



Metagenomic Composition Analysis of an Ancient Sequenced Polar Bear Jawbone from Svalbard.

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Abstract: The sequencing of ancient DNA samples provides a novel way to find, characterize, and distinguish exogenous genomes of endogenous targets. After sequencing, computational composition analysis enables filtering of undesired sources in the focal organism, with the purpose of improving the quality of assemblies and subsequent data analysis. More importantly, such analysis allows extinct and extant species to be identified without requiring a specific or new sequencing run. However, the identification of exogenous organisms is a complex task, given the nature and degradation of the samples, and the evident necessity of using efficient computational tools, which rely on algorithms that are both fast and highly sensitive. In this work, we relied on a fast and highly sensitive tool, FALCON-meta, which measures similarity against whole-genome reference databases, to analyse the metagenomic composition of an ancient polar bear (*Ursus maritimus*) jawbone fossil. The fossil was collected in Svalbard, Norway, and has an estimated age of 110,000 to 130,000 years. The FASTQ samples contained 349 GB of nonamplified shotgun sequencing data. We identified and localized, relative to the FASTQ samples, the genomes with significant similarities to reference microbial genomes, including those of viruses, bacteria, and archaea, and to fungal, mitochondrial, and plastidial sequences. Among other striking features, we found significant similarities between modern-human, some bacterial and viral sequences (contamination) and the organelle sequences of wild carrot and tomato relative to the whole samples. For each exogenous candidate, we ran a damage pattern analysis, which in addition to revealing shallow levels of damage in the plant candidates, identified the source as contamination.

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