Low mitochondrial genetic diversity of *Engraulis ringens* compared to its congeners from coastal upwelling systems

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Introduction

The Southeastern Pacific Ocean is characterized by highly variable environmental conditions, exhibiting oceanic features that challenge its marine inhabitants. Fluctuations in the abundance of the Peruvian anchovy (*Engraulis ringens*), in response to both natural and anthropogenic pressures, suggest that the species possesses a high capacity for adaptation. By exploring how genetic variation is distributed within and among related taxa across space and time (i.e., phylogeography), we can gain insights into evolutionary history and infer some of the factors driving genetic diversity. Although mitochondrial DNA has limitations in reconstructing the complete history of a species, it provides a preliminary view of global or regional patterns, drawing on public databases enriched with mitochondrial DNA sequences collected over several years in different regions around the world.

OBJECTIVE:

This study employs a phylogeographic approach using mitochondrial DNA (mtDNA), to compare the genetic diversity of *E. ringens* with related taxa across global upwelling ecosystems. By leveraging large-scale public datasets, we interpret these genetic patterns in light of species-specific demographic histories and habitat characteristics.

Material and methods

Workflow

1 Sampling

Individuals were collected from the Northern, central, and southern Peru, from 2016 to 2016. Sampling was performed using the scientific purse seine operations conducted by IMARPE. Additionally, ten specimens of Argentine anchovy (*Engraulis anchoita*) were analyzed.

2 DNA, PCR & Sequencing

Total DNA were extracted from muscle tissues. The 5' mtDNA control region (CR) and complete Cytochrome b gene (Cytb) were amplified. A total of 236 individuals were sequenced for Ctyb (913bp), and 445 for CR (420 bp).

3 Genetic diversity

Haplotype diversity (Hd) and nucleotide diversity (π) were calculated with DnaSP². Genetic diversity was compared with published values of eight nominal species of the genus. A total 13 studies were consulted to compiled the genetic diversity indexes.

Genealogy

E. ringens haplotype networks were obtained using the Statistical Parsimony method (TCS) implemented in PopArt. Also published DNA sequences of five nominal Engraulis species were included to evaluate genealogy: E. encrasicolus, E. japonicus, and E. australis from the Old World lineage; and E. mordax, and E. anchoita from the New World lineage.

Neutrality test

Tajima's D test was performed using DnaSP² and statistical significance was assessed using the beta approximation³.

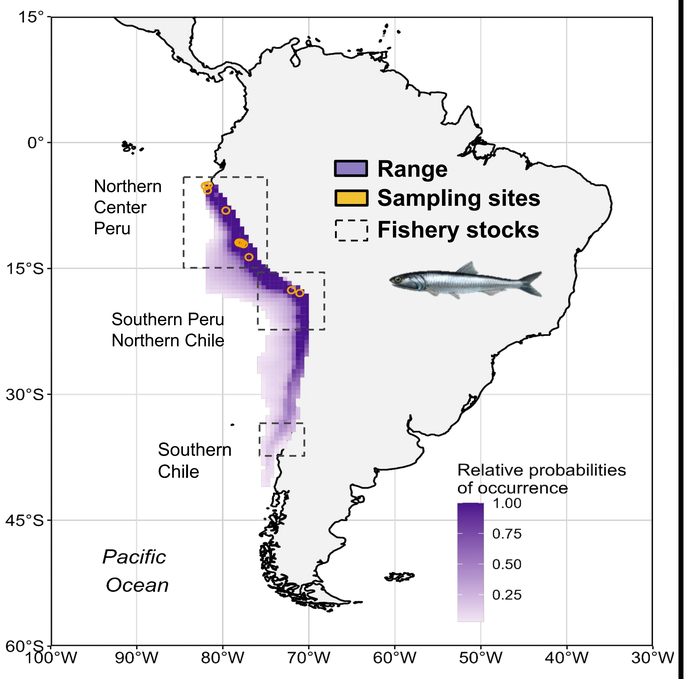

Figure 1. Peruvian anchovy distribution range from AquaMaps[1], showing modeled occurrence probability. Sampling sites are shown in yellow. Fishery stocks are depicted schematically as approximate reference areas.

