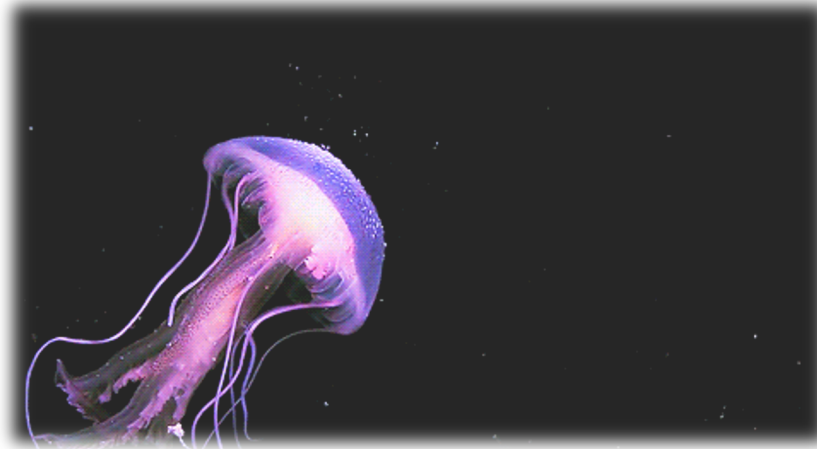# The Life of Moon Jellies

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Intro To Genomics 485

Outline:

- General information (fun facts)

- Genome outcome

- Genome paper

- General genome information

- Sequencing stragedy

- Genome assembly

General information (fun facts):

- The jellyfish got its name from the whitish-translucent moonlike circular bell.

- Its scientific name is Aurelia aurita.

- The body of these creatures is made up of 95% water, 3% protein, and 1% mineral.

- Moon Jellyfish typically live about 12 to 15 months.

- A group of jellyfish is termed as 'smack', and when several smacks gather together to form a larger group, it is called a 'bloom'.

General information (fun facts):

- Moon jellies are the favorite prey of some predators, like the ocean sunfish

- They eat tiny zooplankton and small fishes. They eat, the food items can be seen in the jelly's stomach

- Moon jellyfish live in the Atlantic, Pacific and Arctic Oceans near the coastline. In most cases, they are harmless to humans.

Genome outcome:

- The genome of the moon jellyfish (Aurelia), is from a cnidarian with a medusa life stage and analyses suggest that is a gene gain .

- Loss in Aurelia is comparable to what has been found in its morphologically simpler relatives—the anthozoan corals and sea anemones.

Genome paper:

The genome of the jellyfish *Aurelia* and the evolution of animal complexity

David A. Gold [1,2,12]*, Takeo Katsuki [3,12]*, Yang Li[4], Xifeng Yan[4], Michael Regulski[5], David Ibberson[6], Thomas Holstein [7], Robert E. Steele[8], David K. Jacobs[9] and Ralph J. Greenspan [3,10,11,12]*

General genome information

- A genome is the study of an organism's whole set of genetic information.

- A genome includes all instructions instructions of hereditary for maintaining life and as instructions for reproduction.

- *Aurelia* genome is larger than sequenced anthozoan genomes, but smaller than some strains of *H. vulgaris*

- The *Aurelia* assembly is more fragmented than the anthozoan genomes

Sequencing stragedy:

- Genome sequence was reconstructed by shotgun approach using a combination of Illumina paired-end, mate-pair and PacBio data.

- In total 30166 protein coding genes were predicted and 172 differentially expressed genes.

- Initial scaffolding was performed using error-corrected PacBio reads.

Sequencing stragedy:

sequencing method	sequencing strategy	sequence coverage/depth	contig N50	scaffold N50	number of contigs	number of scaffolds	number of predicted genes
pacbio and ilumina	shotgun approach	60 total coverage	170,088 bp	7744 scaffolds	213,756 bp	7744 scaffolds	>40,000 genes
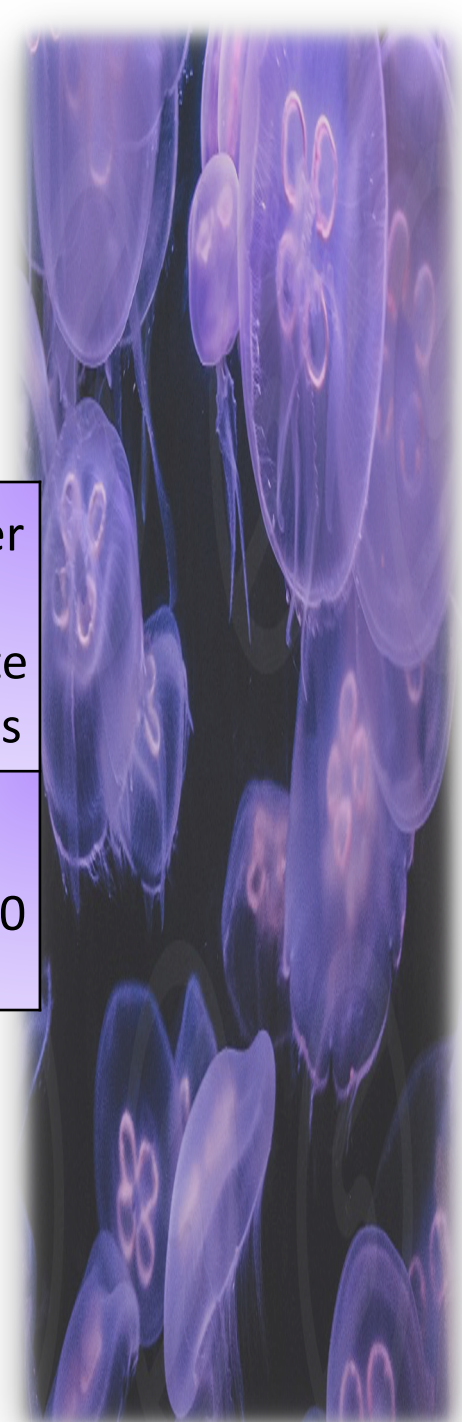
Genome assembly:

- Our final assembly has a total size of 713 megabases (Mb).

- Only contigs >1 kbp were used for the subsequent scaffolding steps. Initial scaffolding was performed using error-corrected PacBio reads.

- Scaffolds larger than 2 kbp were used to calculate the final assembly.

Genome assembly:

- The 250-bp paired-end reads were assembled into contigs using DISCOVAR de novo .

- De novo transcriptome assembly was performed using Trinity

- Trinity models and the Uniprot Swissprot protein data set were mapped to the genome using exonerate80 and GMAP81.

Questions:

- What do you call the group of moon jellies?
- What is the genome size of the moon jelly?