

THE END CRETACEOUS MASS EXTINCTION EVENT

– RECOVERY AND EVOLUTION OF LIFE

B. Schaefer¹, M. J. L. Coolen¹; C. C. Cockell²; K. Grice¹ and expedition 364 scientists

¹Curtin University, Perth, Australia

²University of Edinburgh, Edinburgh, United Kingdom

The End-Cretaceous Mass Extinction event was one of the five largest mass extinction events in the Phanerozoic (Wiese and Reitner, 2011) and the only one proven to be associated with a meteorite impact (e.g. Hildebrand, 1991; Schulte et al., 2010). The impact crater at Chicxulub in Mexico is the largest terrestrial crater with a peak ring and a global ejecta area. For the first time the peak ring of the crater has been cored by the Integrated Ocean Drilling Program (IODP) 364 drilling expedition “*Chicxulub: Drilling the K-T Impact Crater*” in 2016 to study how the peak ring was formed and how microbial and aquatic life evolved post impact. While the impact event has been fairly well studied for fossilising taxa, the post impact recovery and evolution of the majority of “soft-bodied” plankton and invertebrates is largely unknown. In this study molecular fossils and geo-molecules will be analysed using organic and isotopic geochemistry parallel to a molecular biological approach. It has been shown that ancient DNA can be preserved for hundreds of thousand years and be used for ecosystem reconstruction (Coolen and Overmann, 2007) . For this project, it will be explored to what extent ancient plankton and vegetation DNA can be recovered from Cenozoic marine sediments overlying the Chicxulub impact crater and if this DNA is suitable to study the post-impact recovery and if possibly living bacteria in the Cenozoic record can provide information about post-impact environmental and depositional conditions. Further, the study of microbial metagenomics in the impact breccia and the peak ring below the marine Cenozoic sediments will reveal the diversity and function of microbial communities that at some point in history must have been able to recolonise the fractured impact rocks after the crater had sufficiently cooled down to sustain microbial life.

Initial results show that the meteorite-impacted breccia and overlying marine Cenozoic sediments contain up to 800 picograms genomic DNA per gram of rock/sediment. Polymerase chain reaction (PCR) revealing the presence of environmental ribosomal RNA genes of all three domains of life (bacteria, archaea, and eukaryotes). The taxonomic diversity of these organisms are to be revealed (in progress) through ultra high throughput sequencing of the recovered rRNA genes. The amount of genomic DNA that has thus far been recovered from the rock and sediment samples should be sufficient for subsequent metagenomic sequencing of functional genes to infer the potential roles of these deep subsurface microbes (e.g. Orsi et al., in review).

The coupling of the microbial metagenomic datasets with organic and isotopic geochemistry proxy data and in the context of geological data through collaboration with the other IODP 364 science party members will contribute to a deeper understanding of environmental factors that control life in the deep biosphere, its ability to recover and evolve after major extinction events, and the possibility of life to form on other planets (Grice et al., 2000; Orsi et al., in review; Whiteside and Grice, 2016).

References

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