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Illuminating the Polar Night: an Analysis of Phytoplankton Communities in Svalbard through Citizen Science and Genetics

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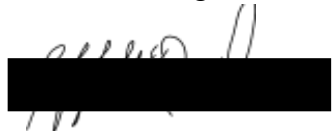
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Acknowledgements:

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Abstract

In 2019, citizen scientists overwintered in Svalbard, a high-Arctic region experiencing extreme seasonal changes including the prolonged darkness of the polar night. During their expedition, they collected phytoplankton samples that were processed using RNA sequencing methods to investigate gene expression patterns throughout the transition into winter. This study presents a short time-series analysis of Arctic phytoplankton gene expression before and during the polar night, linking shifts in gene ontology (GO) terms across Biological Process (BP), Cellular Component (CC), and Molecular Function (MF) categories with environmental variables such as temperature, sea ice thickness, salinity, and sunlight duration. Early sampling revealed upregulation of genes related to salt stress and light response, while the coldest day exhibited widespread activation of cold response pathways and energy metabolism components. During the polar night, most gene expression declined, with selective maintenance of critical cellular functions and ion transport activities, suggesting molecular strategies that enable survival under harsh environmental extremes. This research fills key knowledge gaps about phytoplankton activity during the darkness of the polar night and demonstrates the value of citizen science in advancing polar research and engaging the public with climate-related environmental change. Further studies are needed to explore causal relationships and refine our understanding of phytoplankton responses in a rapidly changing Arctic.

Introduction

“Day 29. -10 Celsius... Light here is such a powerful element. The natural light is over-the-top beautiful and ever-changing... We'll only have daylight for the next 7 hours and every day this month less and less until October 26th - I think that's the date? - When the sun has forever dipped below the horizon below 5° until February. It's a little bit hard to imagine and even believe... I wonder who I will become in the dark ha ha poor Hilde – I write with a smile.”
— Sunniva Sorby, 2019

The polar night begins. A period of near-total darkness and extreme weather conditions that lasts from mid-November to the end of January. This excerpt taken from the journal of Sunniva Sorby was written in the weeks leading up to the onset of total darkness. Sorby, a historian, expedition leader, and citizen scientist, kept journal entries documenting her and her expedition partner, Hilde Fåln Strøm, overwintering in Svalbard during the Hearts in the Ice expedition of 2019. They embraced the unknown and trusted their mission to connect others to the Arctic through citizen science. This drive led them to become the first women in history to overwinter in Bamsebu, a remote trapper's hut near Van Keulenfjord in Svalbard, an archipelago between mainland Norway and the North Pole. The isolation led to limited supplies, no immediate access to civilization, and the opportunity to be completely present with life. The quiet space of the polar night revealed darkness both outside of and within themselves, pushing them to connect to their deepest human purpose.

Prior to their expedition, Sorby and Strøm generated a network of scientific collaborators in an effort to collect useful data during their stay. In combining key institutions and researchers, they were trained to perform protocols through the framework of citizen science, meaning as non-scientists they voluntarily participated in scientific research projects. Through their efforts in this remote region, they created accessible datasets and raised public awareness about climate change issues in Svalbard. A timely concern given that the Arctic is warming four times faster than the global average (Rantanen, 2022). Specifically, the period of the polar night is notorious for being one of the most data-limited seasons and with their efforts researchers could begin to answer long-standing scientific questions from these remote regions of the world. They participated in a multitude of citizen science projects including: taking photos of auroras with Aurorasaurus, flying drones to gather environmental data with BCIT, looking at microplastics with the Norse Polar Institute, taking ice core samples with UNIS, looking at clouds with NASA Globe Observer, observing marine mammals (including polar bears) with UNIS, and collecting phytoplankton samples with Fjord Phyto (Hearts in the Ice, 2019).

These phytoplankton samples collected in collaboration with Fjord Phyto, a program monitoring phytoplankton responses to glacial meltwaters in the poles, are the focus of this study. Sorby and Fåln Strøm used the organization's protocols to gather water samples that could later be analyzed by researchers at Scripps Institution of Oceanography to better understand how phytoplankton respond to the darkness of the polar night at a genetic level (Cusick, 2020). Although, collection sounds simple enough, the changing environmental conditions provided their own set of challenges.

“Day 15. Really cold morning, likely the coldest day yet -5 but that's nothing for what's to come... We held our phytoplankton net, dipped our brown jar in for salt water and lowered the Secchi disk in for a reading—close to 4 meters. Success and such a great feeling when we finish our projects.” — Sunniva Sorby, 2019

These samples were taken from surface seawater to target phytoplankton, tiny single-celled protists ranging in size from 0.002 mm to 1 mm. These organisms are found throughout all marine environments and are the primary producers that serve as the foundation of the marine food web. They convert sunlight into energy and produce over half of the oxygen on Earth (Falkowski et al., 1998; Field et al., 1998). Their growth and distribution are influenced by factors such as light availability, temperature, and nutrient concentrations. Consequently, changes in phytoplankton species composition can serve as early indicators of broader ecosystem shifts (Behrenfeld et al., 2006). The abundance of phytoplankton has far-reaching effects, impacting fisheries productivity and playing a critical role in carbon sequestration by absorbing carbon dioxide during photosynthesis (Le Quéré et al., 2005). Monitoring phytoplankton dynamics provides valuable insights into ocean health, climate regulation, and potential changes in marine food webs. Understanding their cellular responses, particularly during the often-overlooked polar night, is essential for predicting how marine ecosystems will respond to dramatic seasonal variations.

