

## **'Resurrection ecology' of 600-year-old water fleas used to understand pollution adaptation**

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In this picture, a hatching Daphnia (bottom) and a pair of dormant Daphnia eggs (top-isolated from an ephippium, a kind of protective case produced by the 'mother Daphnia' in which the eggs get buried in the sediment. Credit: Dagmar Frisch

One of the leading threats to lakes since the rise of agriculture are runoffs from fertilizer, in the form of high phosphorus levels. These can



trigger devastating events like eutrophication, where deadly algal blooms thrive on phosphorus, and in the process, outcompete and choke off vital nutrients from the rest of the lake.

But to best learn how organisms can adapt to eutrophication events requires comparing samples before and after the event —-a seemingly impossible feat to study eutrophication—-since it arose with modern agricultural 100 years ago.

So, by taking advantage of the unique genomic model organism of tiny waterfleas, or Daphnia, an international team of researchers has now analyzed Daphnia from a phosphorus-rich Minnesota lake —-and compared it to revived, 600-year-old Daphnia dormant eggs found in the bottom sediments—— to better understand how these creatures cope with a dramatic <u>environmental change</u>.

Dagmar Frisch and her colleagues, based in the University of Birmingham's School of Biosciences, used the 'resurrection ecology' of Daphnia and new analysis tools to perform the study. The team was only able to make these discoveries by comparing the responses of modern Daphnia with their 600-year-old ancestors.

Both the modern and the ancient samples studied came from the same lake in Minnesota where eutrophication first started at the beginning of the 20th century. "We used existing data and state-of-the-art <u>analytical</u> <u>methods</u> to connect patterns of gene expression with the physiological responses that allow these animals to deal with increased environmental phosphorus" said author Dagmar Frisch, an expert in environmental paleogenomics. "This allowed us to identify which part of the gene network was accountable for the newly evolved response."

"Because Daphnia is such a central species in <u>aquatic ecosystems</u>, our study ultimately improves our understanding of how aquatic ecosystems



can mitigate some of the effects of <u>eutrophication</u>, one of the major global threats to freshwater environments," said co-author Dörthe Becker, an expert in environmental 'omics'.

They were able to show a large cluster of several hundred genes uniquely adapted in modern-day Daphnia to high phosphorus levels. Many of these were involved in vital, core <u>metabolic pathways</u> necessary for Daphnia survival.

"We used network analysis methods to find out which <u>genes</u> 'communicate' with others to form clusters (or "modules"), and how this gene communication has changed in a keystone species over the last 600 years. In addition, we were able to connect these modules with particular observed traits, which was achieved for the first time in resurrection ecology," said co-author Marcin Wojewodzic.

"Our study emphasizes that evolution is a result of molecular fine-tuning that happens on different layers, ranging from basic cellular responses to complex physiological traits" said Becker. "The approach we used allows a more holistic view of how animals can and do respond to environmental change, and by that improve our understanding of organisms as integrated units of biological organization," said Frisch.

Next, the team will continue to explore how these networks and other molecular processes, including epigenetics play a role in evolutionary adaptation to changing environments.

**More information:** Dagmar Frisch et al, Dissecting the Transcriptomic Basis of Phenotypic Evolution in an Aquatic Keystone Grazer, *Molecular Biology and Evolution* (2019). <u>DOI:</u> <u>10.1093/molbev/msz234</u>



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