A Comparison of Mitochondrial Genomes of Five Species of North Pacific Krill

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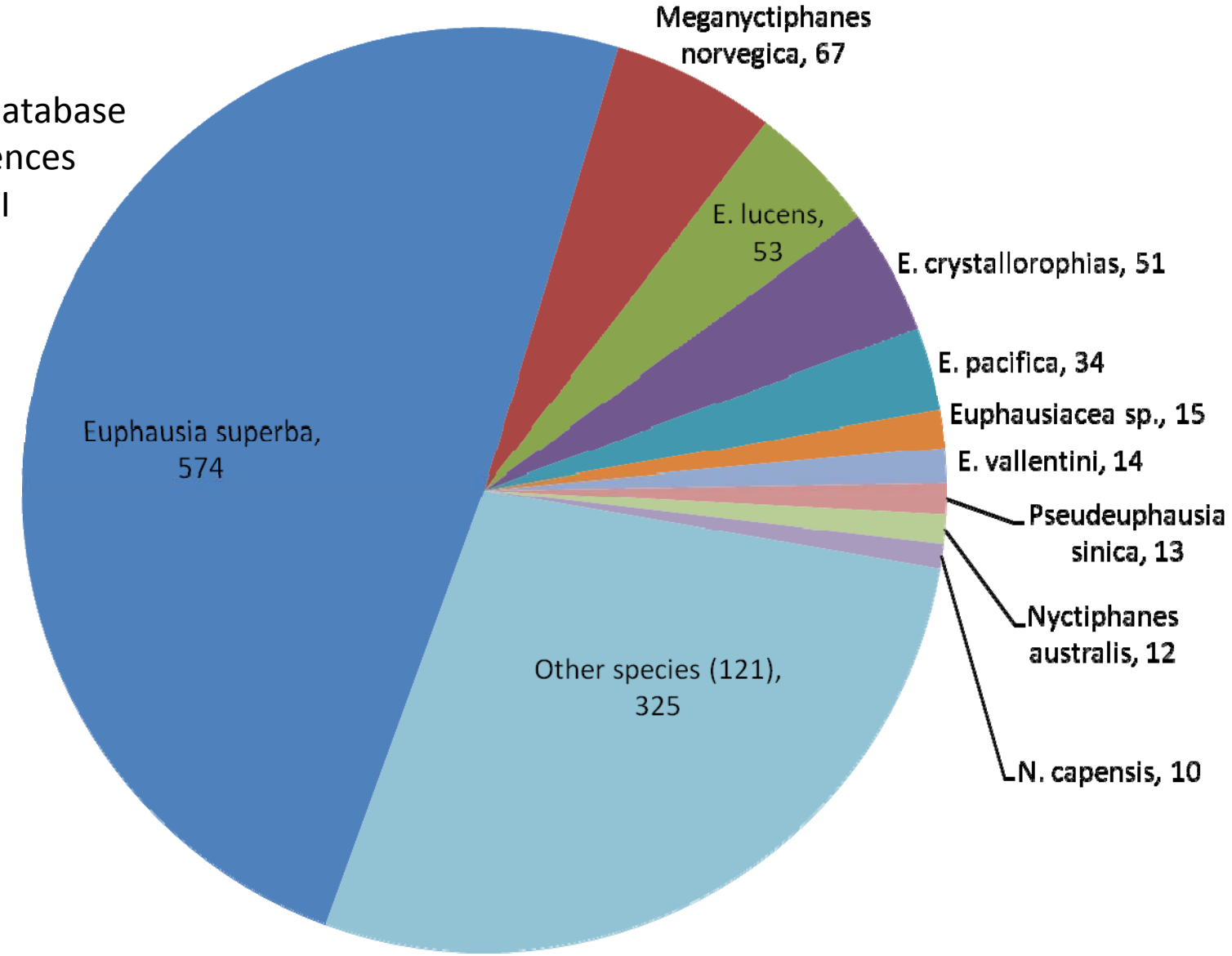
Intellectual Merit

- Krill are a critical link between producers and higher trophic levels
- The body of research is growing
  - Phenology
  - Comparative Physiology
  - Reproduction
  - Mortality
  - Growth Rates
- However, little is known about krill genetics

“Krill” Sequences (Genbank)

Nucleotide Database
- 1168 Sequences
- 286 Not COI



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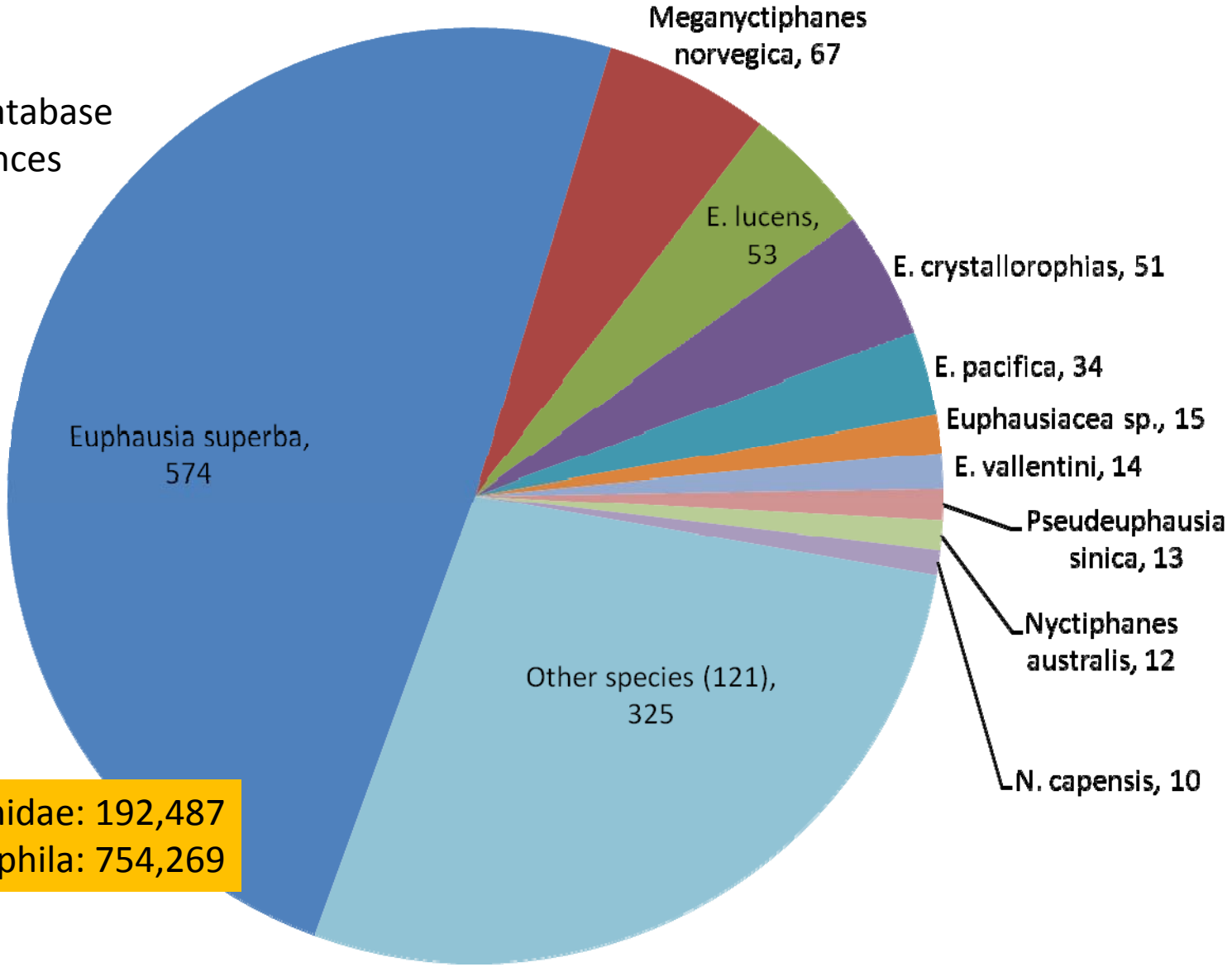
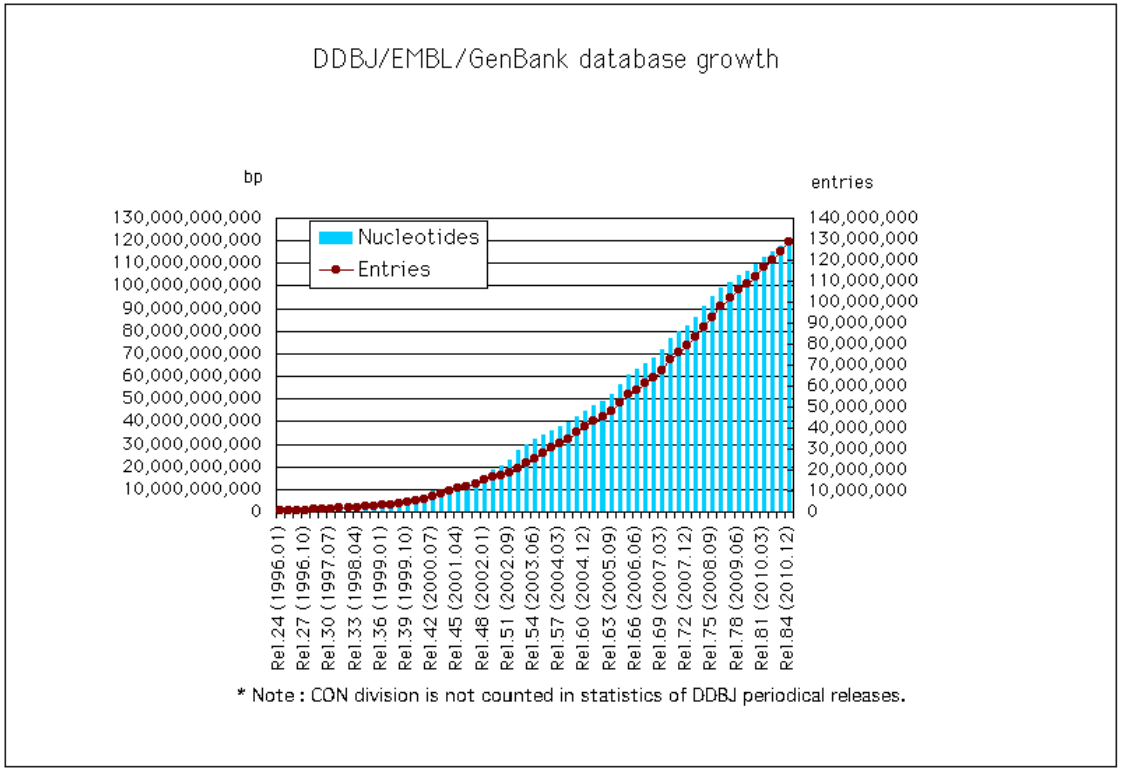