Until recently, it was widely believed that the absence of light during the polar night led to a significant decrease in primary production, rendering phytoplankton largely inactive (Pace, 2012; Berge, 2015). This assumption contributed to limited sampling efforts during winter months, leaving a gap in our understanding of polar marine ecosystems. However, emerging research has revealed that some phytoplankton species remain metabolically active even in the prolonged darkness (Berge, 2015). This growing body of evidence challenges previous assumptions and highlights new opportunities to investigate the ecological roles of phytoplankton throughout the polar night. Despite the logistical challenges posed by the remote and resource-limited environment, the citizen science approach enabled Sunniva and Hilde to make valuable contributions to this sparse dataset, providing important insights into phytoplankton activity during this understudied period.

Methods

Study Site: Svalbard is a remote Norwegian archipelago located in the high Arctic that is characterized by glaciers, deserts, and unique biodiversity such as Arctic foxes, bearded seals, Svalbard reindeer, belugas, and walruses (Coulson, 2042, Figure 1). Bamsebu, a historic trapper's hut located near Van Keulenfjord, was originally built in the early 20th century. Since its construction, it has offered refuge to trappers, travelers, and expeditioners braving the harsh Arctic conditions.

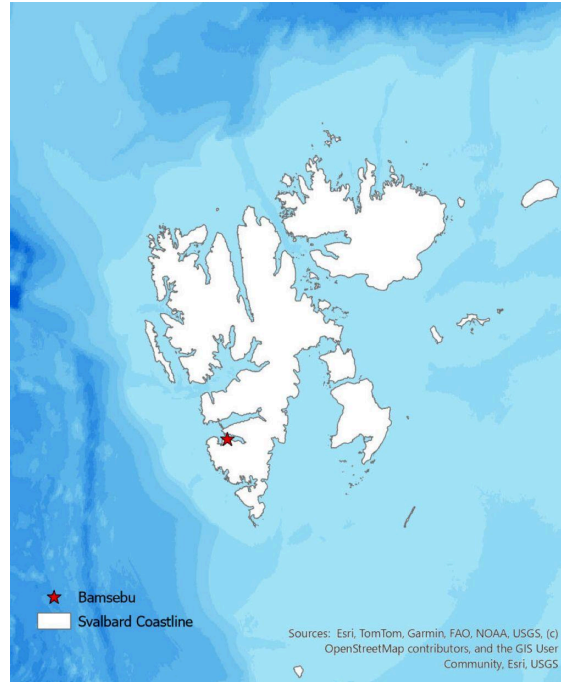


Figure 1. Map of the Svalbard and the trapper's hut, Bamsebu. Bamsebu served as the field base for all of Sorby and Strøm's field work during their 2019 Hearts in the Ice expedition.

Sampling: Sorby and Strøm collected ten sea surface water samples in the bay outside of Bamsebu using a 20-micron net starting on September 24th until December 28th, 2019. The first six samples were before the polar night and the last four samples were during the polar night (Supplemental Table 1). After net towing, they filtered the concentrated biomass through a 0.2 - micron filter which was then preserved in a stabilizing solution (RNAlater) and frozen until processing by scientists at home institutions.

RNA sequencing: RNA extraction and sequencing was done at the University of California San Diego, J. Craig Venter Institute and UC Davis Sequencing Core then used to examine the phytoplankton's gene expression across the ten water samples. After sequencing, gene-level expression data was normalized in two steps. First, each gene's raw count was divided by its length to account for size differences between genes. Then, expression values were normalized to the total RNA read count per sample to ensure comparability across samples of different sizes. This method ensures that larger samples do not skew results by having more reads of a gene simply due to sample volume. A more detailed description of the procedures are available in Willis (2025).

Gene Ontology (GO) Analysis and Data Processing: Gene Ontology (GO) Analysis and Data Processing: Following assembly and annotation, open reading frames (ORFs) were translated using FragGeneScan and functionally annotated via multiple protein domain databases, including EggNOG v5 (Willis, 2025). To enable downstream analysis of gene expression patterns, Gene Ontology (GO) terms were used to classify annotated ORFs. GO terms, which offer a

standardized vocabulary for gene functions across organisms, were used to classify expression data (EMBL-EBI, n.d.). GO terms with a total row sum of at least 20 transcripts per million (TPM) were retained for analysis. GO terms were organized into three main ontologies using the BiocManager R package: Biological Process (BP), which includes broader physiological or cellular responses, Cellular Component (CC) which indicates the cellular location or structure where a process takes place, and Molecular Function (MF), which describes the activity of specific molecules (Gene Ontology Resource, 2025).

GO Enrichment Analysis: A GO enrichment analysis was conducted to identify stress-related responses among BP terms. This process guided the selection of BP GO terms, which included response to cold (GO:0009409), response to salt stress (GO:0009651), and response to light stimulus (GO:0009416). These terms were chosen because they represent the most environmentally relevant physiological responses observed during the polar night.

