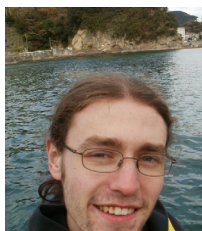


Survivors of the Sea: Investigating the genomics and survival strategies of the diatom *Skeletonema marinoi*

In this thesis, I use the genome of the marine diatom *Skeletonema marinoi*, along with transcriptomics data, to investigate its ability to form resting stages that can survive in dark, anoxic sediments for over a century. While the longevity of these dormant cells is well known, the precise mechanisms they use to survive these periods without access to oxygen or sunlight is not well understood. Transcriptome sequencing was used to compare gene expression between vegetative and resting cells of *S. marinoi*, revealing major shifts in core metabolic pathways and consistent upregulation of genes relating to protein synthesis. When examining biases in allelic expression, I identified a number of genes that undergo major shifts in allele-specific expression between the resting cells and their vegetative counterparts. These included genes from several pathways pertaining to the diatoms' silica cell wall.

The *S. marinoi* reference genome was also used as part of a new bioinformatic tool – Bamboozle – to identify novel, intraspecific genomic barcoding loci capable of tracking the relative abundance of strains in co-culture.

This thesis has provided some insights into the activity of 'dormant' diatom resting stages, and highlights potential avenues for future studies of these fascinating phytoplankton.



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ISBN 978-91-8069-399-8 (PRINT)
ISBN 978-91-8069-400-1 (PDF)
<http://hdl.handle.net/2077/78323>

Ph.D. thesis

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PH.D. THESIS

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