Salmonidae: 192,487
Drosophila: 754,269

New Sequencing Tools



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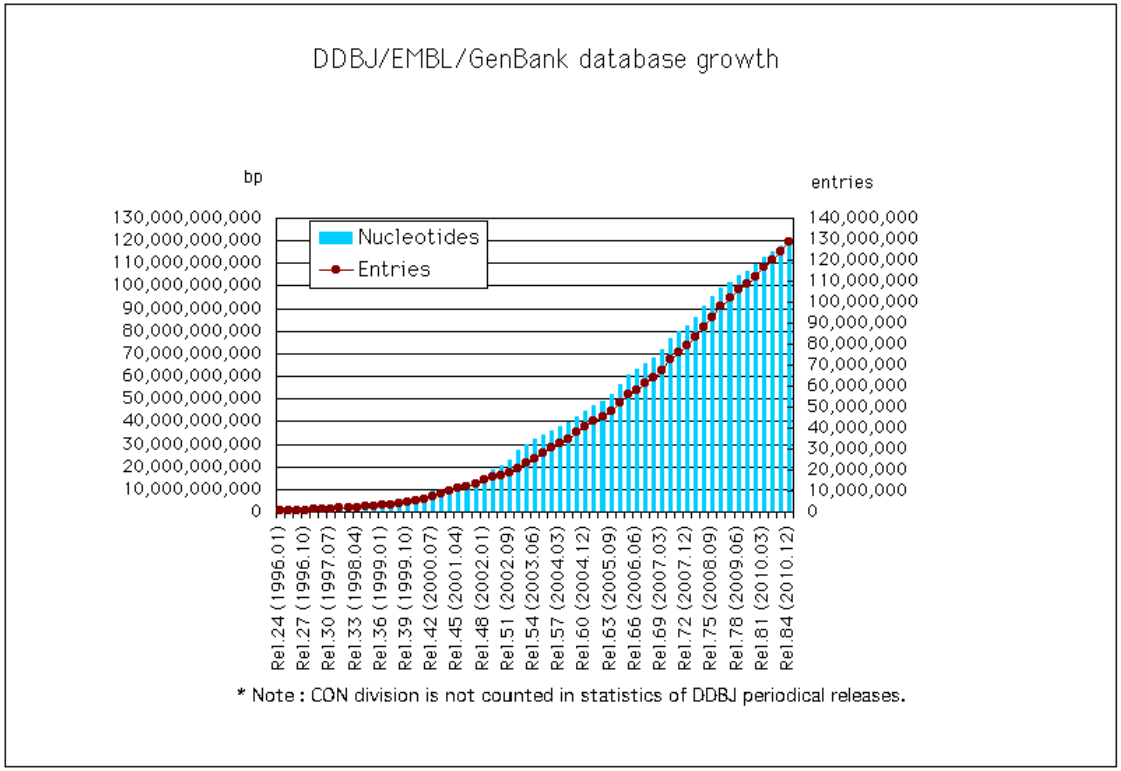

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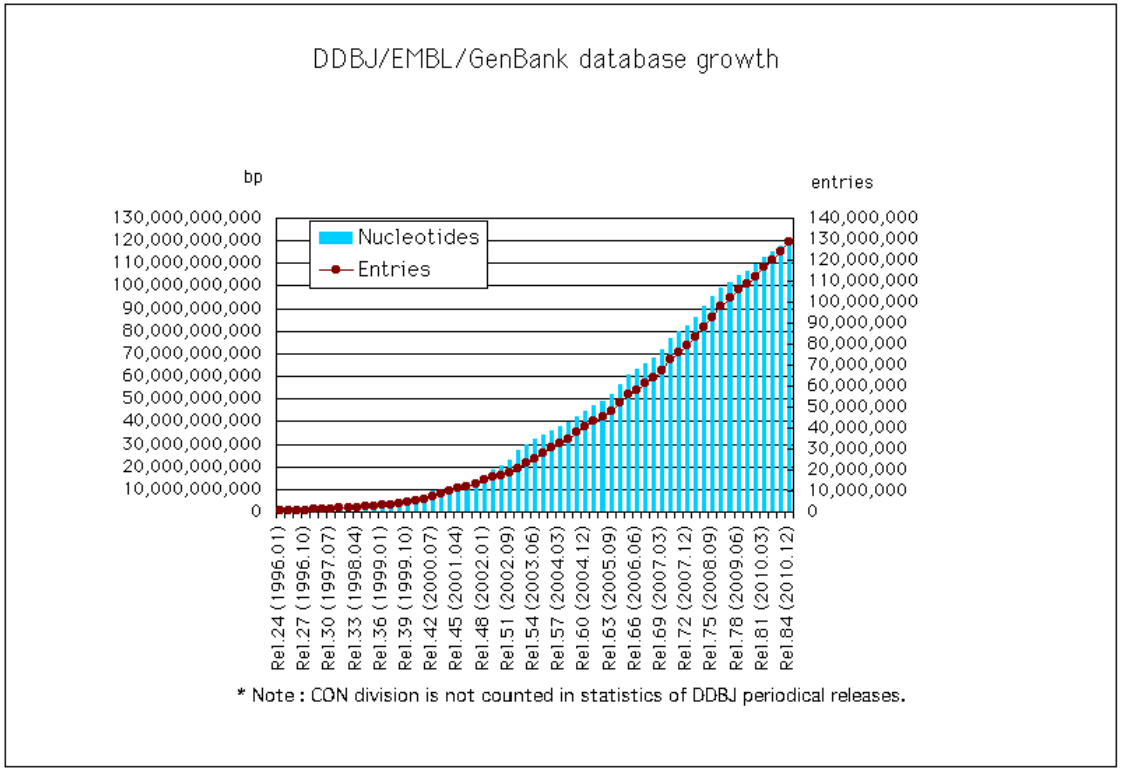