CC GO Terms and MF GO Terms: CC and MF GO terms were selected based on their relevance to the chosen BP terms and the environmental data obtained from the Copernicus Marine Service. It is important to note these terms were subjectively chosen. A complete list of all GO terms included in the analysis is provided in Supplemental Table 2.

Data Visualization and Figure Generation: A variety of R packages were used to generate visual representations of the data. The packages *readxl*, *pheatmap*, and *RColorBrewer* were used to create heatmaps of GO term expression. For line graphs visualizing environmental variables over time, *tidyverse* and *readr* were used. Boxplots comparing the distribution of GO term counts across the BP, CC, and MF categories were created using *ggplot2*, *dplyr*, *tidyr*, *readr*, *hrbrthemes*, and *viridis*. Each figure was generated to show different aspects of the data, including molecular response patterns and environmental trends.

Environmental Data: Satellite-derived environmental data was obtained from the Copernicus Marine Service on May 9, 2025. This platform provides high-resolution oceanographic datasets that are widely used for marine research. For this study, a region in the Arctic was selected, encompassing 20 satellite pixels spanning latitudes 77.45° to 77.63° N and longitudes 14.5° to 15.7° E. This area surrounds the general location of biological sampling. While exact sample coordinates were not available, this spatial window was chosen to ensure representative environmental coverage of the study region. For each sampling date, mean values were calculated across all 20 pixels to estimate environmental conditions. This averaging approach captures spatial variability while preserving ecological relevance for comparisons with gene expression data.

Statistical Tests: To test whether gene expression levels differed between groups, either Welch's t-test or the Student's t-test was used, depending on the data distribution and the similarity of group variances. Before selecting the appropriate test, the Shapiro-Wilk test (Shapiro and Wilk, 1965) was used to assess normality, and Levene's test (Levene, 1960) was used to evaluate the

equality of variances across groups. Welch's t-test, which does not assume equal variances or sample sizes, was used when these assumptions were not met (Welch, 1947). In cases where both normality and homogeneity of variance were met, the standard Student's t-test was applied (Student, 1908). Both methods are well-established in gene expression analyses for detecting differences between experimental conditions (Ruxton, 2006). Results of the Shapiro-Wilk and Levene's tests are provided in Supplemental Table 3a, and the results of the t-tests are presented in Supplemental Table 3b.

Preliminary Results

Pre-Polar Night and Polar Night Variation: Differences were observed between the pre-polar night and polar night periods across all measured environmental variables (Figure 2). Air temperature was higher prior to the polar night (mean = 0.67 °C) compared to the polar night period (mean = -1.61 °C), with a Welch's t-test confirming this difference ($t = 3.84, p = 0.0093$). There was also a clear change in sea ice thickness, rising from a mean of 0.048 m in the pre-polar night to 0.44 m during the polar night ($t = -4.38, p = 0.0023$). Salinity also showed an evident increase during the polar night (mean = 35.23) relative to the pre-polar night period (mean = 33.96; $t = -5.72, p = 0.0004$). Lastly, sunlight hours dropped to zero during the polar night (mean = 0.00) from an average of 7.76 hours pre-polar night ($t = 5.48, p = 0.0028$) (Supplemental Table 3b). Collectively, these results demonstrate significant environmental transitions associated with the onset of polar night (Figure 2).

