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EDITORIAL

Another useful property of mtDNA: editorial comment on the highlighted article by Lou et al. (2018)

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Mitochondrial DNA (mtDNA) has been the marker of choice since the advent of phylogeography, and for good reasons. Foremost, mtDNA is haploid, i.e., represented by a single variant of the molecule, as opposed to two sets of nuclear chromosomes in diploid organisms. This reduces effective population size (N_e) by half compared to nuclear DNA, and also facilitates sequencing and genotyping (all base pairs are expected to be homozygous in a haploid marker, circumventing the need to identify and distinguish alleles in heterozygotes, either physically through cloning or bioinformatically). Furthermore, contrary to the nuclear genome that is transmitted by both parents, mtDNA is maternally inherited. This reduces N_e by another half, resulting in an expected N_e for mtDNA that is a fourth of nuclear DNA. Lower N_e results in stronger genetic drift, providing higher resolution for phylogeographic analysis. In the era of whole genome sequencing (WGS), these advantages of mtDNA are balanced by the much larger volume of data provided by the nuclear genome. Yet, another property of mtDNA is that cells typically harbor many copies of the mitochondrial genome versus just a few of the nuclear genome, resulting in higher sequencing coverage for mtDNA than for nuclear DNA.

Lou et al. (2018) leveraged this property to recover the full mitochondrial genomes of 189 Atlantic silversides (*Menidia menidia*) at a mean coverage of 153× from a low-coverage (1.3×) WGS experiment (Therkildsen and Palumbi 2017). They carefully addressed a number of potential issues with mtDNA, including the fact that it is a circular molecule (which complicates mapping in the absence of edges) and the possibility of heteroplasmy (the occurrence of several mtDNA variants) or mitochondrial insertions into the nuclear DNA. The *M. menidia* mitochondrial genome was 16,454 base pairs long, providing significantly more data and phylogeographic resolution than an earlier *Marine Biology* study based on a 340 base pair segment of the mtDNA control region (Mach et al. 2011). It also provided the opportunity to search for signs of selection at the 13 protein-coding genes present in the mtDNA and apply approximate Bayesian computation (ABC) analysis for demographic inference.

Yet notwithstanding its many advantages, mtDNA also comes with a number of limitations. One generalization emerging from whole genome analysis is that evolutionary histories vary along the genome. In this regard, as a single molecule that lacks recombination, mtDNA essentially behaves as—and provides a sample size of—one locus. A related matter is that in the presence of whole genome data, and particularly high-coverage data, the gain from adding mtDNA may be marginal unless there is a specific biological motivation to do so such as mito-nuclear interactions or sex-biased dispersal. The analysis of the nuclear genomic data will allow to establish to what extent this applies to *M. menidia.*

Compliance with ethical standards

Conflict of interest The author declares that he has no conflicts of interests.

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