Digest: Mito-nuclear interactions modulate life-history phenotypes in the wild

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Footnote: This article corresponds to Rank, NE, Mardulyn P, Heidl SJ, Roberts KT, Zavala NA, Smiley JT, Dahlhoff EP. 2020. Mitonuclear mismatch alters performance and reproductive success in naturally-introgressed populations of a montane leaf beetle. Evolution. doi:10.1111/evo.13962. https://onlinelibrary.wiley.com/doi/10.1111/evo.13962

Abstract: Do mito-nuclear interactions impact life-history traits? Rank et al. (2020) found that these genomic interactions are of great importance in wild populations of the leaf beetle *Chrysomela aeneicollis* and may explain why populations are highly differentiated.

Main Text:

Mitochondria are essential organelles for life in eukaryotes, taking center stage in the process of cellular respiration. This process is regulated via a series of finely coordinated obligate interactions of molecules encoded by two genomes: nuclear and mitochondrial. Both genomes are required to work harmoniously to provide cellular energy, and thus their interaction is vital for the maintenance of mitochondrial integrity and the viability of eukaryote life (Lane 2005). For the past two decades, many studies have shown high levels of phenotype-changing genetic variation within the mtDNA genome. These findings run counter to the traditional paradigm in which mitochondrial genetic variation was expected to be evolving neutrally (Rand 2001; Burton, et al. 2013). It remains unclear whether mitochondrial genetic variation is accumulating adaptively under selection, or non-adaptively under mutation-selection balance.

A series of observations has led to the hypothesis that genetic variation found within the mitochondrial genome has been shaped by natural selection imposed by the prevailing thermal climate (Mishmar, et al. 2003; Ruiz-Pesini, et al. 2004). For instance, some studies have detected positive selective sweeps in the mitochondrial genome (Meiklejohn et al. 2007), while others have found that the frequencies of particular mtDNA haplotypes change with latitudinal or altitudinal variation (Silva et al. 2014; Camus et al. 2017). While a few studies have shown evidence for mito-nuclear coadaptation (Immonen et al. 2016; Morales et al. 2018; Healy and Burton 2020), obtaining evidence from natural populations is a complex endeavor.

In this issue, Rank et al. (2020) investigated links between mito-nuclear genotype and components of fitness in natural populations of the leaf beetle *Chrysomela aeneicollis*. They first examined a 65 km latitudinal transect and found that populations at the north and south edges had distinct mito-nuclear genotypes, with intermediate populations showing signs of intermixing (Figure 1A). The authors then focused on the region where intermixing occurred. They compared individuals whose mitochondrial and nuclear genotypes “matched”—i.e., both came from either the northern or southern population—to individuals with “mismatched” mitochondrial and nuclear genotypes, where the two genomes came from different populations. They examined how matched or mismatched genomes impacted key life-history traits, including fecundity, larval development, and male mating frequency.

Rank et al. (2020) found that beetles with matched mito-nuclear genomes typically outperformed genomically mismatched beetles, which moved slower, mated less, and were less fecund (Figure 1B). Notably, these effects were amplified following heat treatment. In addition, the direction of the mito-nuclear mixing was not symmetrical; beetles with northern nuclear genomes and southern mtDNA suffered the most. In sum, the authors’ results demonstrate that mito-nuclear interactions are of great importance to life-history evolution and may play a large role in maintaining population structure.

Mito-nuclear interactions have been largely overlooked in natural populations and have the potential to play an important role in many evolutionary processes, from responses to disease to speciation. This study provides a robust ecological experimental framework to test the effects of mito-nuclear epistasis, which can further the goal of understanding genotype-specific effects on traits that shape life history evolution.

Figure Legend

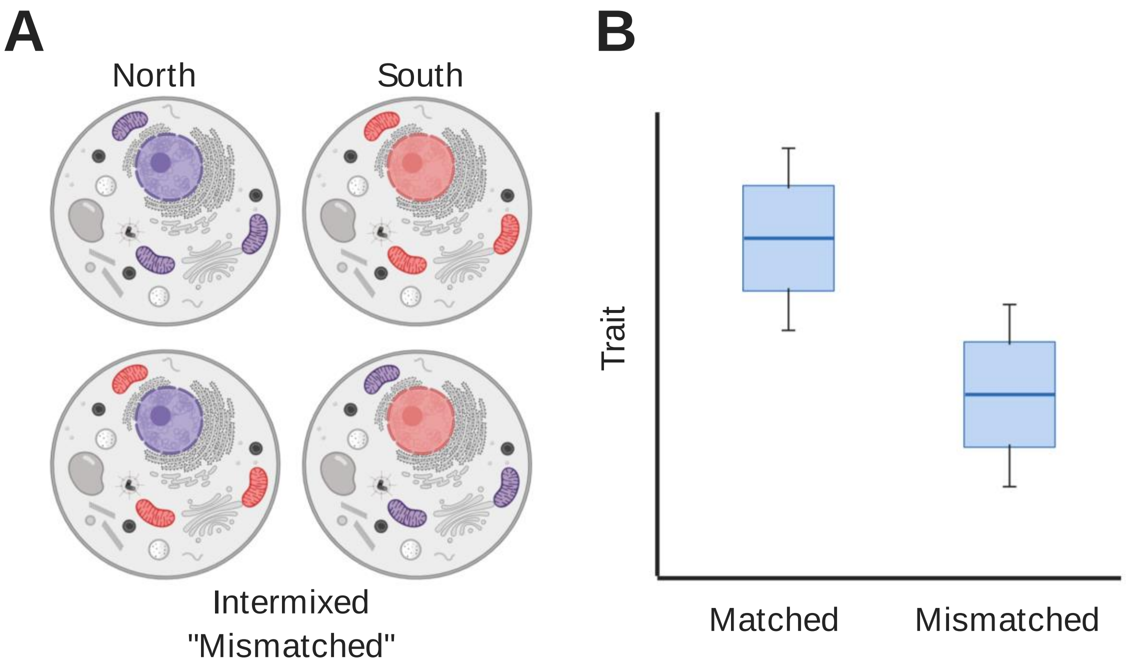

Figure 1: (A) Visual representation of mito-nuclear genotypes across the sampling locations. **(B)** Overview of main findings, whereby matched genotypes mostly outperformed mismatched individuals.

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