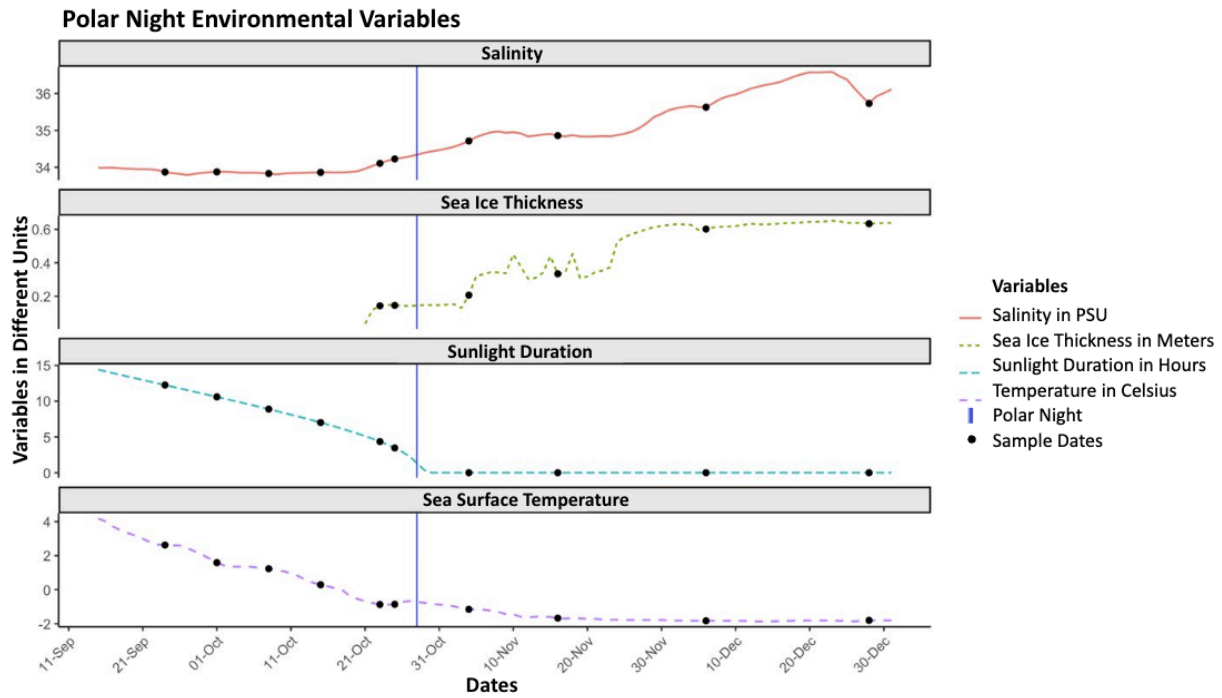


Figure 2. Time-series plots of environmental variables measured from September 13 to January 1, 2019. The x-axis is labeled at 10-day intervals and each variable is plotted with its own y-axis scale denoting the appropriate units. Panels display salinity, sea ice thickness, sunlight duration, and sea surface temperature. Lines are colored and styled by variable. Black dots indicate sample collection dates. A vertical blue line marks the onset of the polar night on October 28, 2019.

Community GO Term Expression: GO term expression totals were grouped into three categories: Biological Process (BP), Cellular Component (CC), and Molecular Function (MF). The total number of GO terms in each category are available in Supplemental Table 4. Notably, expression peaks were observed on September 24 and November 4, with overall expression levels declining during the polar night (Figure 3).

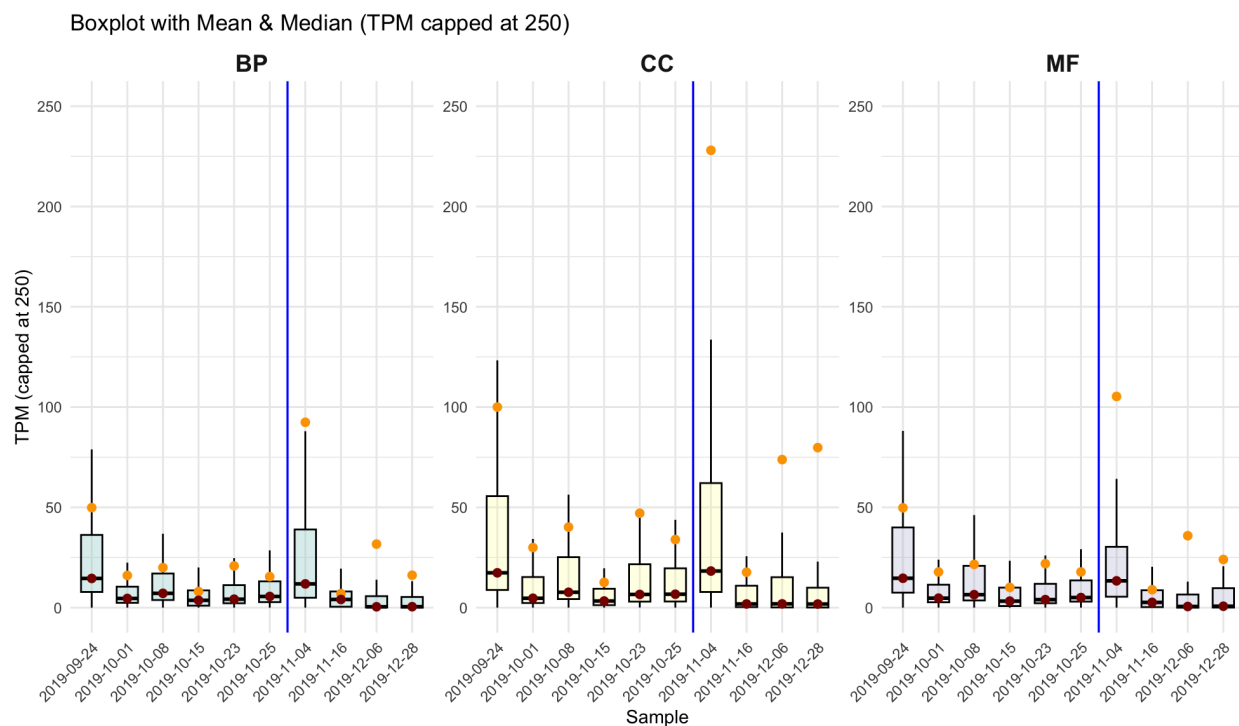


Figure 3. Box plots showing transcripts per million (TPM) of GO terms across ten sampling dates, categorized by Gene Ontology domains: BP, CC, and MF. Orange points indicate the mean expression, while dark red points represent the median. The blue line marks the division between samples collected before and after the onset of the Polar Night. TPM values have been capped at 250 to better visualize the overall expression patterns across all GO terms.

GO Term Pattern Interpretation: In the first sample collected on September 24th, BP such as response to salt stress and response to light stimulus are upregulated, while response to cold is downregulated (Figure 4). There is upregulation in CC, including the plasma membrane and vacuole and downregulation of the chloroplast, mitochondrion, and cell wall (Figure 5). All MF are upregulated, except for monoatomic ion transmembrane transporter activity (Figure 6).

