

# Causes and consequences of mitochondrial mutation rate variation

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**Objectives**

## Introduction

Eukaryotes rely on the coordinated action of gene products encoded in both the nuclear and mitochondrial (mt) genomes to generate energy (Fig. 1). Therefore, it is hypothesized that coevolution between interacting mt and nuclear genes should be a common feature of eukaryotes<sup>1,2</sup>. One way to test this is to examine lineages with variable rates of mt evolution. In taxa where mt rates are fast, rates of evolution in interacting nuclear genes should also be fast, resulting in a pattern of “evolutionary rate covariation” (ERC)<sup>3,4,5</sup>. Mt evolution rates vary tremendously across eukaryotes (Fig. 2)<sup>6</sup>, providing many opportunities to test this hypothesis. However, this raises another question: why do mt rates vary so substantially? In plants, a lineage with high variable mt evolutionary rates (Fig. 3), recombination-mediated mechanisms act to repair mtDNA damage. Therefore, plant lineages with low copy numbers of mt genomes may have compromised recombination-mediated repair efficiency, leading to high rates of mt mutation and evolution.

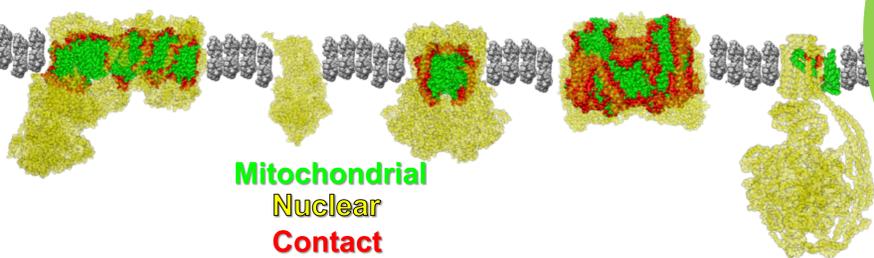


Fig. 1. The machinery used by eukaryotes to generate cellular ATP (OXPHOS complexes of the electron transport chain) are made up of proteins encoded by two genomes. Identity is based on mammals.

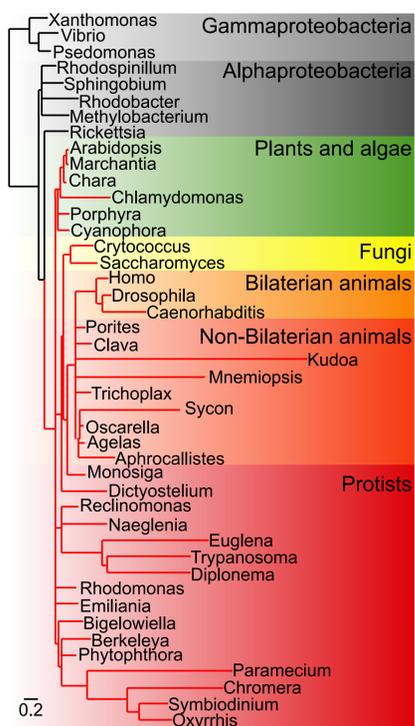


Fig. 2. Mitochondrial evolutionary rates vary tremendously across eukaryotes. Branch lengths show amino acid substitution rates in the mitochondrial gene COX1<sup>6</sup>.

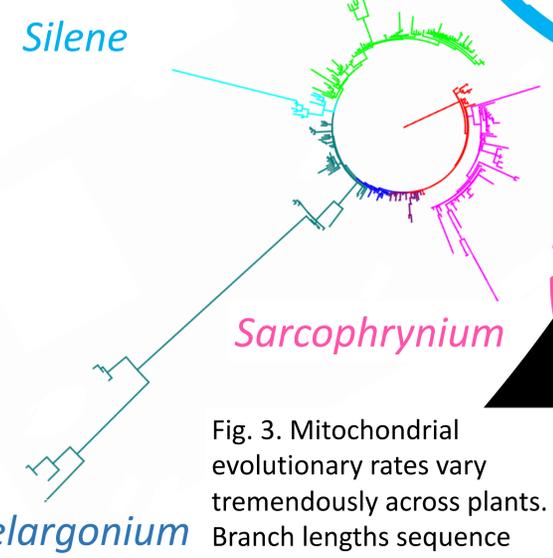
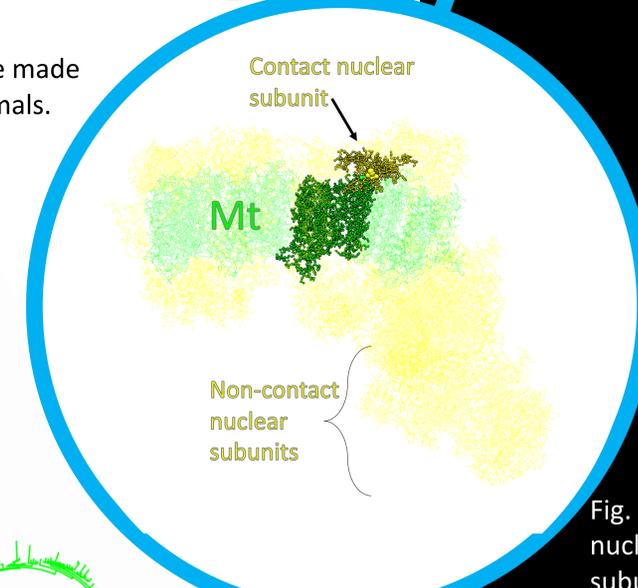
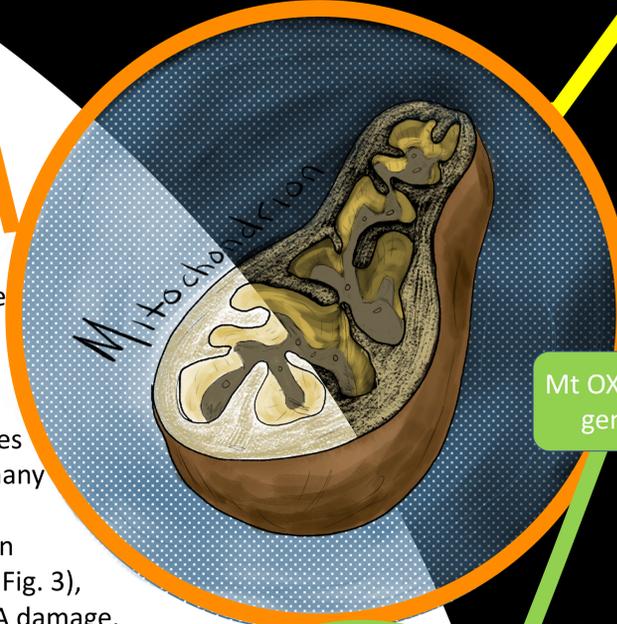


