







## so much names...

COI is a gene that encoded a protein called mitochondrially cytochrome c oxidase I. the gene is also called COX1, CO1, COI or MT-CO1<sup>1</sup>.

## DNA Barcoding

COI is often used as a DNA barcode to identify animal species, this because its mutation rate is often fast enough to distinguish closely related species<sup>1</sup>.

## In the human...

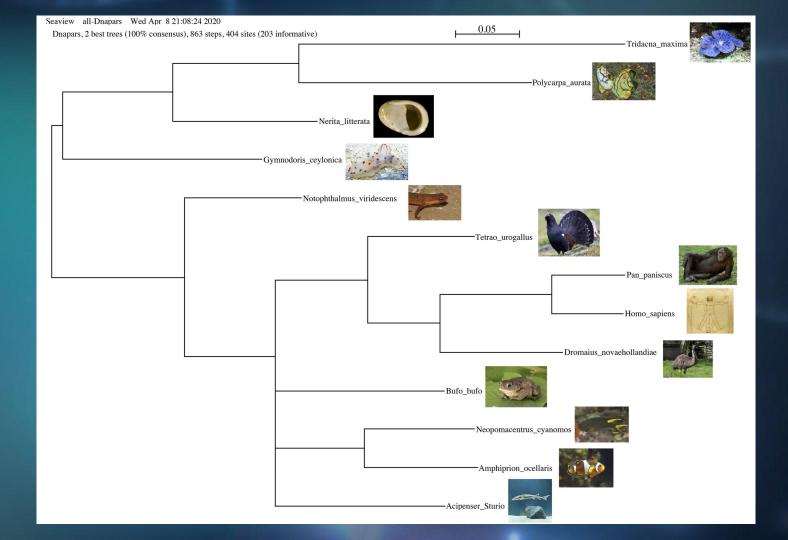
... the gene is located from nucleotide pairs 5904 to 7444 on the guanine-rich heavy (H) section of mtDNA (Mitochondrial DNA)<sup>1</sup>.

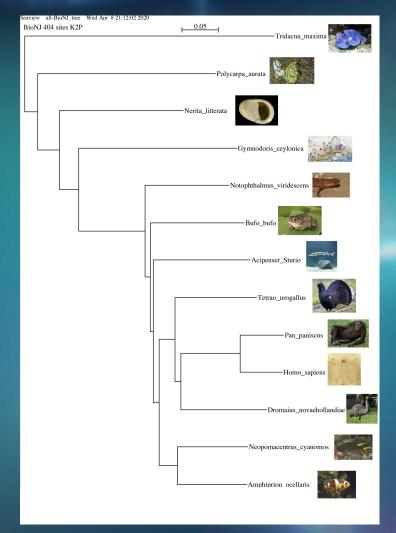


For the assignment was required to take in account different species:

- Polycarpa aurata = marine invertebrate animal
- Neopomacentrus cyanomos = fish native to the Indo-Pacific region from the Persian Gulf
- Acipenser sturio = it is a species of sturgeon previously found on most coasts of Europe
- Homo Sapiens = humans
- Pan paniscus = an endangered great ape
- Nerita litterata = Philippine marine mollusks
- Maxima clam = species of bivalve mollusc found throughout the Indo-Pacific region
- Gymnodoris ceylonica = a species of sea slug
- Bufo bufo = common toad
- Notophthalmus viridescens = common salamander of eastern North America
- Amphiprion ocellaris = common clownfish (remember nemo?)
- Tetrao urogallus = western capercaillie
- **Dromaius novaehollandiae** = emù

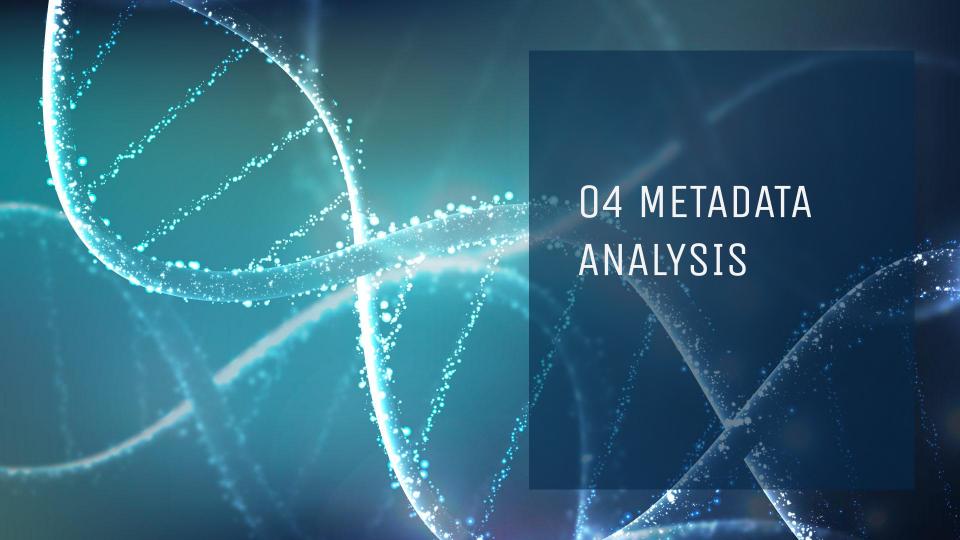






Likewise as seen before, this tree assembles the different species taken in account reasonably.