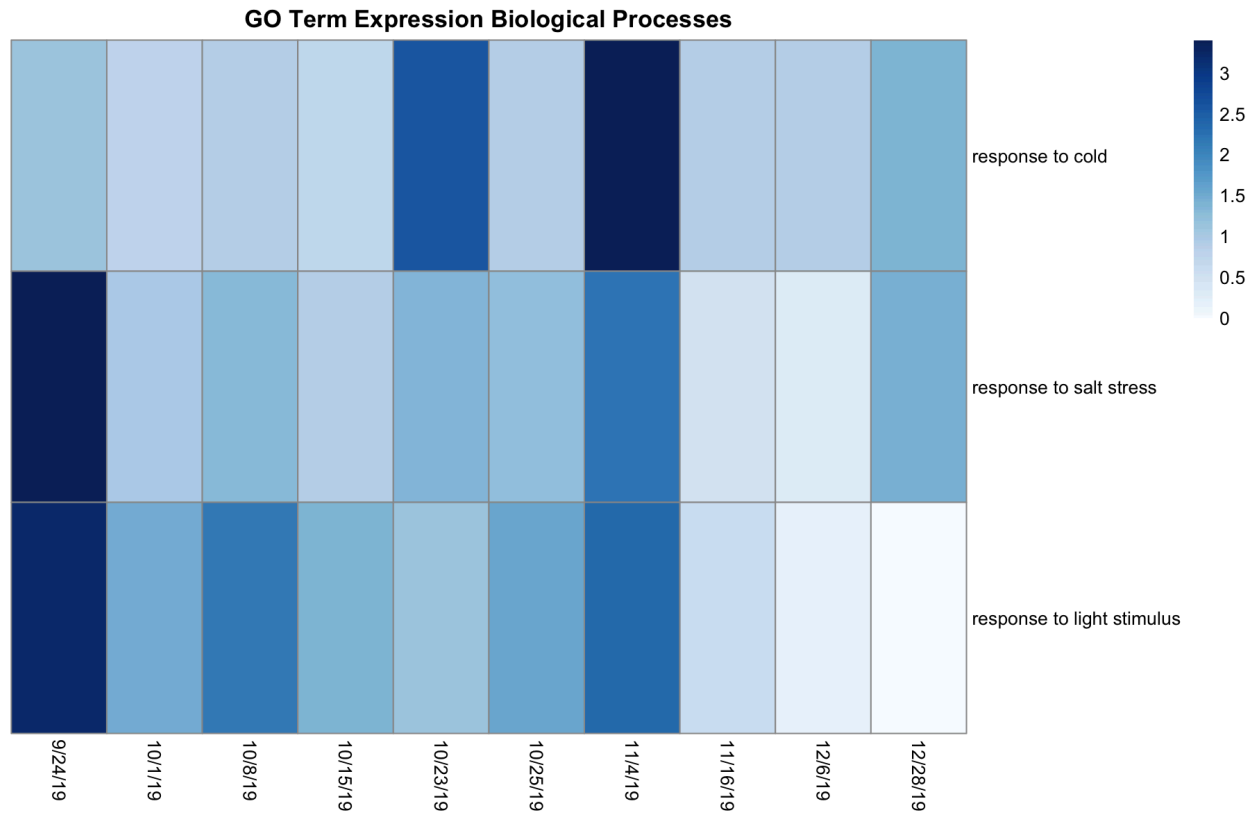


Figure 4. Heatmap shows normalized gene expression levels for BP GO terms, with GO terms on the y-axis and ten sampling dates on the x-axis. The color gradient indicates expression intensity, ranging from light blue (low expression) to dark blue (high expression).

