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Evolutionary and ecological effects of metal pollution on coastal diatoms

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Abstract

Oceans are changing rapidly in response to human activities, such as toxic pollution, eutrophication, and climate change. Diatoms are major primary producers in the oceans with short generation times, flexible reproductive strategies, and high standing genetic diversity. These traits should facilitate rapid evolution, potentially increasing the resilience of individual species and buffer against the effects of global change. In my thesis, I use the Baltic Sea and metal pollution as a model system to study the evolution of diatoms in response to global change. I use two native species, *Skeletonema marinoi* and *Thalassiosira baltica,* to investigate evolutionary and ecological responses to metal pollution at a mining-exposed inlet. The mine, Solstads gruva, has been active for 400 years, and the ore was deposited on the shore of a five km^2 large inlet, Gåsfjärden.

I first tried to use a resurrection approach to study evolutionary processes backward through time. However, cross-contamination from contemporary cells at the sediment surface made age determination inconclusive. As previous studies have not quantified contamination directly, this finding suggests that phytoplankton survival in sediment may have been overestimated, and evolutionary interpretations possibly confounded. I re-directed focus on the contemporary diatom population present on the sediment surface. I found noticeable species differences between *S. marinoi* and *T. baltica* in tolerance towards non-essential metals (silver, cadmium, and lead) and indications that *S. marinoi* had evolved elevated tolerance towards copper and cobalt at the mining-polluted inlet. Moreover, I showed that metal pollution modifies competitive interactions between *S. marinoi* and *T. baltica*. Specifically, both species had large and overlapping, intraspecific variability in tolerance to copper, and evolution through selection on standing strain diversity modified the competitive outcome between them.

To better understand selection and other evolutionary processes, we collect and analyze whole genome sequencing data from 55 strains of *S. marinoi.* We developed a bioinformatic tool that can identify the most allele-rich loci across a species genome and used it to localize three hypervariable loci in *S. marinoi* with at least 100 unique alleles amongst the 55 diploid genomes. I used the barcode loci to track selection in an artificial evolution experiment with a relatively high diversity consisting of 58 strains. The barcodes enabled me to enumerate and quantify fitness of individual strains under co-cultivation. I showed that under intense copper stress, and within 42 days [or 50 generations], one or two strains outcompeted the other conspecific strains. Future studies utilizing the barcode loci should be able to track evolution in more complex ecological settings and with much higher genetic diversity than what was possible with existing technologies. Finally, I link the copper tolerance phenotypes with genomic changes in copy number variance of metal detoxifying and transporting genes. Although I found copy number variance to be prevalent in genes encoding metal binding proteins, this did not correlate with copper tolerance in strains, suggesting that other genetic mechanisms were responsible for the evolved copper tolerance in the population. In summary, my thesis enhances our understanding of the evolutionary potential of phytoplankton in general, and metal tolerance in diatoms specifically. This evolution can be rapid; genetic diversity can be created within centuries, and selection on this diversity provides populations with the capacity to adapt to environmental change on timescales relevant for seasonal blooms.