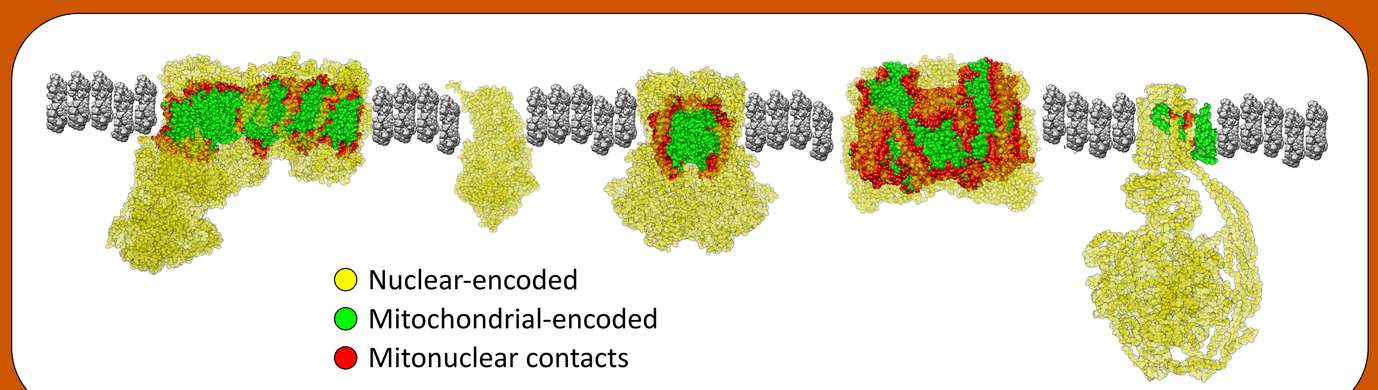
Predictions stemming from mitonuclear coevolution were not supported across diverse topics



Mitonuclear coevolution: implications (or lack thereof) for mother's curse, doubly uniparental inheritance, and speciation

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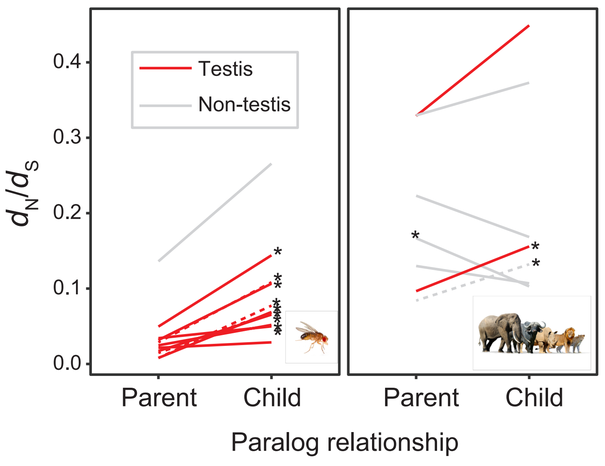
SUMMARY

- Mitonuclear coevolution, the notion that changes within one genome exert selection for complementary changes in the other genome, has been proposed to be ubiquitous in eukaryotes
- We refuted several predictions arising from mitonuclear coevolution related to three broad topics:
  1) mother's curse – nuclear OXPHOS paralogs do not likely compensate for male-harming mt mutations
  2) doubly uniparental inheritance – male-specific mt genomes do not evolve to maintain mitonuclear interactions
  3) speciation and nuclear compensation – rates of speciation and mt evolution are not correlated; nuclear-encoded sites that contact mt sites are not under positive selection

Mother's curse

Hypothesis: Male-specific nuclear-encoded OXPHOS paralogs are under selection to offset mother's curse mutations in mtDNA[1,2]

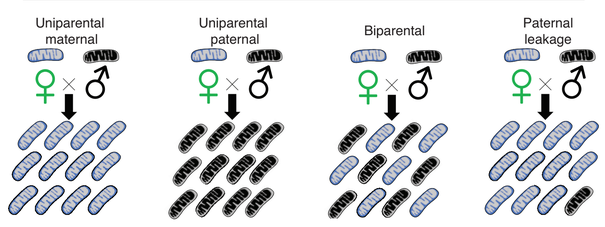
Results[3]*:* Nuclear-encoded OXPHOS paralogs with testis-specific expression show