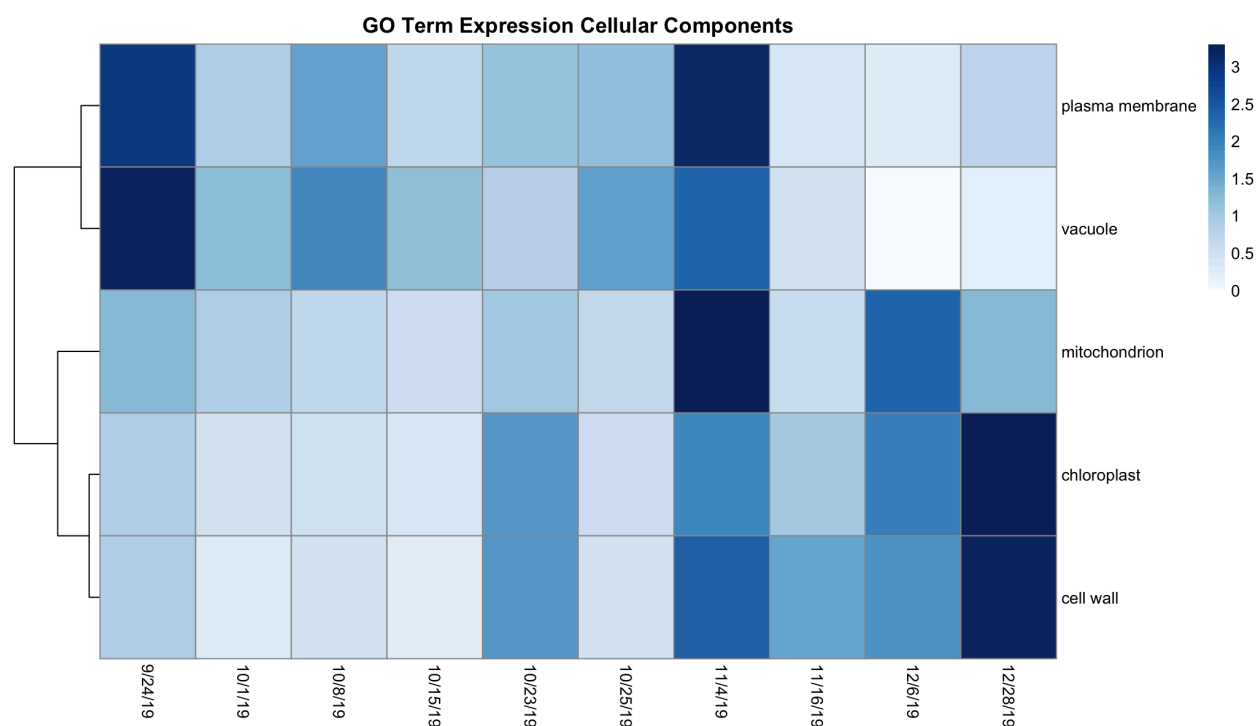


Figure 5. Heatmap shows normalized gene expression levels for CC GO terms, with GO terms on the y-axis and ten dates on the x-axis. The color gradient indicates expression intensity, ranging from light blue (low expression) to dark blue (high expression). Clustering on the left organizes CC by similarity in expression trends over time.

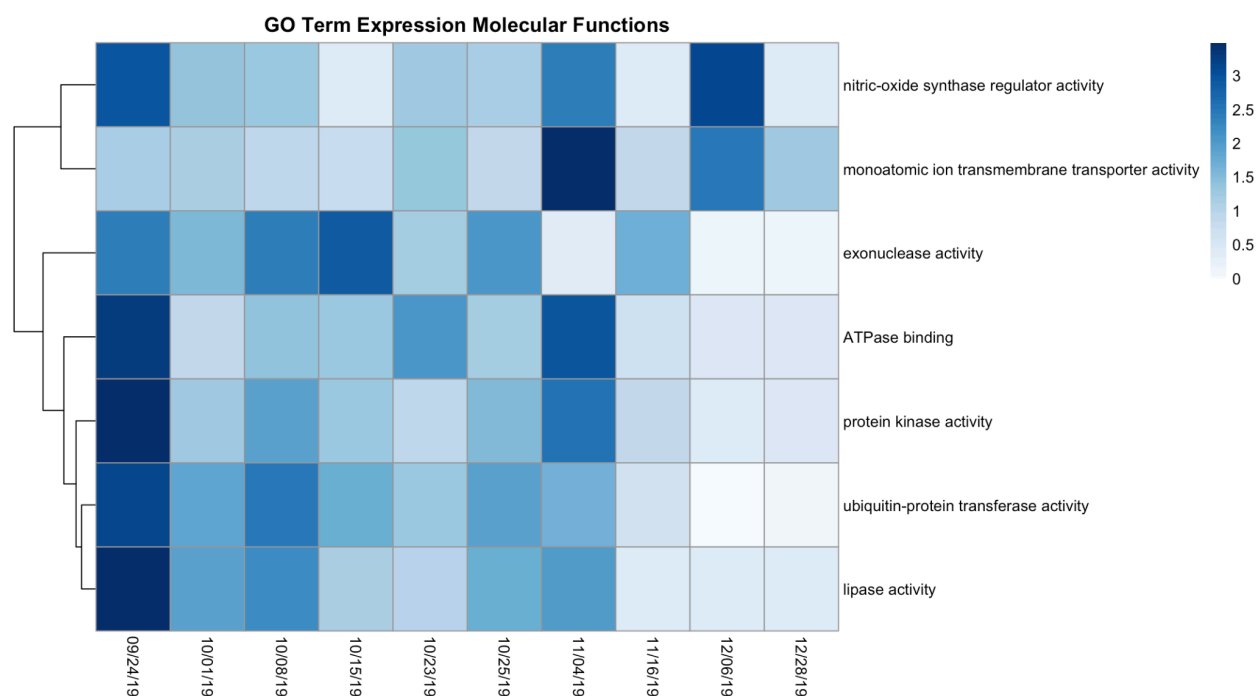


Figure 6. Heatmap shows normalized gene expression levels for MF GO terms, with ten sampling dates on the x-axis and GO terms on the y-axis. The color gradient indicates expression intensity, ranging from light blue (low expression) to dark blue (high expression). Clustering on the left organizes CC by similarity in expression trends over time.

Between October 1st and October 25th, most BP showed downregulation, with the exceptions of response to light stimulus on October 8th and response to cold on October 23rd (Figure 4). Cellular components were also downregulated, though the plasma membrane and vacuole remain active on October 8th, and the chloroplast and cell wall are upregulated on October 23rd (Figure 5). MF showed a mixed pattern of expression. Notably, exonuclease activity is slightly upregulated on October 8th, while protein kinase activity, ubiquitin-protein transferase activity, and lipase activity exhibit increased expression on both October 8th and October 15th.

