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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

Plants with reproductional organs have lost the capability to carry out photosynthesis and have become parasites. Additionally, through further research, it can be stated that parasites are defined as angiosperms(flowering plants with reproductional organs) who develop haustoria roots which deprive them of the capability of undergoing photosynthesis, due to the roots extracting water and nutrients from the plant. A mushroom-like parasitic plant known as the Balanorpha has a prominence of parasitism, which I can infer may be due to the unique genetic code it has of a great number of adenine and thymine codons. This research provides us with an interesting chance to study the effects of genetics on genome evolution, and combine the studies of molecular biology and evolution which differ in their outlook on discovery with respectively reductionist and systemic thinking.

Abstract

Plastid genomes(chloroplast DNA) have a great variation in size and genetic content across nonphotosynthetic plants, however, parasites have a greatly reduced form of these genomes within them. The parasitic Balanorpha plastid genomes lack many features found in

standard plastids, such as the ability for protein synthesis resulting in it being forced to import all tRNAs needed for translation. Through some research, I realized that genomes with a high quantity of guanine and cytosine bonds are more stable due to the extra hydrogen bond it has over adenine and thymine bonds, alongside being highly associated with features such as gene density, size, and methylation patterns. I can infer that parasites find it easier to evolve in organisms with smaller amounts of Guanine and Cytosine bonds, thus increasing the percentage of adenine and thymine bases within the plastid. Although 90% of parasites are hemiparasites (undergo partial photosynthesis) 10% are holoparasites (no photosynthesis at all).

Results

The Balanophora plastids the *Balanophora laxiflora* and *Balanophora reflexa*, have incredibly similar genomes due to indels(mutations) in each genome which balance out in length, allowing us to infer that parasitic mutations occur similarly within both of these species. They both have 19 functional genes in common, with no organelles or features that are used in Glycolysis, The Krebs Cycle, the Electron Transport Chain, or even Transcription. This realizes an interesting idea, that the parasitic mutation cripples all processes that require energy due to depleting the plant's capability to gain energy, this may force the plant into finding a host to gain nutrients from to survive, or simply dying. Due to the modification or absence of a UUC codon, which is necessary to undergo protein synthesis, within both plastids, they cannot code for proteins leaving them vulnerable.

Balanophora plastids typically have unusually high gene densities(ratio of the number of genes per the number of base pairs) which is calculated by finding the number of genes per million base pairs. This means that Balanophora plastids would have a high number of overlapping base pairs (nucleotides coding for more than one protein) which through my research occurs due to the genome length being compressed, but being forced to code for the same number of proteins. This would tie into the article's previous statement of the genome being reduced by the parasitic mutation, and result in parasitic plastids being greatly more compact and thus having a higher gene density. Also, Balanophora plastids have a great number of deletion indels (deleting mutations) reducing gene length. This leads me to theorize that deletion indels can result in the creation of a parasite, by restricting the capability for protein synthesis.

Discussions

The low percentage of Guanine and Cytosine codons results in codon reassignment within the Balanophora which leads to deviating from its canonical genetic code. The Balanophora contains a variety of deletion indels within its genome resulting in its high AT

content concentration and the deletion of Cytosine and Guanine bonds. This results in codon usage biases (allowing for multiple amino acids to be created under a single codon) to generate the necessary proteins for survival. This codon usage bias centers at the heart of the Balanophora plant's applications as it provides scientists the opportunity to study the way deletion indels can be used to generate multiple amino acids within a codon.

Material and Methods

The plastome assemblies, defined as the way the plastid's genome was assembled, were investigated by using an ORF finder(something finding all reading frames for a genetic sequence). I can infer that this was used to find all the amino acids that could be coded per codon due to the codon usage biases because I already know that each individual reading frame correlates to a unique amino acid. Using BLAST and DOGMA they strategically located the start and stop codons based on their position relative to the expressed genes.

Questions

How does HGT contribute to evolving plants from autotrophs to heterotrophs that can develop haustoria roots?

What happens to the free codons that form as a result of the deletion indels?

How can be the genetic drift leading to the development of deletion mutations be modified using synthetic biology?

Can we apply the research of codon usage bias from parasites to humans, to perhaps create necessary proteins?

Problem to Solve

This research has proved to provide many promising applications of the effects of a high genetic density of codon usage bias, so the central issue of the article is that scientists can we either lengthen or decrease the length of a genome by either increasing or minimizing deletion indels? However, an alternative perspective to that could be that would it be possible to use insertion indels to increase the length of a genome as well, to fill in the empty blanks left by deletion indels, and as a result modify the canonical genetic code.

So in conclusion the central problem of this article is how can we use mutations to modify the properties of the Balanophora plant, which is a perfect target due to its high rates of codon usage bias.