Fig. 3. Mitochondrial evolutionary rates vary tremendously across plants. Branch lengths sequence divergence in COX1<sup>7,8</sup>. Lineages of interest are highlighted.

- Test for mitonuclear coevolution in mammals by examining ERC in mt and interacting nuclear genes
- Determine if plant lineages with fast mt evolutionary rates have low mt copy numbers

## Methods

- 50 mammal species with reference genomic data were used to create phylogenies using 5 amino acid datasets:
  - Mt targeted: Mt OXPHOS genes, Nuclear OXPHOS genes, Nuclear mt ribosomal genes
  - Control: Nuclear glycolysis genes, Nuclear cell cycle genes
- Branch lengths between different datasets were correlated after controlling for background rates using a set of random single-copy orthologues
- Sequencing reads from total cellular DNA from leaf tissue were mapped to mt, plastid (pt), and nuclear gene sequences and read depth was used to estimate relative mt and plastid copy number in three plant lineages with variable mt evolution rates

## Results

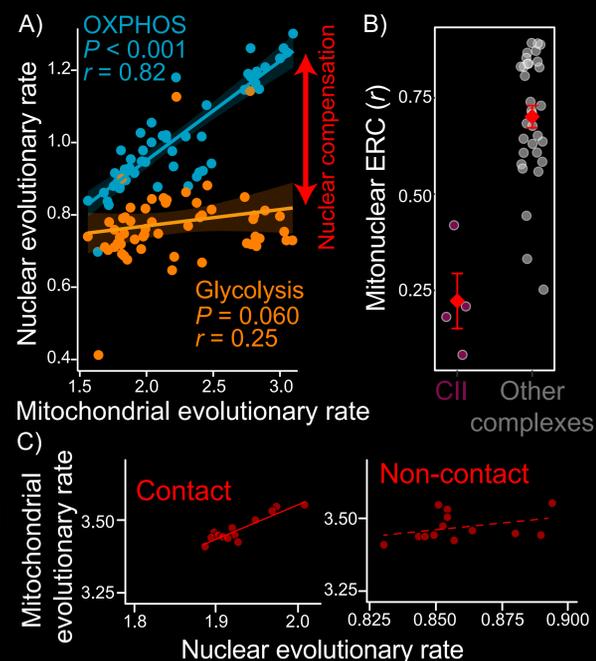


Fig. 4. A) ERC is strongest between mt and interacting nuclear genes, B) except for those that lack mt-encoded subunits. C) ERC are strongest within taxa (primates are shown) when using “contact” nuclear subunits (see left).

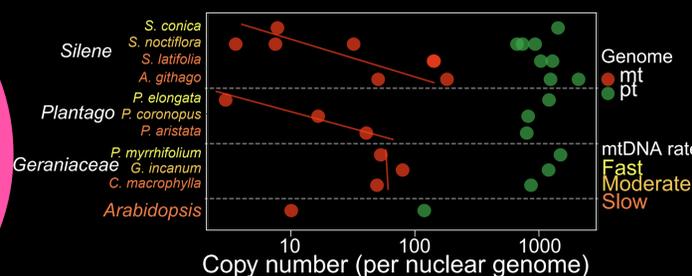


Fig. 5. Mitochondrial genome copy number is reduced in *Silene* and *Plantago* species with fast mt evolution, but not in Geraniaceae.

## Conclusions

Variation in mt evolutionary rates may be caused by variation in mt genome copy number in some plant lineages. Variation in mitochondrial evolutionary rates was used to detect signatures of mitonuclear coevolution in mammals.

### Literature cited

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