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Biological Phenomena 1: The Ice Man

The Iceman, A mummy more than 5000 years old that was discovered in the Italian Alps, is an archaeological discovery that gave scientists a deeper understanding the the history of humans. Samples taken from the Iceman are the oldest samples ever taken from a human being to have been fully genetically sequenced. Having a human sample this old be analyzed has given researchers an idea of how humans may have migrated and lived throughout europe. High throughput genome sequencing in the form of next-gen sequencing technology has both answered many questions and has raised new ones for the Iceman mummy (who has also been nicknamed Otzi.) The sequencing efforts have shown that his eyes are brown and that his diet restricted dairy foods containing lactose. Obviously certain things were discovered simply upon physical examination of the body in its frozen state (like cause of death via arrow, and his last meal which was ibex meat) but without High throughput sequencing, his lineage and origin would have been unknown. Mainly, the Iceman's Y chromosome, which shed light on his ancestry and relation to modern-day sardinians. One of the strengths of using HTS in this case, is just how small of a sample was actually needed to sequence the entire genome. Only 20 nanograms of DNA was needed, and this is crucial especially if the body in question is extremely fragile and under protection. The weakness of HTS in this case however, is that although researchers were able to sequence the entire genome of the Iceman, there are many abnormalities and variations within the sequence where scientists aren't sure if they have any clinical or geographical significance (in regards to disease, ethnicity, ancestry, etc.)

Biological Phenomena 2: Ancient Wood

Another example of using high throughput sequencing to study archaeological discoveries, is the DNA sequencing of ancient waterlogged European White Oak. There are a collection of 167 European white oak remains that span a huge historical and geographical range stored at the Danish National High-Throughput Sequencing Center. These remains span almost 10,000 years and throughout the entirety of Europe. Having such a large spanning collection of samples helped biologists and archaeologists understand what are the conditions required for long-term preservation of wood remains. High throughput sequencing in this case helped discover what may cause DNA decay in fossilized plants. The process for HTS in this case involved collecting maternally inherited chloroplast haplotypes from the samples which are important because these are the specific categories of plant DNA most susceptible to DNA decay. The strength of using HTS in this case lies in the fact that this is DNA that is incomplete in most cases, but using NGS sequencing methods still allows us to perceive the larger genomic map of these subfossils. This

however is a double edged sword, because herein also lies the weakness of HTS and NGS sequencing techniques. Although these DNA sequencing techniques allow us to work with incomplete and decayed samples, they still don't allow to understand all the different variables in play such as human intervention or human induced deforestation and ecosystem manipulation, and how that may play a part in DNA conservation.