

Khan Inan
Professor Truong
BI-GY 7683

The Genome Size of the Largest Animal to Have Ever Lived on Earth: The Blue Whale

Rationale

My rationale for studying the genome of the blue whale is that since it is the largest animal to have ever lived, is its size also reflected in its genome? In other words, does it have as large of a genome as one would imagine? There are many interesting facts related to genetics that arise when discussing the genome size of a species. For example, since humans are such intelligent creatures, one would imagine that they'd have an extremely complex and large genome. There are, however, unicellular organisms like the amoeba that have a genomes hundreds of times the size of the human genome. I find it very interesting to look into the genome size of the Blue whale, which is larger than any animal alive today, and larger than any prehistoric creature or dinosaur.

Hypothesis

My hypothesis regarding the genome size of the blue whale is that it is not very large at all, and genome size in general is not proportional to organism size

Experimental approach

My experiment to determine the genome size of a blue would begin with obtaining a tissue sample of a blue whale or blue whale carcass. This is necessary because it is extremely helpful to have cells from the animal you are studying, because genetic material can be studied from them. The general process from here is fairly simple, and is not unlike the experiments that many students do in high school and elementary school when they are isolating the DNA of a strawberry. First the cells must be destroyed in such a way that there is disruption of structures down to a cellular level. There are mechanical and chemical methods of doing this, but I think using a lysing enzyme would be the best and most efficient method. From here it is a matter of separating the cell debris from the genetic material. One method of doing this is precipitation since DNA can be dissolved. Once DNA is isolated, using a High Throughput Sequencing method like sequencing by synthesis would allow mapping of the millions of sequences and give us an idea of the general genome size of the organism.

Anticipated Results

Upon calculating the genome size of a blue whale, I anticipate that it will not be nearly as large and complex as one would expect. On a genetic level there are many things that affect the genome size of an organism such as amplification, deletion, mutation etc. and these things happen over the course of evolution. Factors like this are unrelated to the general real-world size of the entire organism and have more to do with things like the cell size, rate of metabolism, lifespan, etc.

Challenges

The main challenge with my experiment would most likely be practical issues, such as sample contamination or variation within tissue samples. Thankfully, i'm not looking for anything specific from within the DNA sequence of a blue whale, but much rather the broader general size of the genome map for a blue whale. Still these issues are important to address, and I believe the best way to eliminate any variables would be to run the sequencing test multiple times. Something as basic as increasing sample size can have a huge impact on gene sequencing results. Let's say, for example, that we are successful in sequencing the genome of a blue whale using state-of-the-art technology and HTS, how would we be certain that this is an accurate representation of the genome size? I think the best way to validate our results would be to compare it with already available reference genomes for the organism. We aren't looking for something exactly the same as the reference genome, but something at least similar.

High Throughput vs Low Throughput (traditional) Sequencing

This experiment would be a great chance to test the general notion that HTS is the preferred choice for sequencing a huge number of targets. In this case, if it's the entire genome of an organism like the blue whale, something smaller scale like sanger sequencing simply would not work. Additionally High throughput methods have advantages like more sensitivity to variations, more data for the same amount of DNA and higher sample throughput (which means that cell samples can survive the testing) which is important since tissue samples may be difficult to obtain.

Useful Reference

A high-quality blue whale genome, segmental duplications, and ... (n.d.). Retrieved October 3, 2022, from https://assets.researchsquare.com/files/rs-1910240/v1_covered.pdf?c=1659454155