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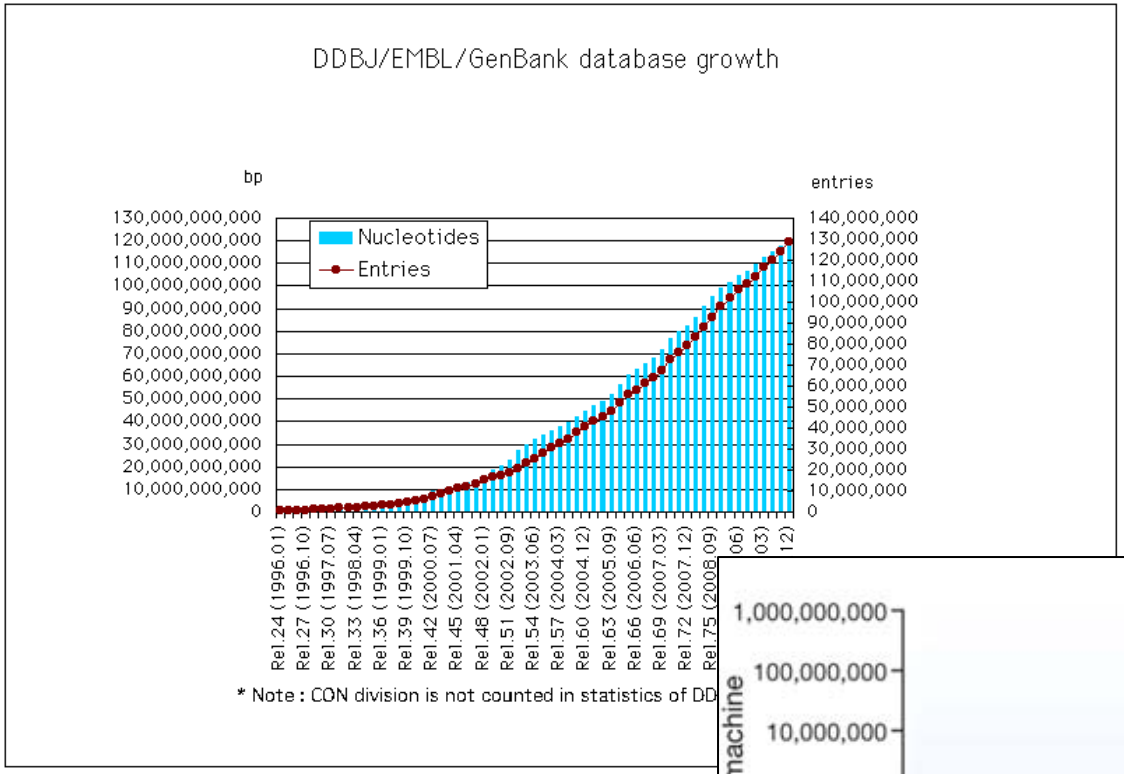
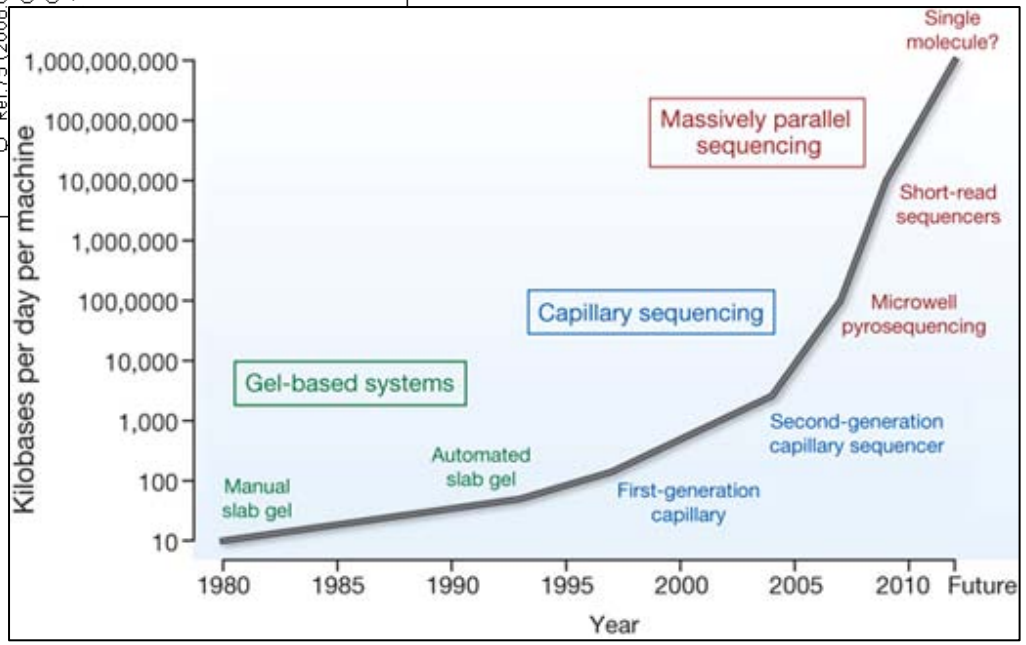
BUT

This growth has been accompanied by technological improvements that we can take advantage of.

