A MINIMALLY DESTRUCTIVE PROTOCOL FOR DNA EXTRACTION FROM ANCIENT TEETH

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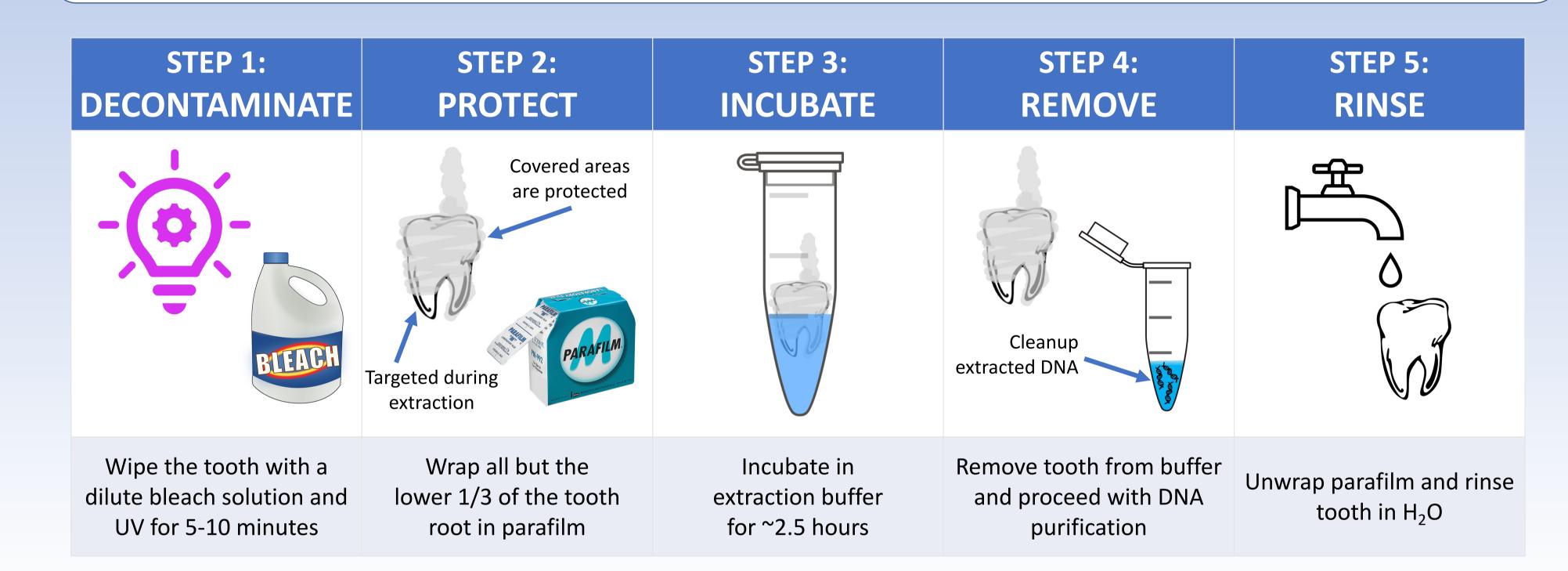
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As the field of ancient DNA has grown, the destructive nature of sampling from



skeletal remains has become a growing area of ethical concern. Ancient DNA sampling methods — although optimized for efficient DNA extraction — are typically destructive, relying on drilling, cutting or grinding-based approaches to produce powder from parts of bones and teeth. There are concerns regarding the physical impact of invasive sampling on ancient remains, particularly on key skeletal collections. Here we describe a minimally destructive protocol for extracting DNA from the outermost cementum layer of ancient teeth.





THIS MINIMALLY DESTRUCTIVE EXTRACTION APPROACH PERFORMS COMPARABLY TO DESTRUCTIVE, POWDER-BASED METHODS

We sampled DNA from 30 multirooted teeth using the minimally destructive extraction (MDE) protocol on one root from each tooth and a destructive approach using powder sampled from a whole tooth root (WTR) from the same tooth. We find no significant difference in DNA quality between the two methods.

