
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

Plants that lose their ability to do photosynthesis and become parasites have reduced genome sizes. Its genome also consists of an abnormally high amount of adenine and thymine base pairs. These observations can be used to low genome complexity that can explain evolution

Abstract

Parasitic plants can be split into photosynthetic and non-photosynthetic. The non-photosynthetic ones are called holoparasitic and are considerably more interesting with a larger variation in genome size and AT content. The most interesting and the one studied in the study are the holoparasitic Balanophoraceae and its largest genus, Balanophora. They have extremely small genomes while also appearing non green, club shaped, and having small flowers. As a result, they most likely seem like a good genus to examine the effects of evolution.

Results

The two species examined, *B. reflexa* and *B. laxiflora*, have very high gene densities and overlapping of genes. This means that they have a very small genome size populated with AT pairs. *B. laxiflora* is the most biased to amino acids, only coding for Asn, Ile, Leu, Lys, Phe, and Tyr. Furthermore, their genetic code is altered since they have large amounts of stop codon codes in their DNA making it likely that they instead code for Tryptophan. However, they don't do RNA editing to alter the TAG when it is read making it more likely that they have a different genetic code. They also use their plasmids to store lipids instead of starches.

Discussions

Since TAG is read as a codon for Tryptophan in plasmids but as a stop codon in the nucleus and mitochondria, the idea that some tRNA only target plasmids rises. Furthermore, the high AT amount in the DNA and compactness of genes can be explained by mutations and natural selection. Most of these mutations are deletions. However, there may not be a relationship between AT concentration and gene compactness. They also lack tRNA genes, requiring them to import tRNA molecules. Its nucleus is different from its plastid in that it doesn't have bias.

Material and Methods

A plastid was formed through BLAST searches and joining ends of DNA if they paired. PCR was also used to amplify the total amount of DNA. ORF finder was used to analyze the plastomes which was used to create GC plot, check codon usage, and amino acid usage. The genes then underwent phylogenetic analysis excluding their RNA genes.

Questions

I don't understand the dn/ds ratio and its importance.

How is it possible for plants to have a plastid because I thought that only prokaryotes had plastids?

What were the different softwares used in this study and how were they used to develop the paper?

Problem to Solve

Use evolution of genetic code to understand the distinction of protists from their other kingdom counterparts. This can be done in a similar process as the one performed in this experiment by taking the DNA of plant-like protists and comparing them to those of the holoparasitic plants discussed.