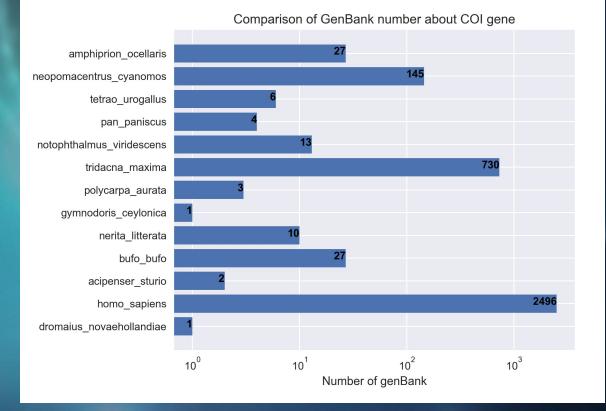
Similar species are represented closely while the ones that are not similar are separated from each other.



Homo sapiens has a greater number of GenBank file, followed by Tridacna Maxima and Neopomacentrus Cyanamos.

The **Tridacna Maxima** has the widest range of all giant clam species<sup>1</sup>.

The **Neopomacentrus Cyanamos** has been found as an invasive species in the Gulf of Mexico and it is widespread in general<sup>2</sup>.

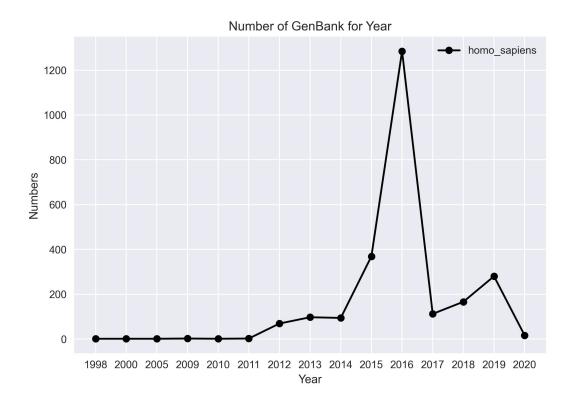


L: Tridacna Maxima

<sup>2:</sup> Neopomacentrus Cyanamos

The increasing trend could be caused by the decreasing of sequencing cost<sup>1</sup>.

The first human genome took \$2.7 billion and almost 15 years to complete. Now genome sequencing and analysis cost around \$1,400. The sequencing can be done in a few days, and analysis in a few weeks<sup>2</sup>.



<sup>1:</sup> Graph of cost per Human Genome

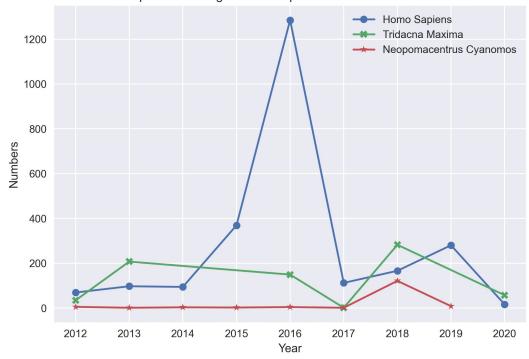
<sup>2: &</sup>lt;u>Unlocking my genome: Was it worth it?</u>

The **Home Sapiens** study has the higher number of sequencioning.

The comparison has been made in the largest common interval of date.

Only in 2013 and 2018 **Homo**Sapiens has been overcome by
Tridacna Maxima. This could be
caused by Australian coral reef
declines showed first in the end of
2012<sup>1</sup> and irreversibly confirmed in
2018<sup>2</sup>.

## Comparison among first three species for numbers of GenBank



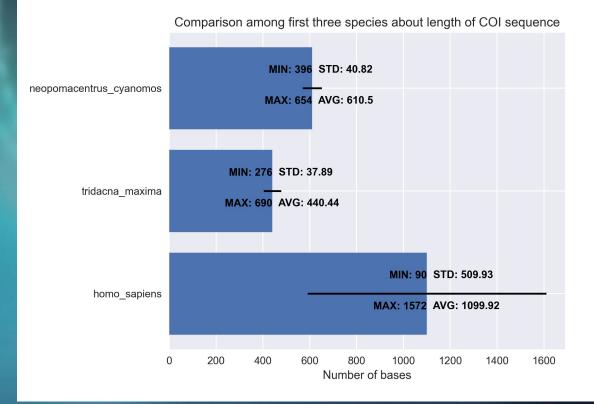
<sup>1:</sup> In 27 anni persa meta' grande barriera corallina

<sup>2:</sup> La Grande Barriera corallina è cambiata per sempre, colpa dei cambiamenti climatici.

The **Homo Sapiens** COI gene length is 1540 bases<sup>1</sup>, parts of the gene surrounded area could have been included in the sequence. The standard deviation value should be investigated...

Others studies about **Neopomacentrus Cyanamos**<sup>2</sup> confirm the length of the COI gene.

No resources found for **Tridacna Maxima**...



Cytochrome c oxidase subunit I

<sup>2:</sup> DNA barcoding of marine ornamental fishes from India



- Why these countries?
- What are related papers talking about?
- Why is there a big gap among Homo Sapiens COI sequences?
- Regarding GenBank per country by other species?



In(number) of GenBank

0

