
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

There has been a growing number of parasitic flowering plants that have plastid genomes of a smaller size and reduced gene content. One of these groups of plants is the *Balanophora*, which has developed a novel genetic code in its miniaturized plastid genome. Investigating this plant helps us better understand limits of genome complexity and the causes of radical genome evolution.

Abstract

Although plastomes are known to vary greatly in size and gene content, two investigated *Balanophora* plastomes have features that are rarely seen in other genomes. The two plastomes are some of the most reduced plastomes known and have no tRNA genes. The genomes are also one of the most AT-rich genomes, which is a potential consequence of the genetic code of the *Balanophora* plastids. There is also a significant difference in the plastomes of photosynthetic and nonphotosynthetic angiosperms. The nonphotosynthetic angiosperms vary much more greatly in size and gene content and have lost many of the genes that are involved with photosynthesis, ATP synthesis, and transcription. The holoparasitic Balanophoraceae are some of the most intriguing angiosperms because the family includes many bizarre plants. Their plastomes are also found to be unusual with the first case of a code change in land plant plastomes.

Results

Both analyzed Balanophora plastomes had a similar length that consisted of genes coding for similar functions and both were found to have a single tRNA gene. The Balanophora plastomes have a high percentage of overlapping genes, and the many overlaps of the genomes likely arose from a common ancestor due to continued downsizing of the genome. The plastomes were found to be extremely AT-rich in comparison to many other gene sets. However, the study could not support that the reason for this occurrence was due to greater efficiency or nitrogen availability/energetic costs. Analysis of the Balanophora plastomes also resulted in the conclusion that a genetic code change resulted in reassigning TAG from a stop codon to a Trp codon and the discontinuing of TGG usage. The Balanophora plastid genes have a relatively high divergence, but are still likely to code for functional proteins. Lastly, the Balanophora tissues were found to contain lipids that could possibly have been synthesis in plastids.

Discussions

The novel genetic code in the Balanophora plastome could be explained through a variety of hypotheses, such as the codon-capture hypothesis or the translation hypothesis. The codon-usage bias of Balanophora is likely explained by mutational forces and natural selection, which have led to high deletion rates. These unique features of the Balanophora plastome likely indicate that it will be lost in a gene transfer to the nucleus.

Material and Methods

The assembly and analysis of the plastomes in the Balanophora plants was done by a variety of bioinformatics tools, such as BLAST, ORF Finder, and DOGMA, and was validated through PCR amplification. The GC content was analyzed by CodonW 1.4, and the nuclear codon usage was analyzed with the help of GenBank.

Questions

What could be the cause for the unusual amount of lipid droplets in the Balanophora tissues?

Would the loss of the Balanophora plastome to the nucleus have a large impact on the functioning of the plant?

When did scientists begin to realize this increase in the evolution of novel genetic code in plastid genomes?

Problem to Solve

The scientists in the article were unable to come to a conclusion that would support their hypotheses as to why the *Balanophora* plants used TAG as a codon for tryptophan rather than its more common function as a stop codon.