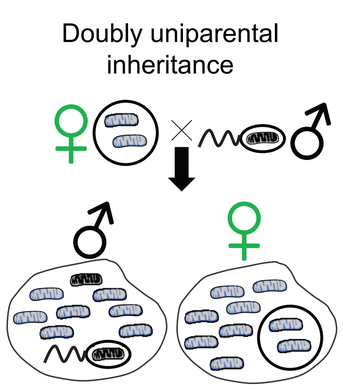


Elevated d_N/d_S …

… but due to relaxed selection[4]

Doubly uniparental inheritance



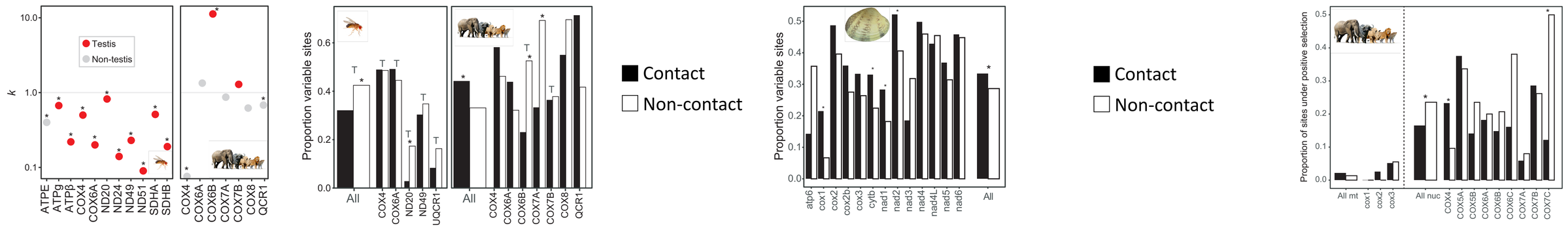


Hypothesis: Male-specific mt genomes should evolve to maintain mitonuclear interactions

Results: Only a single male-specific, nuclear-encoded OXPHOS paralog was found (*SDHC*) and

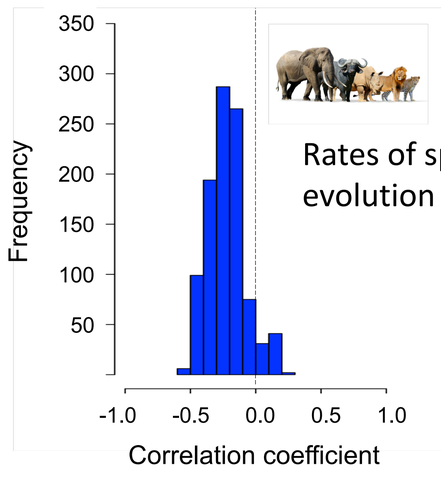
Contact
Non-contact

Contact
Non-contact



and no excess of changes at contact residues

contact residues are subject to more, not fewer changes in the male mtDNA



Rates of speciation and mt evolution were not correlated[5]

Speciation and nuclear compensation

Hypothesis: Mitonuclear genotypes are coadapted within a species due to nuclear compensation for deleterious mutations

Results:

Nuclear contact sites were not especially under positive selection[6]

Take a picture to download the poster

Species/datasets used here

49 mammals from KEGG

12 flies from FlyBase

Ruditapes philippinarum

Ask about ongoing projects in these systems:

Literature Cited

1. Gallach M, Chandrasekaran C, Betran E. 2010. Genome Biol. Evol. 2:835-850.
2. Eslamieh M, Williford A, Betran E. 2017. Genome Biol. Evol. 9(10):2782-2790.
3. Havird JC, McConie H. 2019.. Intgr. Comp. Biol. in press.
4. Wertheim JO, Murrell B, Smith MD, Kosakovsky Pond SL, Scheffler K. 2014Mol Biol Evol 32(3):820-32.
5. Rabosky DL. 2014.. PLoS ONE 9(2): e89543.
6. Yang Z. 2007. Mol Biol Evol 24(8):1586-91.