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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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Date: 11/23/21

Abstract

Hemiparasitic plants range from being fully to minimally photosynthetic, whereas holoparasitic plants aren't at all. They depend on a host plant for materials, and as such, it makes sense why their genome would be different from regular photosynthetic organisms. One of the indications of a holoparasitic species is their small genome size, which may result from the fact that they do not need to create as many proteins as other plants to survive because they can 'steal' such materials from host plants. Additionally, many of the genes in the plastomes of photosynthetic plants code for proteins relevant to photosynthesis. These genes are not useful for holoparasitic plants, so it makes sense that their genome would get rid of them and thus have a smaller size.

Significance

The parasitic plant *Balanophora* is extremely compact, has the most A+T-rich genetic code, and has a new genetic code. As such, it is a worthy

topic to study, and following the evolutionary history of the plant can highlight crucial processes as to how organisms modify their genome over time. In addition, the unusual genome of the *Balanophora* may also be linked to its unusual morphological characteristics.

Results

The *Balanophora* plant typically has a tiny genome length compared to other plants and has a tRNA gene that has only one function (which is unlike most other plastid lineages). Additionally, the plant has an unusually high density of A-T base pairs and overlapping genes. The reason for *Balanophora* compact genome has to do with how the intergenic spacers between genes are very short as well as how the plastid protein genes overlap and are shorter than usual. This observation leads me to think that organisms with a small genome are more likely to be parasites, as small genomes are unlikely to create a wide variety of proteins a regular organism would create. The functional nature of the genes that remain in *Balanophora* also imply that humans can potentially compact genes for protein synthesis and thus reduce the amount of materials to create certain proteins (ex. insulin).

Discussions

Balanophora plants are atypical in how unlike any other organism, TAG (instead of TGA) codes for tryptophan. Additionally, the aforementioned plant is the first land plant to differ from the dominant genetic code. Probable mechanisms behind this fact are the mutation drift model and G/C to A/T replacements in DNA replication. An implication of this is that parasites may be evolving/have evolved to adapt to their own genetic code as a result of tRNA protein deficiencies, thus meaning that there are potentially more land plants out there that have a unique genetic code yet to be found.

Material and Methods

Illumina MiSeq, Illumina HiSeq2000, PAGIT, SAM-tools, and Blast were all used to assemble the *Balanophora* genome and do analysis. The Illumina

HiSeq2000 trimmed the raw sequence reads of DNA from the two species of *Balanophora* mentioned in the article, and BLAST was used to check if genes overlapped. PCR amplification was also used to validate the plastome assembly of *B. laxiflora*.

Questions

What does the position of the window center in a gene tell us? What is its significance?

What does the d_n/d_s ratio tell us?

Why does the *Balanophora* lineage store oil droplets in plastid instead of starch reserves?

Why haven't some photosynthetic organisms shortened their genome over time if holoparasitic plants can get by with an extremely compact genome? Is there some disadvantage to having a compact genome that prevents photosynthetic plants from compacting their genome?

Problem to Solve

The researchers in the article tried to find a viable explanation as to how the nuclear and mitochondrial genomes use UGG for Trp and UAG as a stop codon even though the plastid genome uses UAG for tryptophan. No plastid-like trnW could be found using BLAST; Therefore, we can try to look into the genome of *Balanophora* plastids could uncover the specific candidate translational components needed to explain how the plastid genome can use UAG in place of UGG for tryptophan G.