Extreme Makeover: Fern Edition

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Research Question

Can comparing the plastomes of various ferns provide evidence of genome destabilization?

Background

With a few exceptions, all plants have chloroplasts. Chloroplasts are the organelles responsible for photosynthesis in plants. Interestingly, chloroplasts have their own genome -- called a plastome -- which is separate from the nuclear genome. The genetic composition of ferns, gymnosperm, and angiosperm plastomes are remarkably similar, revealing very little change over evolutionary time. There are however a few notable exceptions to the apparent stability of the plastome. A few lineages of both angiosperm and gymnosperm show dramatically higher rates of mutation and genetic rearrangement than those of their relatives, suggesting major genome destabilization.

Vittariods are a group of ferns that live on the trunks and in the branches of trees in forests. Vittariods are so unique among ferns in structure and life cycle that they have long been thought to be their own family, but recent genetic research has shown they reside within the genus *Adiantum*. Vittariods bear little resemblance to their closest relatives and appear to have quite rapidly diverged from them.

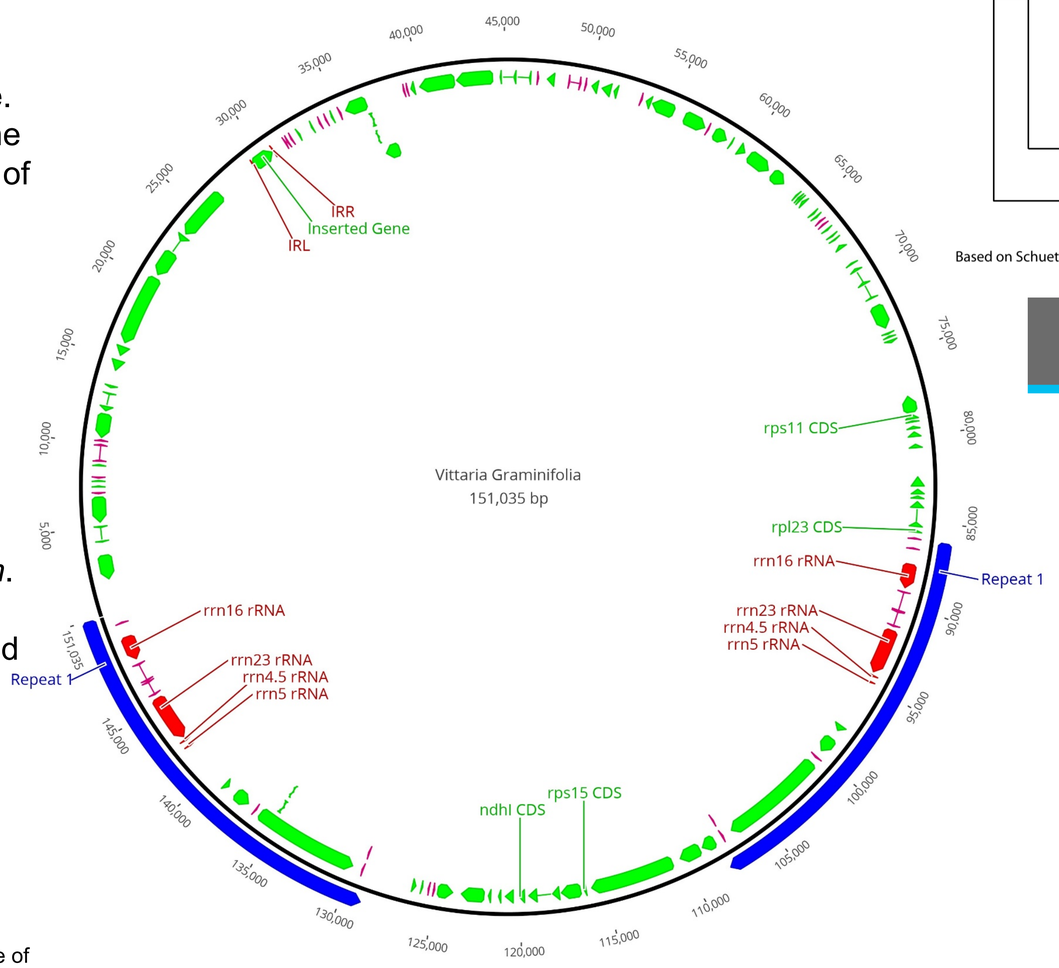
Bottom Left: Shoestring like vittariod ferns.

