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**Coding For Medicine Club**

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**Novel genetic code and record-setting AT-richness in the highly reduced plastid genome of the holoparasitic plant Balanophora - Huei-Jiun Su, Todd J. Barkman, Weilong Hao, Samuel S. Jones, Julia Naumann, Elizabeth Skippington, Eric K. Wafula, Jer-Ming Hu, Jeffrey D. Palmer, and Claude W. dePamphilis**

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Significance   
  
Flowering plants have begun to become parasitical in nature, as they are unable to carry out photosynthesis. The plastids, which include the chloroplasts, of these plants are reduced in size and gene content. The *Balanophora* plant has a very simple plastid genome that is exceptionally streamlined, has evolved a novel genetic code, and possesses the most A and T rich protein coding genes known. These findings allow us to understand the lower limits of genome complexity as well as the mutational and selective forces that drive evolution more deeply.

# Abstract

Balanophora plastomes are one of the most reduced plastomes known. They have no tRNA genes for protein synthesis, meaning they have to import all tRNAs. Their genes overlap, have reduced spacers, have lost all “cis-spliced” introns, and have shrunken protein genes. They are the most A T rich genomes known, and have the most biased codon usage known.

Nonphotosynthetic angiosperms vary much more in size, generally smaller, and gene content, also smaller, as well as GC Base composition, smaller, when compared to photosynthetic ones.

The Balanophora plants are the most bizarre plants observed. They possess some of the smallest flowers in the world. Their plastomes contain novel genetic code that marks the first case of code change in land-plant plastomes, and sets a record for AT-richness and codon usage.

# Results

The plastomes of the balanophora contained very minimal spacers, meaning most of the protein genes are probably annotated. The balanophora genes are collinear with most other angiosperm genes except for a single gene, and unlike most plastomes, those of balanophora lack a large inverted repeat.

The genes of the balanophora are extremely compact and overlap more than usual. The intergenic parts of the plastome are very short.

The protein genes of the plastomes are very sparse in GC content, while the rRNA areas are relatively GC rich. When compared to other AT-rich genomes, the balanophora plastomes were more compositionally biased and were only surpassed by a mitochondrial genome who’s non coding areas contained most of its AT rich content.

Scientists have found that there was a genetic code change - the reassignment of TAG from stop corn to Trp codon, accompanied by the discontinuation of TGG- that occurred in the ancestral balanophora plastome.

The genes in the plastome are found to be highly divergent but still functional.

Balanophora tissues, instead of testing positive for starch storage, showed signs of lipids within themselves.

# Discussions

Balanophora has shown to create new benchmarks in many aspects. Only 2 different non photosynthetic plants, which are all known to evolve radically, share the aspects of compactness and the importation of all tRNA. None approach Balanophora in AT richness, codon usage bias, or having novel genetic code.

Novel genetic code has been seen in other genomes, especially mitochondria. However, the use of TAG as tryptophan is a novel code variant that sets balanophora apart. The reassignment can be explained by the codon capture hypothesis, which states that increased AT richness would cause loss of TAG stops in response to mutation to TAA stops. Duplication of the gene for plastid tRNA(trp) would allow one copy to mutate such that its product recognizes UAG (in the mRNA), which would then allow for the mutation of TGG to TAG (in the DNA), both being deciphered as tryptophan in Balanophora. Because of the AT richness, the extra G in TGGs would be replaced by the A in TAG. If other balanophoraceae plastomes are also AT rich, they may have traveled a different evolutionary pathway and sustained the relatively common TGA-for-Trp change rather than the TAG change.

Once again, the Balanophora is the most extreme genome known in any organism or genetic compartment when it comes to AT content.

The intense streamlining in Balanophora is, as with its AT content and codon-usage bias, driven predominantly by neutral, runaway mutational forces, in this case by exceptionally high deletion rates.

The Balanophora plastome is still functional despite its compaction. It lacks tRNA genes, meaning it needs to import all tRNA.

Due to the large number of TAG codons within the Balanaphora’s plastids, which are novel and cannot be transferred back into the nucleus, it is unlikely that gene transfer to the nucleus will be possible for the angiosperm. This means the plastid DNA may permanently lock in some of its remaining genes and thus the genome itself.

# Material and Methods

An ORF finder was used to read frames of the genetic sequences in the plastome assemblies. This would allow all possible amino acid combinations to be shown, as individual reading frames correlate to different chains of amino acids. Then, through the use of bioinformatic technologies such as DOGMA and BLAST, they were able to locate the start and stop codons based on their position relative to the expressed genes.

# Questions

What does compression of plastomes mean exactly for the future of angiosperm organisms in a larger scope.

Why does Balanophora contain oil reserves in its tissue instead of starch reserves?

Why exactly do holoparasitic plants contain so little GC content?

# Problem to Solve

# The article shows how the plastome of balanophora is able to store TAG/UAG as tryptophan, while being a stop codon in the nuclear and mitochondrial genomes of the same organism. We can try to observe why exactly TAG is able to be interpreted as tryptophan in the plastids of the organism.

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