Results

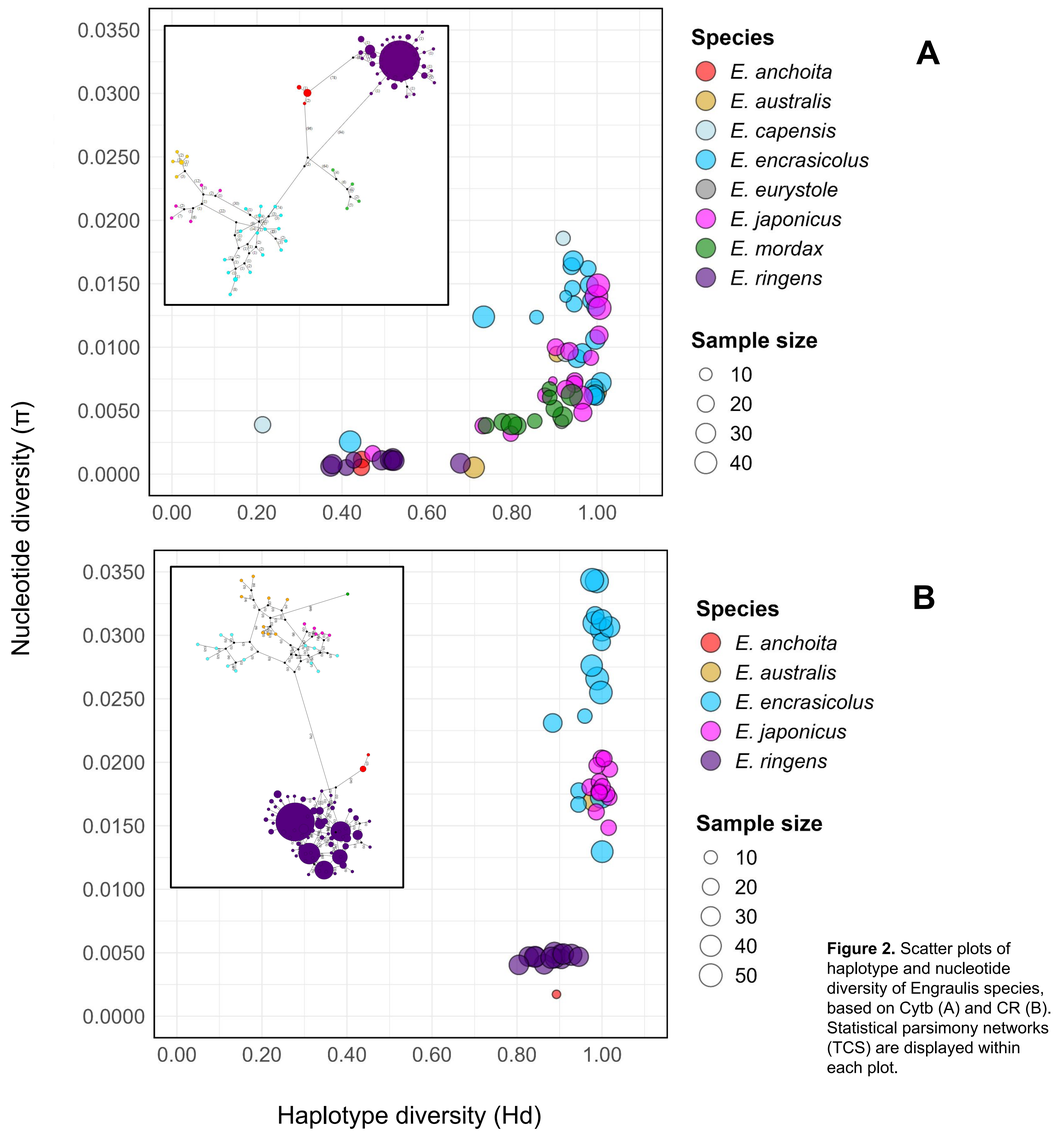

Figure 2. Scatter plots of haplotype and nucleotide diversity of Engraulis species, based on Cytb (A) and CR (B). Statistical parsimony networks (TCS) are displayed within each plot.

Results and discussion

Cytb showed signals of non-neutral processess

- Tajima's D compares two estimators of genetic diversity (π and segregating sites), which are expected to be equal (D ≈ 0) under neutrality and demographic equilibrium.
- Significant negative D values indicated an excess of rare variants, consistent with either population expansion or purifying selection. In the former case, rare variants reflect recent mutations in a growing population, whereas in the latter, they represent deleterious alleles maintained at low frequencies by selection.
- Cytb consistently showed negative D values in *E. ringens* (both per sample and overall). In contrast, CR showed no significant deviation from 0, except when all sequences were analyzed jointly (Total). Assuming stable demography, these results suggest selection acting on Cytb, which exhibits a stronger signal than CR due to its functional nature. However, because few-loci analyses often confound selection with demography, this pattern may instead reflect historical population shifts.
- Disentangling demography from selection requires further study, as anchoveta's population dynamics show demographic changes on short timescales, while its huge population size and highly variable habitat provide fertile ground for an effective role of selection.

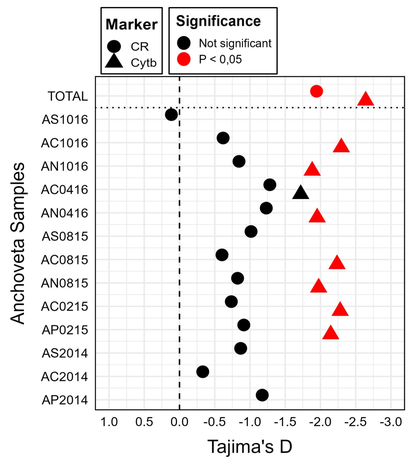

Figure 3. Tajima's D statistic of neutrality for each Anchoveta sample and overall, calculated from Cytb and CR sequences data. Red symbols indicate significance deviation from neutral expectation (P < 0.05).

South American species showed lower mtDNA diversity than Old World lineages

- For the Peruvian anchovy, Cytb showed lower genetic diversity (Hd and π), with reductions of ~2 fold (Hd) and ~10-17 fold (π) relative to Old World species (*E. japonicus* and *E. encrasicolus*), and ~2 fold (Hd) and ~5 fold (π) relative to its Northeast Pacific congener *E. mordax*.
- The Peruvian anchovy shared low-diversity pattern with Brazilian-Argentine anchovy *E. anchoita* (though limited sampling for E. anchoita warrants caution).
- CR confirmed this pattern, where *E. ringens* showed comparable Hd but ~4-7 fold lower π than Old World species, consistent with the higher polymorphism of a non-coding region relative to Cytb.
- Genealogies show shallow coalescence within South American species (haplotypes separated by only 1-2 mutations), despite deep species separation.
- Old World species show deeper genealogies, with more mutational steps among haplotypes within species, but lower interspecific divergence than *E. ringens*, *E. anchoita*, and *E. mordax*.
- Also interesting is that the Asian and European anchovies showed a wider range of nucleotide diversity than Anchoveta and californian anchovy, reflecting a more variable pattern of their diversity along its geographic range.

References

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