New Sequencing Tools





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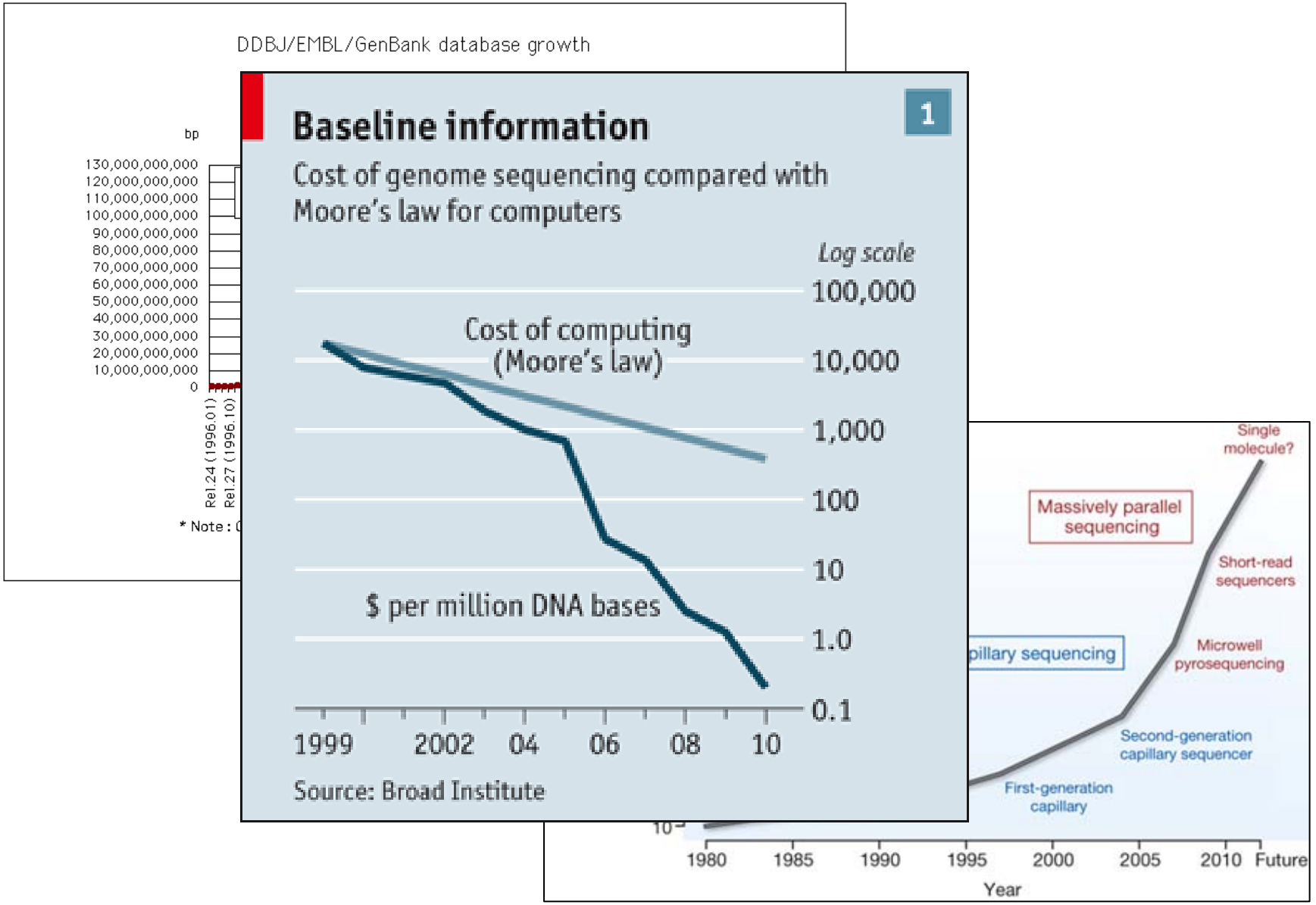
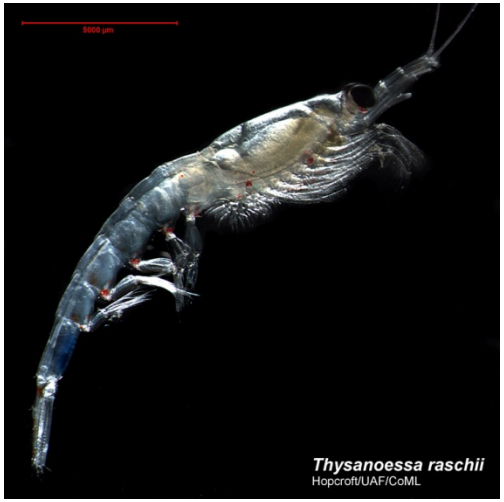


Target Species

Euphausia pacifica

Thysanoessa longipes

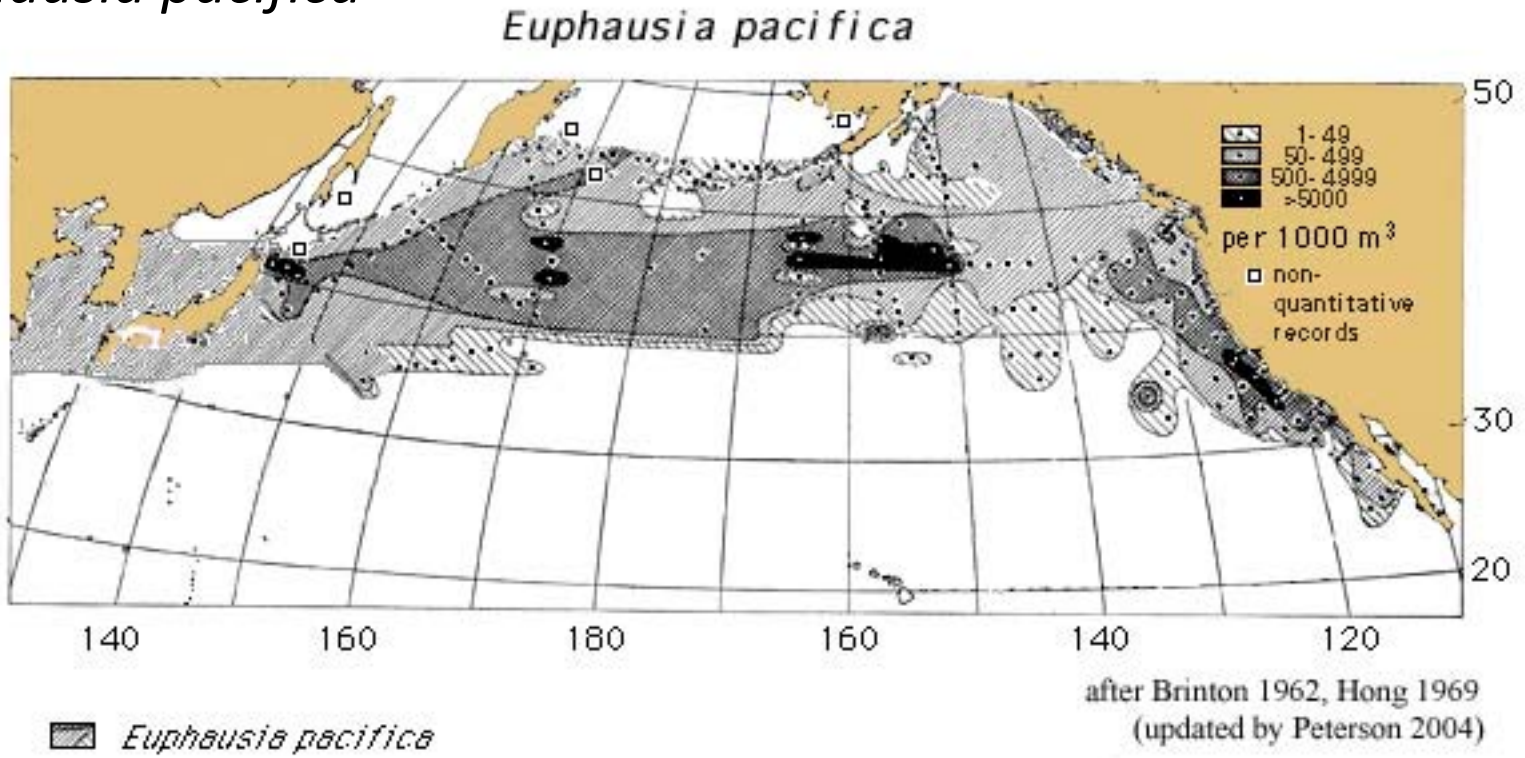
T. raschii



T. inermis

T. spinifera

Euphausia pacifica



Occupies a diverse set of habitats:
Cool, eutrophic upwelling regions
Downwelling region
Oligotrophic oceanic regions

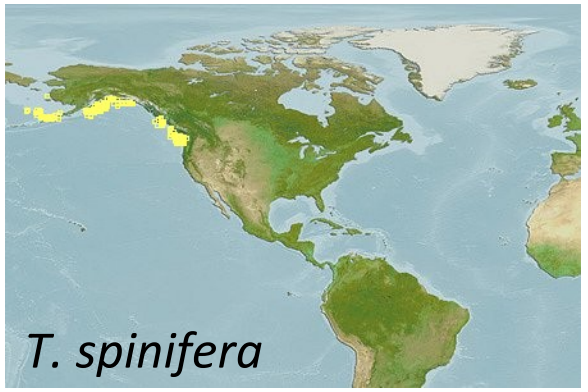
In temperatures ranging from:
Sub-Arctic (the Oyashio)
To
Sub-Tropical (the Kuroshio, Japan Sea, East China, and Yellow Seas)

Very few invertebrates occupy such a wide variety of ecosystems and habitats

Thysanoessa spp.