Top Left: Typical adiantoid fern.

Center: Plastome of *V. gramminifolia*

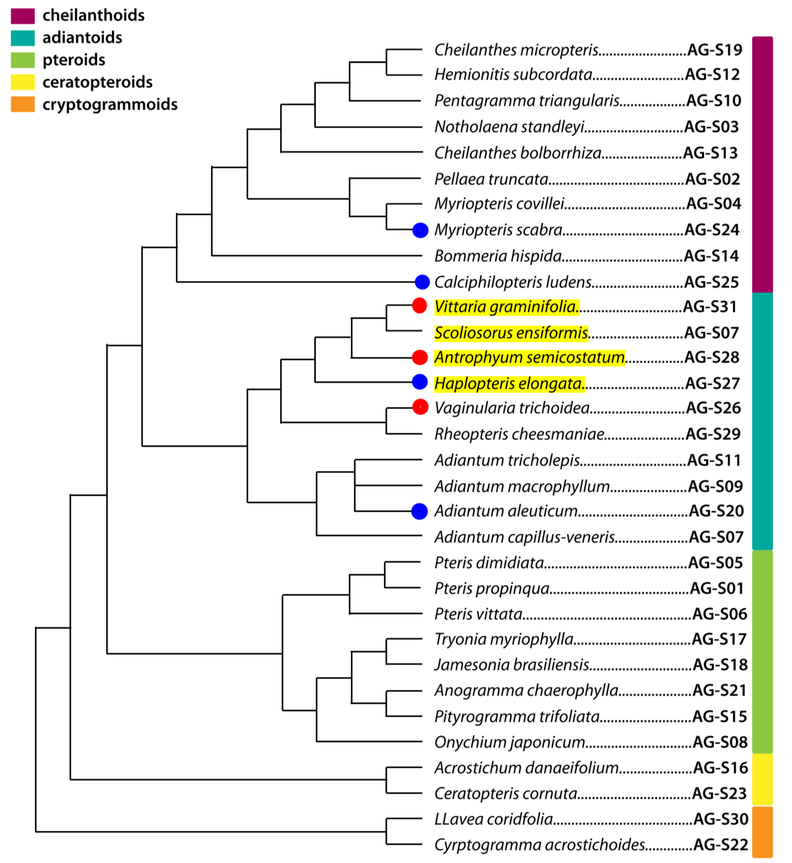
Procedures

We produced assemblies from low coverage genome-skipping analysis of the Pteridaceae family of ferns. The reads were 125 bp paired-end Illumina multiplex sequencing with 300bp inserts. Illumina reads were assembled *de novo* into complete Genomes using NOVOPlasty-master. Subsiquent read mapping was used to ensure that there was sufficient coverage throughout the genome and no false assemblies were produced. Genomes were then compared using geneious and other genome analysis software.



Results

Of the 32 sampled taxa, 24 completely assembled and another 2 produced partial assemblies. As expected, most genomes showed very little variation, but vittariods proved to be interesting. All vittariods excluding *V. Trichodia* had a large inversion within the inverted repeat, which is one of the most stable regions of the plastome. Vittariods were also found to have large insertion sequences which contain an open reading frame. In addition they displayed intense reduction in the length of the inverted repeat and several gene deletions throughout the plastome.



Based on Schuettpelz et al. 2007, Rothfels et al. 2008., Schuettpelz et al. 2016

Conclusion

The prolific mutations in vittariods that simply are not present in other clades, suggest that there must be a reduced efficiency in mechanisms that normally reduce the chance of mutation. While much of the analysis remains to be done, these preliminary results give significant insight into the dramatic molecular changes that have arisen along as a result of the rapid change in morphology of this group of ferns.

Particularly interesting is the prevalence of insertion sequences in the plastome. These insertions resemble the insertion sequences that are quite prevalent in bacterial genomes, but their coding sequences do not match any sequence on GenBank. While we are confident that these insertions are not the result of contamination, we are unsure of their origins.

Works Cited

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