On November 4th, all BP were upregulated, with response to cold showing the highest expression (Figure 4). This aligns with the coldest day in the dataset (Figure 2). All CC are also upregulated, particularly the mitochondrion and plasma membrane (Figure 5). In the MF heatmap, nearly all GO terms are upregulated except for exonuclease activity, and the most highly expressed MF is monoatomic ion transmembrane transporter activity (Figure 6).

The last three samples, collected during the polar night from November 16th to December 28th, show mostly downregulation or minimal expression across all BP, except for a slight upregulation of response to cold and response to salt stress on December 28th (Figure 4). Among the CC, both the plasma membrane and vacuole are downregulated, while the mitochondrion, chloroplast, and cell wall are upregulated (Figure 5). MF are largely downregulated or not expressed, aside from notable activity in exonuclease activity on November 16th, as well as nitric-oxide synthase regulator activity and monoatomic ion transmembrane transporter activity on December 6th (Figure 6).

Discussion

Our samples provide a short time-series analysis for periods before and during the polar night that reveal preliminary patterns in gene expression in response to changing environmental conditions. At the start of the sampling period on September 24th, phytoplankton exhibited upregulation of BP related to salt stress and light stimulus, while response to cold was downregulated, consistent with relatively stable temperatures and sunlight duration before the polar night. Response to salt stress is an important BP in polar environments, which experience seasonal salinity changes from freeze and melt cycles (National Snow and Ice Data Center, n.d.). Phytoplankton mitigate osmotic stress through mechanisms such as osmoprotectant production, enhanced antioxidant defense, and ion transport, which protect CC during salinity fluctuations (Helliwell et al., 2021). Response to light stimulus influences phytoplankton survivability, as

they must tolerate extended darkness and quickly reactivate photosynthesis upon light return to support spring blooms. Species like *Fragilariopsis cylindrus* use chromatin remodeling and gene regulation to control photosynthesis-related BP during light transitions following the polar night (Joli et al., 2025). Upregulated CC such as plasma membrane and vacuole suggested nutrient storage and active transport, while downregulated chloroplast, mitochondrion, and cell wall components likely reflected early energy conservation. The cell wall and plasma membrane provide structural integrity and regulate nutrient transport and stress, signaling key CC functions for maintaining cellular homeostasis under environmental stress (Hamann, 2014). The vacuole also responds by storing nutrients and balancing osmotic pressure, helping phytoplankton cope with fluctuating salinity (Hernando et al., 2015). MF such as ATPase binding, protein kinase activity, and ubiquitin-protein transferase activity support energy use, signaling, and protein turnover. ATPase binding and protein kinase activity enable energy production and rapid signal transduction in response to cold, darkness, and salinity changes (Quintas et al., 2010), while ubiquitin-protein transferase activity is critical for protein recycling during stress (Bidle, 2016).

Between October 1st and 25th, most BP and CC are downregulated, except for varying upregulation in response to light and cold stimuli, and selective CC such as plasma membrane, vacuole, chloroplast, and cell wall. Among BP, response to cold plays a critical role in phytoplankton survival during the polar night. Research on polar diatoms like *Fragilariopsis cylindrus* indicates that under cold conditions, metabolic rates decrease and cell division halts, allowing the cells to sustain essential physiological functions by relying on stored energy reserves (Joli et al., 2025). MF patterns fluctuate with some activities, including exonuclease, protein kinase, ubiquitin-protein transferase, and lipase, showing occasional increases. Lipase activity and ion transporter functions facilitate lipid metabolism and ion homeostasis, supporting growth and survival in fluctuating polar environments (Cantarero et al., 2024)

November 4th, the coldest sampling day, shows upregulation across all BP and CC, particularly in response to cold, as well as in the mitochondrion and plasma membrane components, indicating active physiological responses to environmental stress. The chloroplast, central to photosynthesis, exhibits transcriptional activity even during the polar night's darkness, likely maintaining readiness for the return of sunlight. Similarly, upregulation of mitochondrion, which provides Adenosine Triphosphate (ATP) through oxidative phosphorylation, suggests sustained energy metabolism and a close functional interplay with chloroplasts to maximize energy efficiency under low light conditions (Gain et al., 2021). Most MF are upregulated, with the exception of exonuclease activity, highlighting a focus on protein synthesis and ion transport rather than DNA repair. Controlling the activity of nitric-oxide synthase helps manage how cells take in nutrients and handle stress, which increases the cell's survivability (Moreno et al., 2024).

During the polar night, sampling dates November 16th to December 28th, BP largely exhibits down regulation of all GO terms, with slight reactivation of cold and salt stress responses in the last sample. CC such as mitochondrion, chloroplast, and cell wall remain

upregulated, suggesting maintenance of essential energy and photosynthetic systems even during darkness. MF are predominantly downregulated except for intermittent increases in exonuclease, nitric-oxide synthase regulator activity, and notably monoatomic ion transmembrane transporter activity, which remains highly expressed. These molecular activities likely represent targeted stress responses and ion homeostasis critical for survival during extended darkness and increased salinity.