Occupies similar habitats as *E. pacifica*

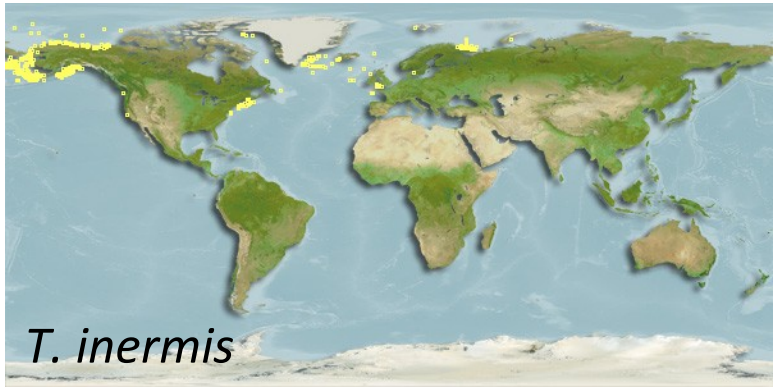
But, divides the range among several species

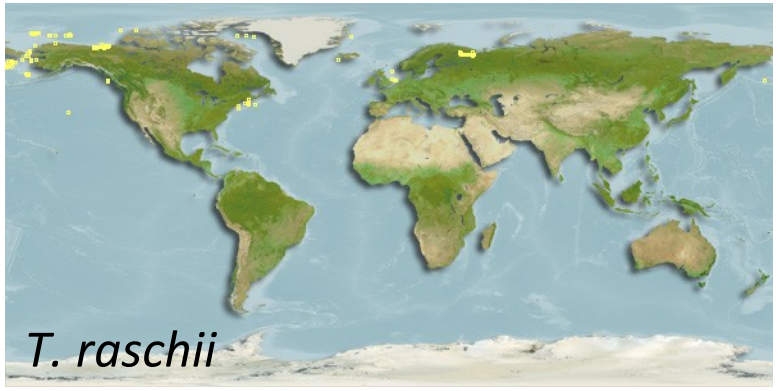


T. spinifera: California Current to Gulf of Alaska

T. inermis/*T. raschii*: Bering Sea/Arctic Ocean to Russia

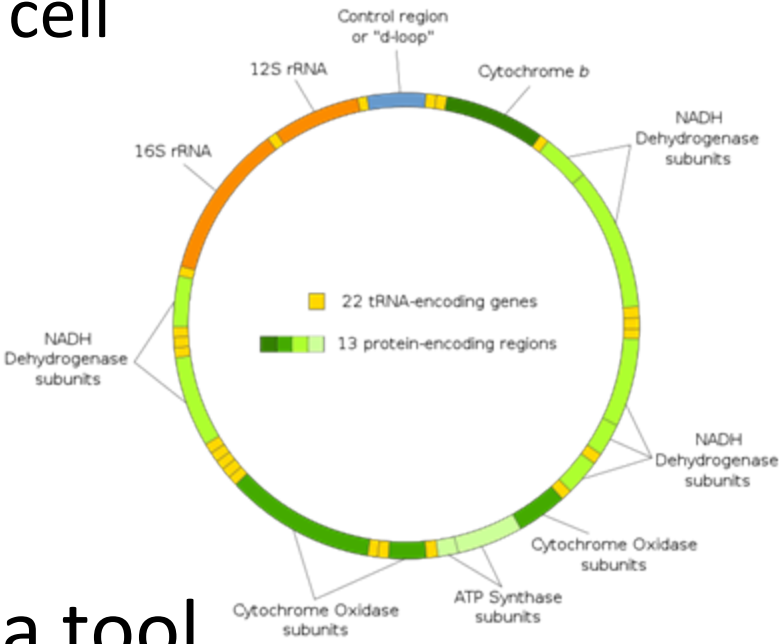
T. longipes: Bering Sea southward to 40°N (Japan), to 50°N (mid-Pacific & North America)





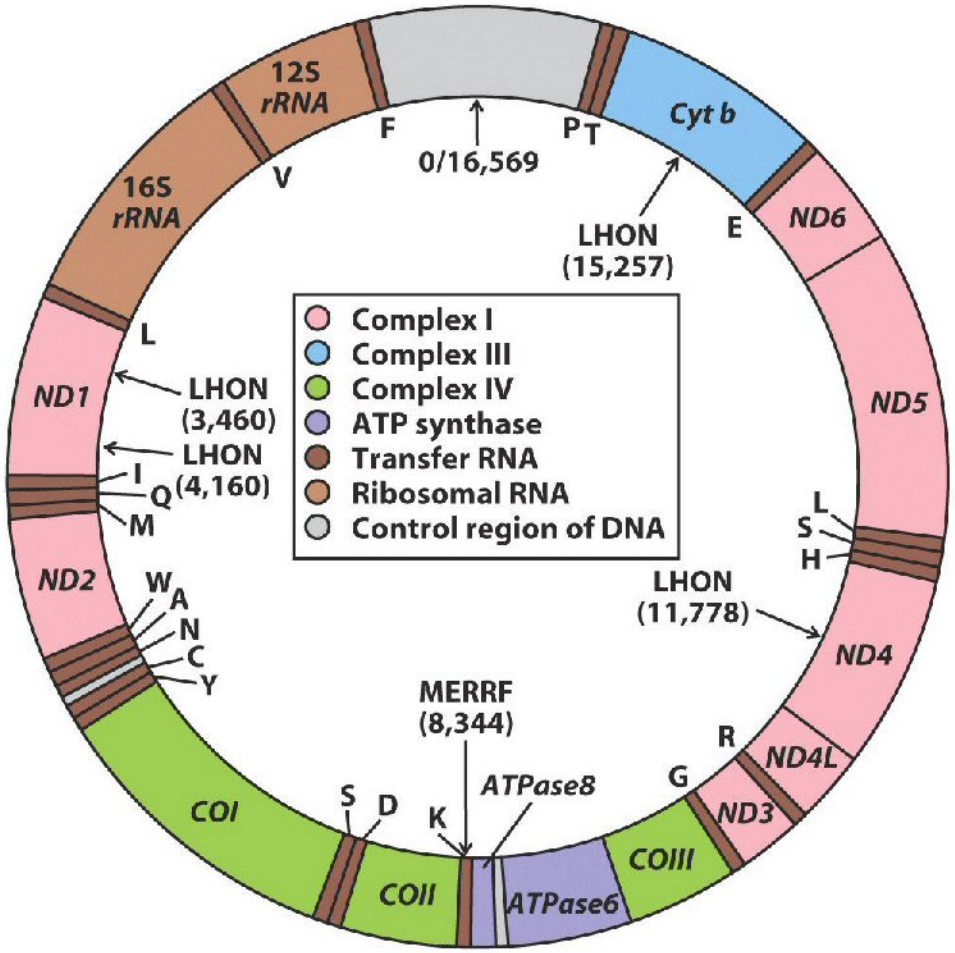
Starting Point: Mitochondrial DNA

- Characteristics of mitochondrial DNA
  - 100s-10,000s of copies per cell
  - High mutation rate
  - “No” recombination
  - Haploid
  - Maternally inherited



- Mitochondrial markers as a tool
  - Phylogenetics
  - Species identification
  - Population genetics

Approach and Methodology



1. Shen et al. *E. superba* mitogenome

Adapted from Shen et al. 2010. Mol. Biol. Rep.

