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 started to change, many becoming parasites and losing their ability to carry out photosynthesis, as well as having their plastid genomes become degraded. The parasitic plant, Balanophora, has an evolved type of plastid genomes and genetic code. The discovery of these novel types of plastid genomes broaden the scientists' understanding of the complex amount of findings within genome evolution.

Abstract

Among the varieties of plants that exist, plastid genomes will vary in size and gene content. Since key lineages have not been explored yet, scientists have investigated the plastid genome sequence and expression for holoparasitic and morphologically different Balanophoraceae, which were proven to display features that had never been seen in any other plastomes

or genomes. The holoparasitic Balanophoraceae are one of the most interesting among the angiosperms that have no existing plastome sequences because the family contains the most bizarre plants, including many that are often confused with fungi. Discovering more about the various plants within the holoparasitic Balanophoraceae may help scientists determine more uses for these plants, which could include a use in the medical field. These plants could play a huge part in the future of science.

Results

The plastid genomes of the Balanophora have colinear gene orders. Even though the two Balanophora have an order that is smaller than all the photosynthetic plants on land, only one gene (rp/14) is not collinear with most of the angiosperms. The plastomes of Balanophora do not have an inverted repeat, however. Another similarity that scientists have begun to search for was the presence of starch grains within the tissues of the plants. By finding the similarities and differences between the plastomes of these families, scientists have begun to learn more and more about Balanophora, which may let them learn more about how they can benefit humankind.

Discussions

Discovering the evolution of plastid genomes in the fast-evolving Balanophora has helped make more discoveries for the 16th other genera. Studying slowly evolving lineages could contribute to the revealing of important conditions for the genetic code switch and other unusual things that happen with the Balanophora plastomes. As more and more discoveries are made, these discoveries will contribute to mankind in some way that will hopefully change things for the better.

Material and Methods

An assorted variety of equipment and materials were used in the research described within this article. This includes the HiSeq2000 (reads with 800-bp fragment sizes) and the Velvet version 1.2.07 (de novo assemblies). By using precision tools and well known machines with specific parameters, the scinets have justified that any measurements that were taken for research were probably accurate and true. This whole section is justification for all the mentioned results.

Questions

How are these parasitic plants affecting our ecosystem today and will the effects be magnified in the coming years?

How did scientists initially discover that there was a difference between Balanoflora and fungi?

Where did scientists get the idea for this specific area of study? What event or occurrence inspired them to think this way?

Problem to Solve

As three RNA genes were excluded from the phylogenomic analysis because of their short length, it would be an issue because it may or may not affect the validity of the results. Scientists should find a way to somehow incorporate these excluded genes into the study, giving them relevance and a purpose in research.