultivated stramenopile lineage MAST8b.

The "universal" genetic code is used by most translation systems across the tree of life, but there are exceptions to every norm in biology. Mitochondrial DNA has proven to be the most fertile ground for the evolution of modified genetic codes. This is not surprising given that mitochondrial genomes have a small number of genes and hence codons, as well as a nucleotide composition bias that causes some codons to be rare or even nonexistent. These codons are prone to propagating throughout the mitogenome with a new meaning. The UGA codon, which ordinarily signals translation termination but has been reassigned to encode tryptophan in many mitochondrial lineages, is the most prevalent codon reassignment. However, unlike nuclear genomes, mitochondria regularly exhibit numerous sense-to-sense reassignments, such as shifts of codon meaning to other amino acids.

Finally, some mitochondria have been found to exhibit the third type of codon reassignment, known as sense-to-stop reassignment, which is not seen in non-mitochondrial translation systems. This type of alteration has been observed in some green algae and vertebrates, albeit the specific mechanism by which the non-standard codons effect translation termination is unknown or debatable.

The topic of how UUA recognition as a termination codon is performed mechanistically remains unresolved despite the intriguing discoveries. The capacity of mitochondria from the green algal group Scenedesminia to use the codons UCA and UCG as non-standard termination codons is thought to be due to changes in the mitochondrial releasing factor mRF1a.

Changes in the meaning of mitochondrial UAG and UAR codons in the Aplanochytrium and LAB14 lineages could be evolutionarily independent, albeit they could be influenced by the same underlying processes that have influenced the evolution of the mitochondrial genetic code in Labyrinthulea. The UAG codon is completely absent in all thraustochytrids, which is interesting.

The capacity for a mitochondrion to self-replicate is planted in its evolutionary history. It is casually thought that mitochondria descend from cells that creates endosymbiotic interbonding with α-protobacteria; they have their own genome for reproduction. However, current evidence suggests that mitochondria may have developed without symbiosis. The mitochondrion is a key regulator of the metabolic activity of the cell and is also an important organelle in both production and degradation of free radicals. It is postulated that higher mitochondrial copy number (or higher mitochondrial mass) is shielding for the cell.

Critically, mitochondrial numbers and morphology vary on the report of cell type and context-specific demand, by means of the balance between mitochondrial fusion/fission regulates mitochondrial distribution, morphology and function.