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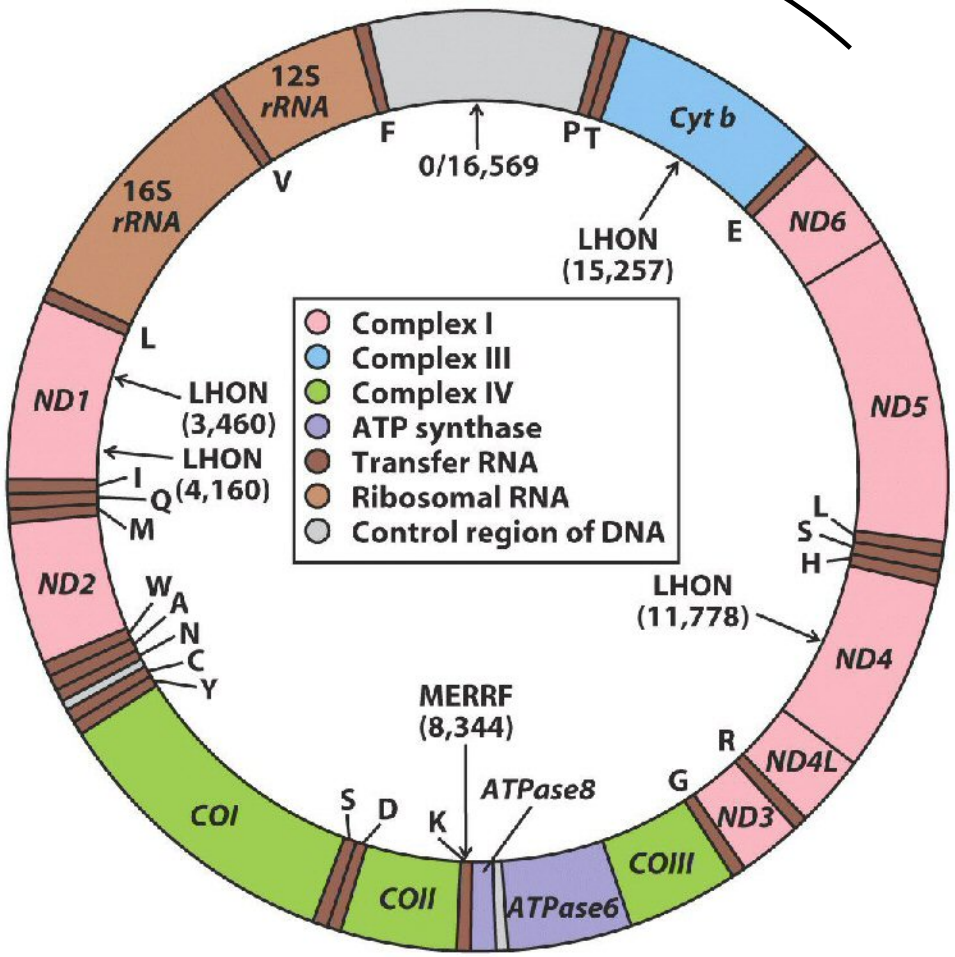

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2. Short PCRs (300-800bp; Shen et al. & degenerate primers)

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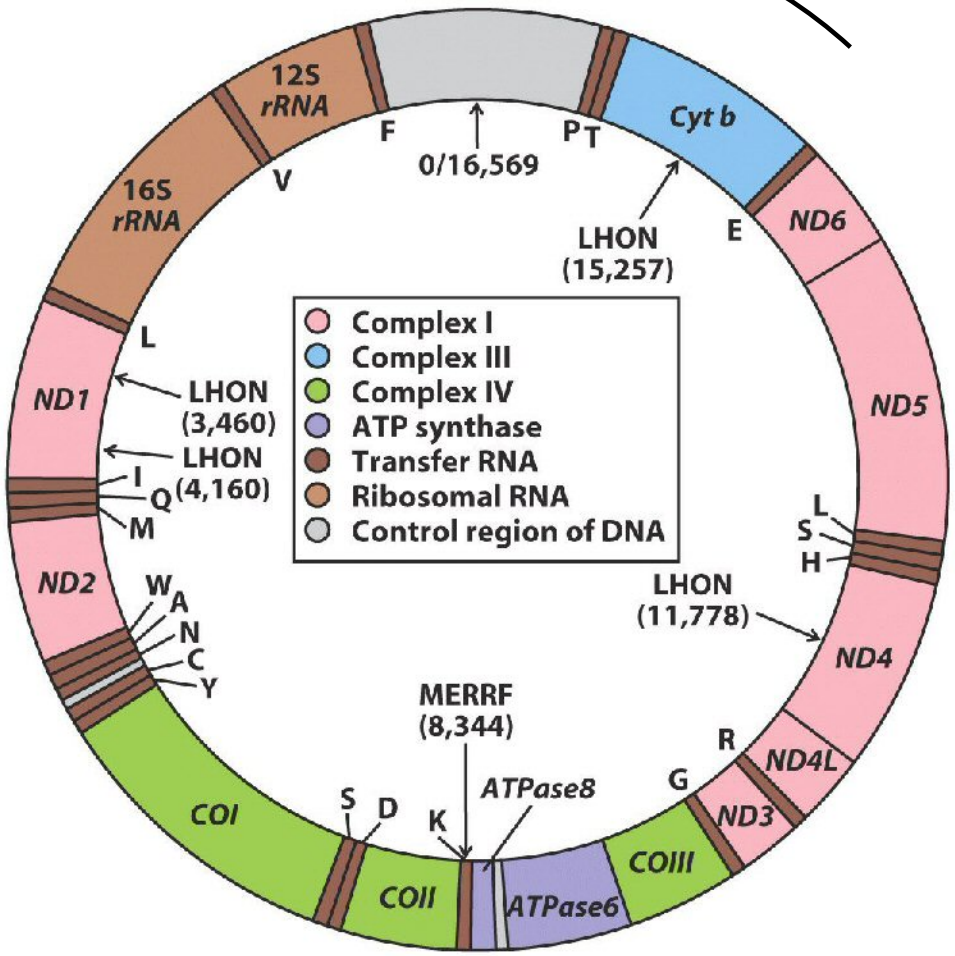

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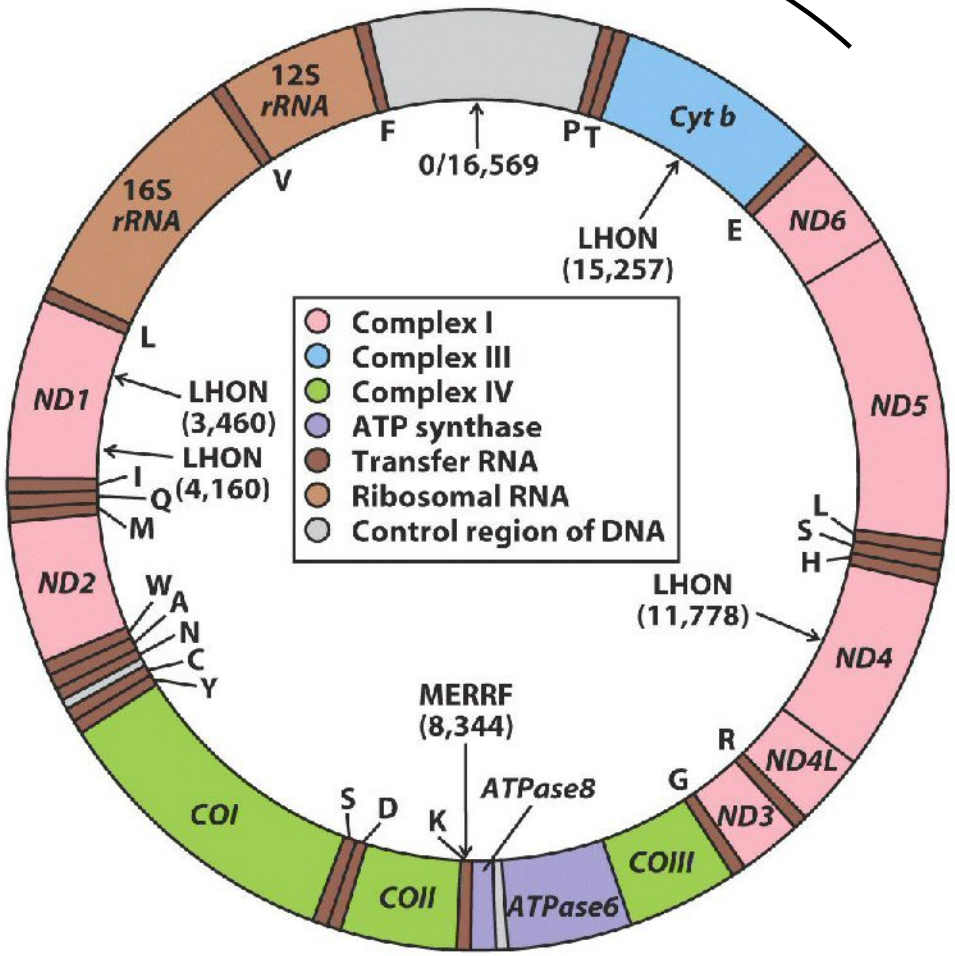

