**Genome Annotation for Antipatharians**

Kayal et al. 2013 selected "The Mold, Protozoan, and Coelenterate Mitochondrial Code and the Mycoplasma/Spiroplasma Code (transl\_table=4)" for their annotations on GenBank. Barrett et al. 2020 utilized the following settings on Mitos2 (Bernt et al., 2013) to confirm annotations: NCBI RefSeq 81 Metazoa and genetic code 4 (mold, protozoan and coelenterate mitochondrial code).

*De novo* assembly was annotated via transferring annotations from Cirrhipathes lutkeni/Stichopathes luteni (<https://www.ncbi.nlm.nih.gov/nuccore/JX023266.1>/<https://www.ncbi.nlm.nih.gov/nuccore/NC_018377.1>) in Geneious Prime 2022.1.1 (Kearse et al., 2012).

Our initial BankIt submission was rejected because the “The Invertebrate Mitochondrail Code” was used, thus stipulating the incorrect reading frame. The second submission to BankIt was mostly correct, however it was still rejected due to *COXI* and *ND5* discrepencies.

Barrett et al. 2020 found that some Antipatharian species possess an intron in *COX1*. In order to amend our annotations we will extract *COXI* and *ND5* from *Antipathes* cf. *dichotoma* (<https://www.ncbi.nlm.nih.gov/nuccore/MT318841.1>), *Phanopathes sp*. (<https://www.ncbi.nlm.nih.gov/nuccore/MT318852.1>), *Stichopathes sp*. (<https://www.ncbi.nlm.nih.gov/nuccore/MZ157399.1>)

The fasta and GFF3 files for all the above were downloaded and placed into a folder in Geneious. Once both documents were loaded both documents into Geneious gene annotations were visible.

In order to extract the gene of interest...

1) select gene (ND5 or CO1)

2) right click "Copy Sequence Name & Bases"

3) go to "Sequence" in the tab/drop down options

4) select "New sequence" and paste the sequence and sequence name here. (Get rid of the name as we are only interested in the bases)

After the gene was extracted a multiple sequence alignment was performed using the Geneious aligner's default settings.

Other tasks that were performed:

-Annotations were exported to a .csv. This was done by going to the Sequence View tab in Geneious and selecting export the annotations to a .csv

-Identify intron regions for each of the above species.

-Extracted intron sequence from the above species.

References

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