Although this analysis has limitations and potential biases, it offers preliminary insights into gene expression patterns and their potential environmental drivers. Further research and controlled laboratory experiments are needed to distinguish correlation from causation between environmental variables and phytoplankton gene expression. Still, this work lays the groundwork for deeper exploration into how phytoplankton respond to extreme environmental changes like the polar night.

Reflection

Despite three months of darkness, phytoplankton continue to function and adjust their genetic responses to their environment by using molecular signaling pathways. While phytoplankton manage light loss by conserving energy and shutting down non-essential processes, humans respond to environmental and emotional stress in similarly flexible ways. In response to the rapid changes occurring in the Arctic, two citizen scientists and explorers Sunniva Sorby and Hilde Fålun Strøm, led a citizen science expedition that gathered valuable datasets for researchers and helped connect people to the rapidly shifting polar environment.

Their expedition served and serves as an example of how both individual and collective actions can drive meaningful change. One person's mission can be the catalyst that inspires others to be curious and seek new ways of understanding, offering fresh perspectives. Citizen science is an invitation to accessible ways for people to participate in research, fostering curiosity and emphasizing the importance of exploring unanswered questions through scientific inquiry.

Today, making science understandable and accessible is more important than ever. In the U.S., shifts in science funding and policy are affecting both ecosystems and people, leaving many disconnected from their work, communities, and sense of purpose. Accessible science through collaboration and connection is essential to keeping science relevant to the public. The efforts of Sunniva and Hilde through their Hearts in the Ice expedition demonstrate how individual actions can contribute to broader changes. Their data from their expedition is still contributing to new projects and discoveries to this day. Citizen science gives people the chance to participate directly in research, creating space for deeper understanding and connection. In a time of uncertainty, these efforts ground science in community and purpose, reminding us that meaningful change begins when people choose to engage.

“I believe so strongly in the two reasons we're up here—for science and connecting people. There needs to be deeper understanding around what in the world is going on out there—not just in the polar regions but everywhere. And it makes us feel like we are doing something meaningful even though we are out in the middle of nowhere. Disconnected but connected.” - Sunniva Sorby, 2019

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Supplementary Information

Supplemental Table 1:

Pre or Polar Night	Dates
Pre-Polar Night	9/24/19
Pre-Polar Night	10/1/19
Pre-Polar Night	10/8/19
Pre-Polar Night	10/15/19
Pre-Polar Night	10/23/19
Pre-Polar Night	10/25/19
Polar Night	11/4/19
Polar Night	11/16/19
Polar Night	12/6/19
Polar Night	12/28/19

Supplemental Table 2:

Ontology	GO Term ID	Description
Biological Process (BP)	GO:0009409	response to cold
	GO:0009651	response to salt stress
	GO:0009416	response to light stimulus

Cellular Component (CC)	GO:0009507	chloroplast
	GO:0005739	mitochondrion
	GO:0005618	cell wall
	GO:0005886	plasma membrane
	GO:0005773	vacuole
Molecular Function (MF)	GO:0051117	ATPase binding
	GO:0004672	protein kinase activity
	GO:0004842	ubiquitin-protein transferase activity
	GO:0030235	nitric-oxide synthase regulator activity
	GO:0004527	exonuclease activity
	GO:0016298	lipase activity
	GO:0015075	monoatomic ion transmembrane transporter activity

Supplemental Table 3a:

Variable	Shapiro-Wilk W	Shapiro p-value	Normality (p > 0.05)	Levene's F	Levene's p-value	Homogeneity (p > 0.05)
Sea Surface Temperature	0.94885	0.6549	Normal	9.6388	0.01456	Not Homogeneous
Ice Concentration	0.94514	0.6115	Normal	4.8444	0.0589	Marginal
Ice Thickness	0.92837	0.432	Normal	2.0361	0.1914	Homogeneous
Salinity	0.95597	0.7391	Normal	0.4576	0.5178	Homogeneous
Sunlight	0.93506	0.4995	Normal	8.0609	0.02184	Not Homogeneous

Supplemental Table 3b:

Variable	t-value	p-value	Significant Difference?	Mean (Not Polar Night)	Mean (Polar Night)	Notes
Temperature	3.8447	0.0093	Yes	0.6701	-1.6125	Temperatures drop during.
Sea Ice Thickness	-4.3824	0.0023	Yes	0.048	0.444	Thickness increases during polar night.
Salinity	-5.7215	0.0004	Yes	33.9624	35.2333	Salinity is higher during polar night.
Sunlight	5.4779	0.0028	Yes	7.7628	0	No sunlight during polar night.

Supplemental Table 4:

GO Ontology Category	Number of GO Terms
Biological Process (BP)	2,347
Cellular Component (CC)	373
Molecular Function (MF)	333

Educational Polar Science Zine

To bridge the gap between scientific research and public engagement, Julia Lowe and I created educational zines (small, foldable magazines) as outreach tools designed to make the complex topic of phytoplankton more accessible and meaningful. Grounded in our own personal capstone projects, the zines combine storytelling, original artwork, and participatory science to highlight the importance of these microscopic organisms and the global connections they inspire. By integrating scientific analysis with creative communication, the zine offers a tangible, shareable way to connect audiences to polar science, the role of phytoplankton in global ecosystems, and the power of community-driven research.