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4. 454 Sequencing

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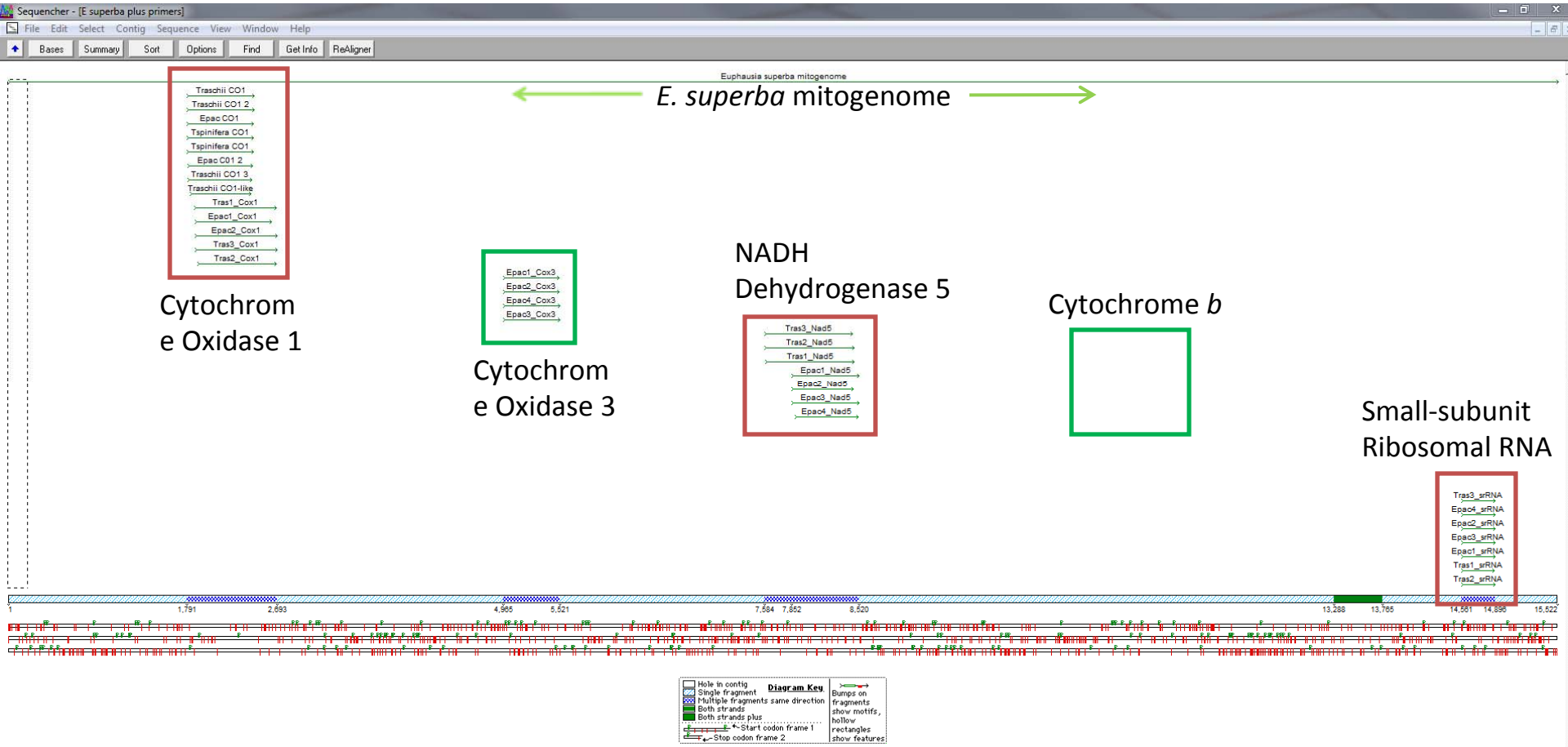
Project Status



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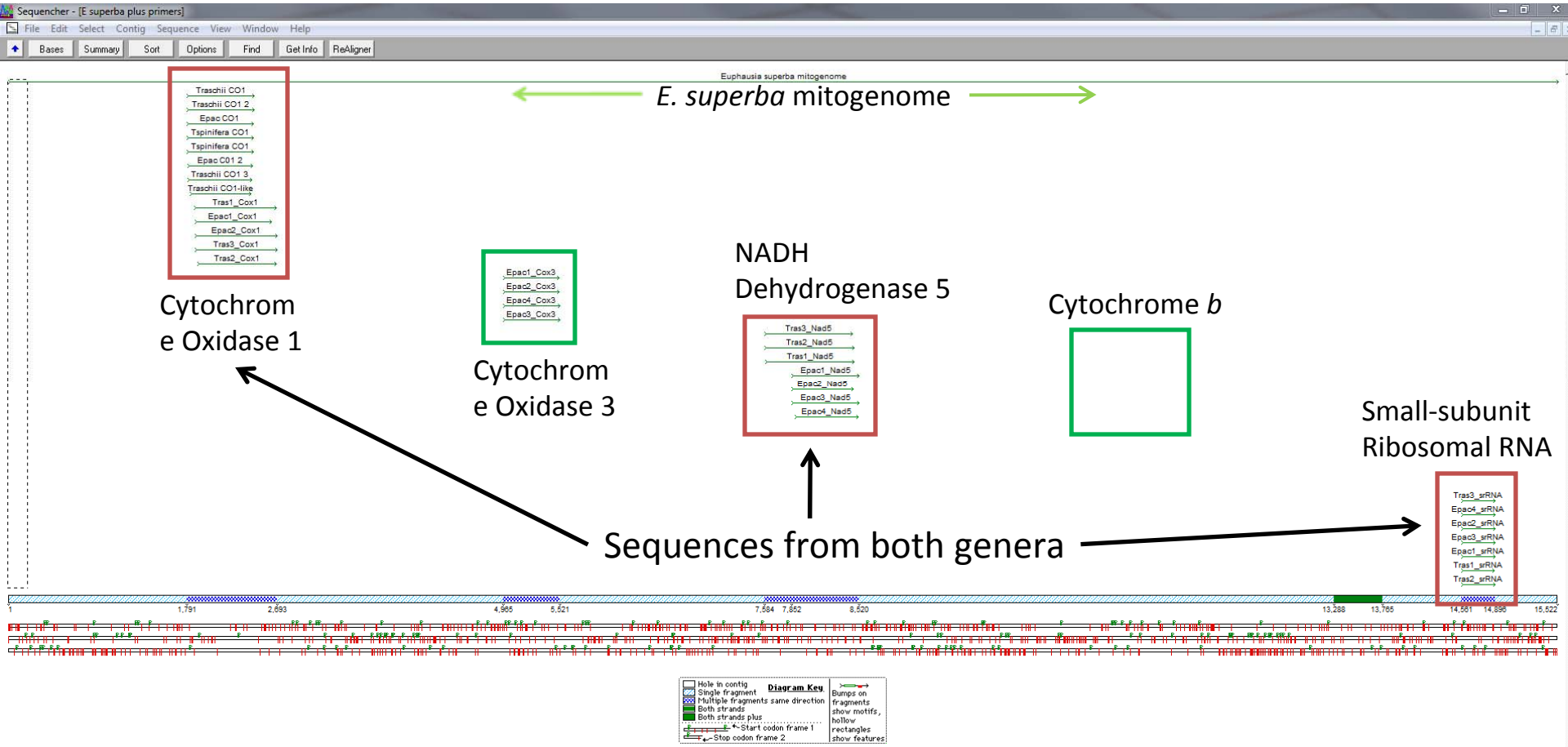

