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Virus

The process I would use to sequence the DNA of a rapidly evolving new virus would be the Sanger method, otherwise known as the chain termination method. The entire process for successfully dealing with this virus is as follows. First the DNA must be sequenced from virus using the Sanger method and from this DNA a DNA vaccine can be developed. How a DNA vaccine works is that it translates the DNA from the virus into a protein and then your body recognizes the new protein as a foreign element. And then the human body's immune system creates antibodies against the protein/virus DNA. This is the eventual outcome, but my rationale for choosing the sanger method is that it is a simpler and more efficient method compared to other DNA sequencing techniques. The reason for why simplicity and efficiency is important in this case is that very often we may need to constantly sequence new strains of the virus as they evolve, much like how we saw with COVID-19. This whole process of Sequencing the virus and creating a DNA vaccine would take possibly several months and then even more time, depending on any new strains that may arise.

New Human Population

For a new human population that has never been studied before, In my opinion the best way to go about sequencing their DNA would be to use Hierarchical shotgun sequencing. Back when efforts were being made to sequence the human genome, a scientist by the name of Craig Venter went with shotgun sequencing in order to sequence the genome faster than the publicly funded Human Genome Project. Shotgun sequencing removes the stages of mapping and is just an overall more efficient process than clone-by-clone sequencing. Additionally shotgun sequencing needs much less DNA than clone-by-clone sequencing. The main reason why I think that Hierarchical shotgun sequencing is the best method for sequencing this new human population is that this technique works very well when there is a reference genome. Why I chose Hierarchical shotgun sequencing over normal whole genome shotgun sequencing is that hierarchical shotgun sequence does better with sequencing complex vertebrates (like humans) that have a lot of repetitive sequences. Since we already have a map of the fundamental human genome to use as a reference, we can assemble this new genome sequence by comparing and aligning it with what we already have. The outcome of this would be a very fast and efficient method of DNA sequencing for this unstudied human population, but the challenge lies the amount of computing power needed and the need to fill in the gaps and correct the errors. But since we already have a very established reference genome, I am assuming that these errors

would be fairly easy to correct. The main advantage of this approach lies in how quickly the DNA can be sequenced leaving more time and resources to be spent on correcting and filling in any gaps and errors. The Genome of this new human population can be sequenced in about a day but it may take much longer if any analysis is to be done, but eventually we would be finished in a respectable time frame.

Frozen Neanderthal Tissue

For sequencing the DNA of a frozen Neanderthal, the best method would most likely be the Maxam-Gilbert method or the Chemical method. This method uses chemicals to modify the DNA and induce cleavage at certain bases. After a series of radiolabelled fragments are created, they are separated by size using gel electrophoresis and then a sequence can be inferred. The main reason why I chose this method is because DNA degrades over time. Even though this Neanderthal may have been preserved fairly well in the ice, its DNA may still purification (which the chemical method allows). Another reason is that the Maxam-Gilbert methods allows us to analyze DNA-protein interactions. This is important because beyond just sequencing this neanderthal DNA, we want to compare their genome to modern humans. The challenge of using this method is that is is fairly complicated, but I feel as though this does not matter because we wouldn't need to do this process multiple times. In addition to this, the neanderthal DNA is not everchanging, and any data collected will stand the test of time.

Newly discovered deep-sea single celled organism

The best method for sequencing the DNA of this newly discovered deep-sea single celled organism would be whole genome shotgun sequencing. We don't need hierarchical shotgun sequencing in this case because this cell most likely has a smaller genome compared to a more complex organism. This method of shotgun sequencing has many advantages, such as being a single step process, creating smaller fragments, creating a more high resolution genome map, and being overall faster than other methods. Since nothing similar to this single-celled organism has ever been seen before, any method that gives us an understanding of the entire genome of the creature is a better choice. We also don't need a genetic map if we go with this method. The main challenge we need to overcome is that there is no reference genome to compare our results with. We can bypass this challenge by running multiple sequences over and over again to eliminate any errors and gaps that may arise. Out of all the scenarios discussed, this newly discovered undersea organism may require the longest time frame to obtain a complete genome sequence. There are doubts to whether it may be finished at all until a closely related reference genome can be found. Unfortunately there aren't many options available to analyze the DNA and genomes of organisms that have been isolated in the broader genetic map of the earth.