Tracing ancient DNA of foraminifera in tsunami deposits (GEN-EX)

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1. Background

Tsunami deposits provide information on the long-term frequency-magnitude patterns of events, which may not be covered by the historical and instrumental record. Such information is crucial for the assessment of coastal hazards and mitigation measures against the loss of life and assets. In order to identify tsunami deposits in the coastal sedimentary record and to infer tsunami characteristics, a wide range of proxies has been established based on studies of recent tsunami deposits. Microfossils (e.g. foraminifera, ostracods, diatoms) are often used to recognize tsunami deposits, and to differentiate them from those of other processes. In terms of foraminifera, tsunami deposits mostly contain allochthonous associations dominated by benthic intertidal to inner shelf taxa. Specimens may originate from outer shelf to bathyal depths; even planktonic forms may occur. Furthermore, changes in test numbers, taphonomy, size or adult/juvenile ratios compared to background sedimentation are common (Pilarczyk et al., 2014; Engel et al., 2016). However, dissolution of microfossils often prevent identification and diminish their value as a proxy (Yawsangratt et al., 2012).

2. Study goals and concept

To address the problem of post-depositional alteration of microfossil associations in tsunami deposits, high-throughput metagenomic sequencing techniques are applied by the GEN-EX project to identify marine organisms in onshore sand layers based on their DNA remains. Metagenomics (or environmental genomics) is related to sequencing DNA directly from the environmental samples, where the genetic material may have been preserved in sedimentary records covering tens of thousands of years. Metagenomics is an emerging technique in environmental research and is used to characterize the diversity of bacterial communities but also higher organisms such as animals, plants and fungi of recent and ancient origin in a variety of settings, including ice, lake sediments, soils, cave deposits, and various types of surface waters. Metagenomics can also be used to detect cryptic diversity, ultimately providing more accurate estimates of biodiversity (Pedersen et al., 2015). Among the broad range of organisms, foraminifera (single-celled protists) show a water depth-related zonation in subtidal environments, and are the first to have been identified successfully in palaeo-tsunami deposits by their DNA (Szczuciński et al., 2016).

The main objectives of GEN-EX include: quantifying the relationship between water depth and the distribution of different foraminiferal taxa where known tsunami deposits are present, using a comparative classic micropalaeontological and metagenomic approach; assessing the potential (based on both approaches) for identifying key indicator species in tsunami deposits in different coastal settings; and establishing how metagenomic approaches can contribute to the differentiation between storm and tsunami deposits.

3. DNA extraction

DNA will be analysed in two types of material – modern extant foraminifera and sediments (tsunami deposits and adjacent layers). DNA extracted from single foraminiferal specimens will be followed by whole genome amplification to obtain sufficient DNA concentrations. Either part of the nuclear 18S rRNA region or the mitochondrial genome (mtDNA) will be amplified, before high-throughput sequencing of the amplicons. Sequences will be edited and aligned, and their identity verified by BLAST (Altschul et al., 1990) searches in Genbank and the Forambarcoding project (http://forambarcoding.unige.ch). A project-specific database of 18S and mtDNA data of the identified recent foraminifera will be constructed.

Sampling of tsunami deposits and DNA extraction follows the protocol of Szczuciński et al. (2016). Suitable primers will be developed from our reference database of recent foraminifera to amplify overlapping short fragments of 18S or mtDNA of the target species. Amplicon concentration will be quantified and prepared for high-throughput sequencing. Sequence data will be analysed with different bioinformatics pipelines (e.g. QIIME), including quality control, removal of barcodes and adaptors, identification and removal of chimeric and redundant sequences, and comparisons with our own and open access databases of 18S data for defining Operational Taxonomic Units with 95% and 97% similarity cut-offs.

4. Study area

One of the study areas, where the eDNA approach is applied, are the Shetland Islands, exposed to the mega-tsunami triggered by the early Holocene Storegga submarine slide off the coast of Norway. Sediment run-up of more than 25 m left a distinct landward-thinning sand layer with an erosive lower contact, large rip-up clasts, fining-upward sequences and marine diatoms in near-shore lakes and coastal peat lowlands. In addition to sediments associated with the Storegga tsunami, two younger tsunami deposits dated to c. 5 and 1.5 ka (Bondevik et al., 2005) are investigated. Sampling for the planned foraminiferal analyses and eDNA extraction of the deposits and their source area, comprising along the beach and subtidal area to the central shelf area is scheduled for the second half of March 2018.

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