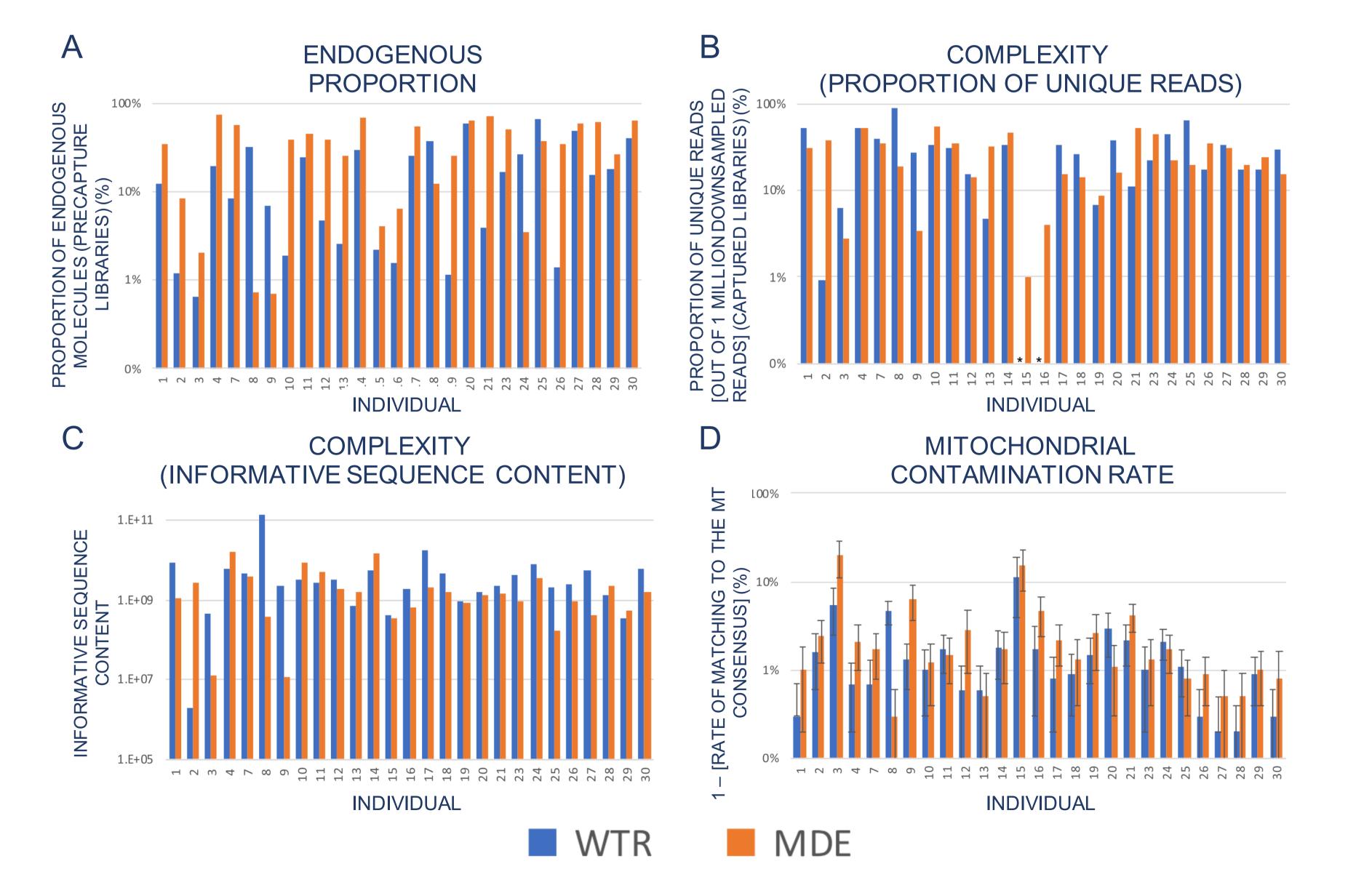


Figure 1. Examples of teeth before and after minimally destructive extraction. Teeth which have been sampled using this minimally destructive extraction protocol were photographed prior to (left) and ~24 h after (right) extraction. Portions of the tooth that were targeted for extraction are indicated with semi-transparent boxes in the after images.

Figure 2. Sample quality. A comparison of the quality of data produced by WTR (Whole Tooth Root) and MDE (Minimally Destructive Extraction) methods in samples that passed quality filtering. (A) The proportion of endogenous molecules in data obtained via shotgun sequencing. (B) The complexity of each sample, as measured by the proportion of unique reads out of 1,000,000 reads sequenced. Asterisks indicate that the total number of unique reads sequenced was below 1,000,000 for the specified sample, and therefore complexity estimates could not be generated. (C) The complexity of each sample, as measured by informative sequence content. (D) The rate of contamination is compared by considering the rate of matching to mitochondrial consensus sequence. Error bars indicate the 95% confidence interval. Only samples that passed quality screening are shown.

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