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Metagenomics of tsunami deposits: developments, challenges and recommendations from a case study on the Shetland Islands (UK)

Max Engel[1,2], Tasnim Patel[3], Sue Dawson[4], Anna Pint[2], Isa Schön[3,5], and Vanessa M.A. Heyvaert[1,6]
[1]Royal Belgian Institute of Natural Sciences, OD Earth and History of Life, Geological Survey of Belgium, Brussels, Belgium (mengel@naturalsciences.be)
[2]University of Cologne, Institute of Geography, Köln, Germany
[3]Royal Belgian Institute of Natural Sciences, OD Nature, ATECO – Freshwater Biology, Brussels, Belgium
[4]University of Dundee, Department of Geography, Dundee, UK
[5]University of Hasselt, Research Group Zoology, Diepenbeek, Belgium
[6]Ghent University, Department of Geology, Ghent, Belgium

Onshore tsunami deposits provide crucial information on tsunami recurrence patterns in flood-prone areas. Their composition is mainly a function of the site-specific coastal sediment system, bathymetry, and onshore topography and flow conditions. Microfossils (e.g. foraminifera, ostracods, diatoms) are often utilised to recognize tsunami deposits and differentiate them from other deposits. Foraminifera found within tsunami deposits mostly comprise allochthonous associations dominated by benthic intertidal to inner shelf taxa. Specimens may also 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. However, post-depositional degradation (e.g. dissolution) of carbonate tests often prevents identification, thereby reducing their value as a proxy.

The project “GEN-EX - Metagenomics of Extreme Wave Events” aims at developing high-throughput, metagenomic sequencing techniques to identify foraminifera assemblages and to unravel their cryptic diversities in onshore extreme wave deposits from their environmental DNA (eDNA) signature. The project has sampled tsunami deposits from coastal peat sections at three sites on the Shetland Islands, UK, dated to approximately 1.5, 5.5 and 8 ka BP, respectively. Tsunami deposits were identified by utilising integrative high-resolution grain-size analysis, CT scanning, multi-sensor core logging and geochemical analyses. When applying classical micropalaeontological techniques, no foraminiferal tests were found in any of the tsunami deposits analysed to date, whilst inter- to subtidal offshore source deposits show moderate to high foraminiferal concentrations, indicating possible severe post-depositional dissolution of foraminifera in the onshore tsunami deposits, which are bracketed in between massive dystrophic peats.

Several different extraction methods, polymerase chain reaction (PCR) protocols (to amplify target regions of the foraminifera DNA) and primers were tested. So far, the S14 F3 and S14 F1 primers were able to amplify the DNA of specific foraminiferal taxa from modern offshore samples, but

this approach was less successful for the palaeo-samples. Current tests are focusing on targeting the amplification of another region of the foraminiferal DNA (V9), with the best available protist specific universal DNA primers at present. Possible reasons for the challenges in amplifying foraminifera DNA in the palaeotsunami samples may be due to the high age of the deposits and time-associated DNA degradation; transportation and storage of samples at ~-20 °C may also be key. However, it is possible that the foraminifera DNA is altogether absent from the sediment collected, even though this is considered unlikely given the number of tests recorded and identified in the potential subtidal source sediments. Thus, at present, a “shotgun sequencing” approach is being applied to these samples to obtain the eDNA signal in its entirety from the remains of all taxa within the sediment.

Finally, our tests so far have further revealed that the extraction method and DNA amplification protocols must be modified individually for each of the different sample types, i.e. modern offshore, modern intertidal and palaeotsunami samples, posing an added challenge to this metagenomics research. A comprehensive summary of all recommendations will be made available in the near future.