## Breaking up DNA-mineral interactions – comparing existing DNA extraction approaches for recovery of short fragments

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Marine sediments as climate archives harbour among other biomolecules, large amounts of extracellular DNA present in various pools. Within the sedimentary matrix, DNA fragments bound to various mineral types remain protected from enzymatic degradation and are under favourable conditions able to survive for millions of years. Once extracted from such a matrix, these fragments form a valuable fingerprint of the past ecosystem structure and climate conditions. However, established DNA extraction approaches are often not evaluated and optimized to account for their effect on the overall retrieval of DNA fragments bound to mineral surfaces in light of unique mineral-DNA interactions. In this project, we evaluated these approaches and their ability to desorb and extract short DNA fragments from pure clay and quartz minerals as well as from different types of marine sediments. We separately investigated the lysis step (DNA release) and purification step (isolation of DNA), assessing five different types of lysis buffers across two commonly used DNA purification approaches: silica magnetic beads and phenol/chloroform purification. Our results show that the choice of lysis buffer significantly impacts the amount of recovered DNA from minerals as well as the range of recovered fragment lengths, with buffers containing higher salt concentrations performing best. While we do not observe considerable differences in the amount of recovered DNA from minerals between the two purification approaches, marine sediment DNA extracts and prepared sequencing libraries exhibit varying degrees of quality. With this study, we highlight the importance of lysis buffer choice in sedimentary DNA extractions and demonstrate its impact on the recovery of short fragments. We attribute equal importance to the choice of DNA purification approach in order to facilitate successful downstream processing of DNA extracts and subsequent analysis.