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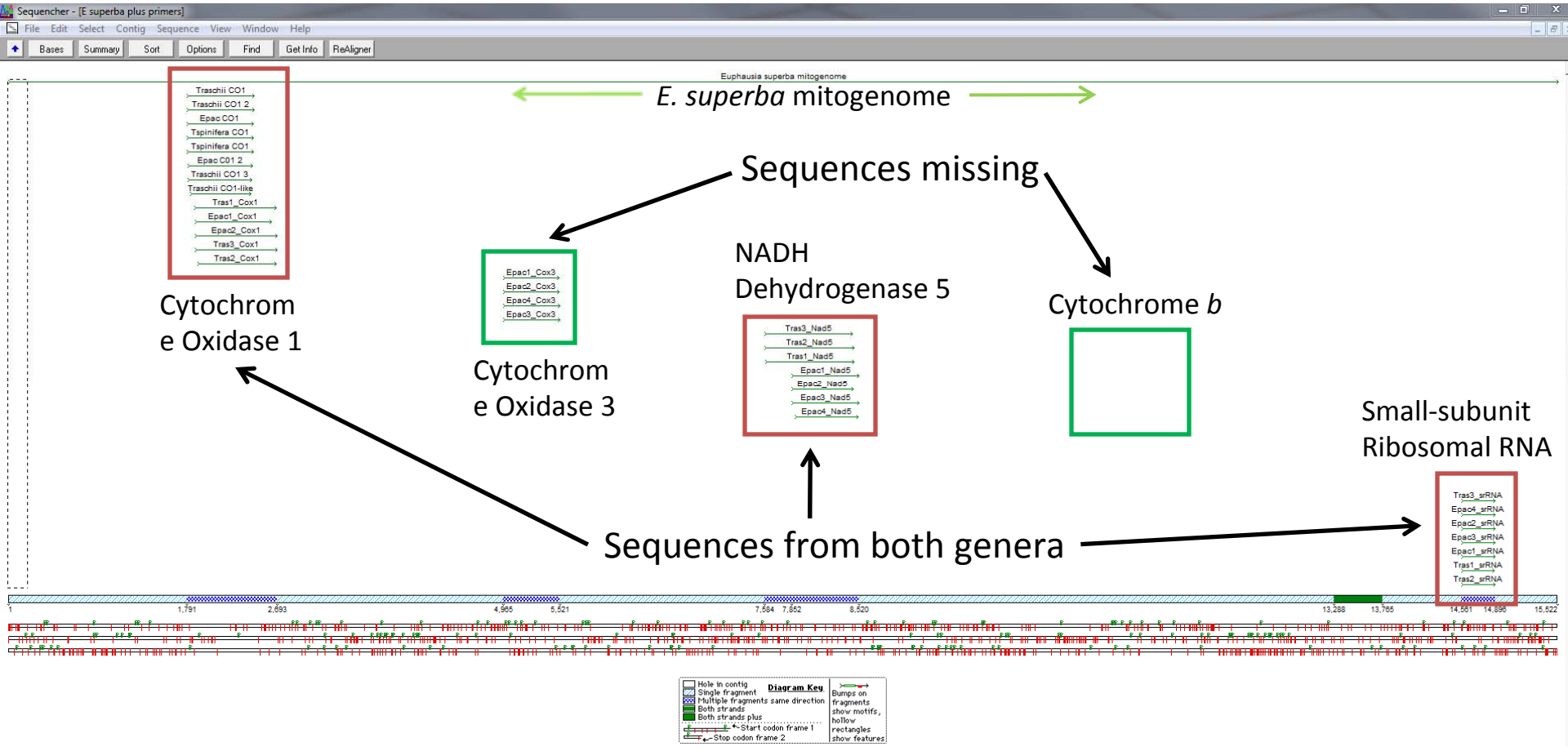

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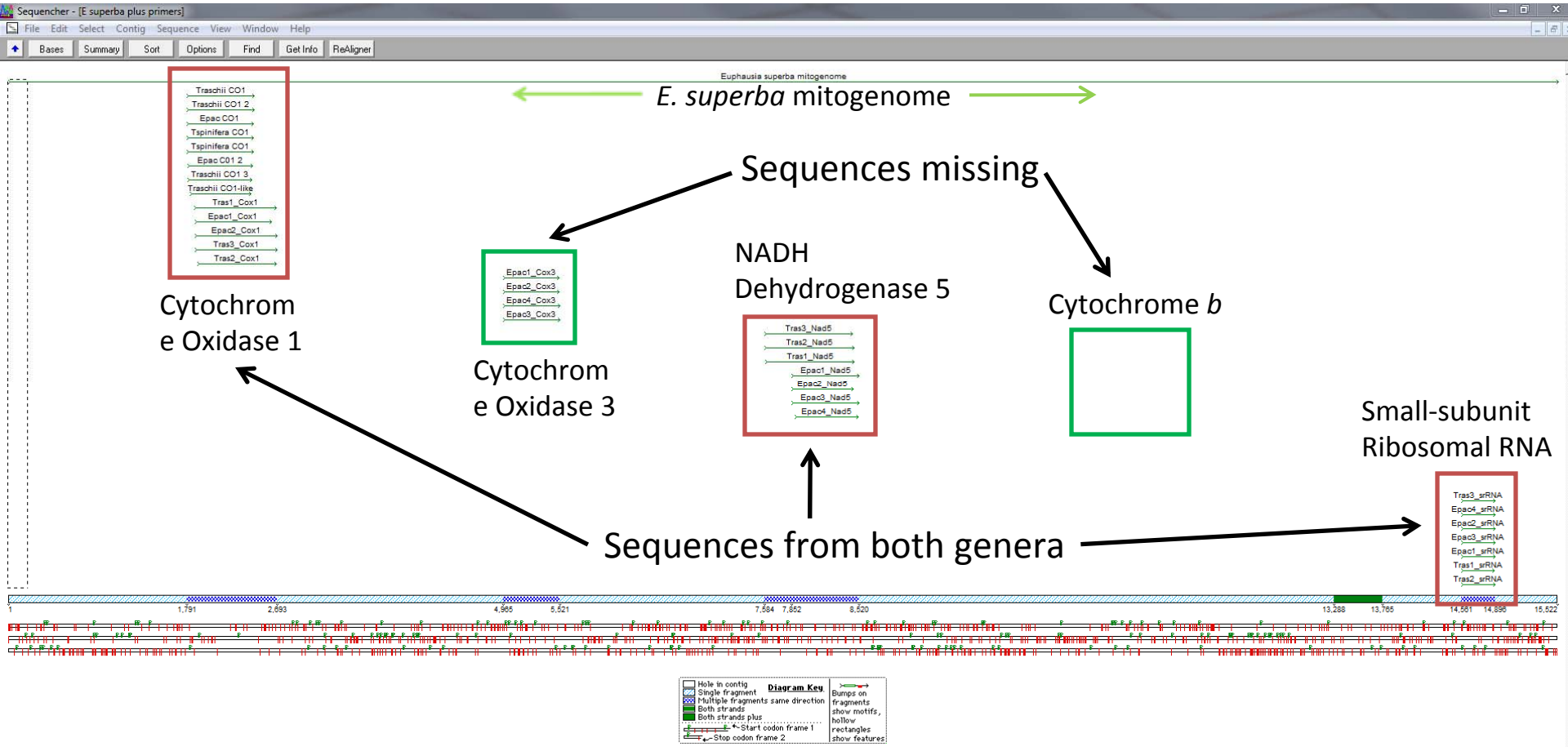

Lots of work still to do…

Where are we now?

Ultimately, we seek to answer the question:

What genetic or genomic characteristics distinguish the cosmopolitan *E. pacifica* and allow it to populate such a wide variety of ecosystems and become dominant among the plankton?

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Current Projects: Tool Building

- Mitochondrial Genomes
- Microsatellite Development

Where do we go from here?

1. Population Genetics
   - *Euphausia pacifica* – North Pacific
   - *Thysanoessa raschii* – North Pacific, Arctic, North Atlantic

2. Reference Transcriptomes
   - Approaching the genome
   - What genes are expressed?
   - How do expressed gene sequences differ?
     - *E. pacifica*
     - *Thysanoessa* spp.

3. Changes in Gene Expression
   - What happens with climate change?
   - Temperature acclimation experiments
     - *E. pacifica*
     - *T. spinifera*