Detecting and modeling *Karenia mikimotoi* abundance in the Gulf of Maine

Erica Lei and Nicky Ling

Introduction

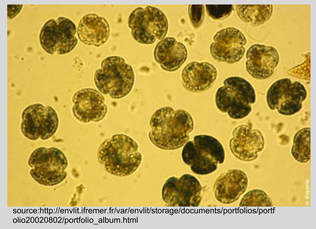
The dinoflagellate *Karenia mikimotoi* is a common phytoplankton found in harmful algal bloom (HAB) events (Brand et al. 2012). Presence of the organism in the nearshore Gulf of Maine was not studied or documented until a bloom took place in 2017, leading to a loss of $250,000 from Maine's economy (McGuire 2017). To mitigate economic loss from harmful algal blooms (HABs), it is necessary to track the presence and abundance of this species in the Gulf of Maine and to model environmental conditions that could contribute to possible HABs of this species.

In this study, we will investigate the presence of *K. mikimotoi* in the Damariscotta River Estuary using an environmental DNA (eDNA) approach and analyze how its abundance is related to two environmental factors: the sea surface temperature (SST) and the photosynthetic available radiation (PAR).

source: https://www.wxnmh.com/thread-781487.htm

Left: a *Karenia mikimotoi* dominated red-tide event.

Right: *Karenia mikimotoi* individual cells.



source:http://envlit.ifremer.fr/var/envlit/storage/documents/portfolios/portfolio20020802/portfolio_album.html

Methods

- Collect water samples around 1:00 pm on Sep 12, 19, 26, Oct 3 and 10 by casting PVC Niskin Type Sampler at two depths, "shallow" (1m) and "deep" (4 - 7m).
- Vacuum-filter the samples using 0.2 µm filter paper.
- Store the filter paper at 4˚C for eDNA extraction.
- Extract eDNA using DNeasy PowerWater Kit protocol (Qiagen, Germantown, MD).
- Run a real-time qPCR based on the methods of Yuan et al. (2012).
- Acquire temperature and radiation data from UMaine LOBO buoys.
- Abundance of *K. mikimotoi* in samples is expressed in gene copies rather than cell counts because the exact number of 28S genes in a single *K. mikimotoi* genome is not known.

Figure 1

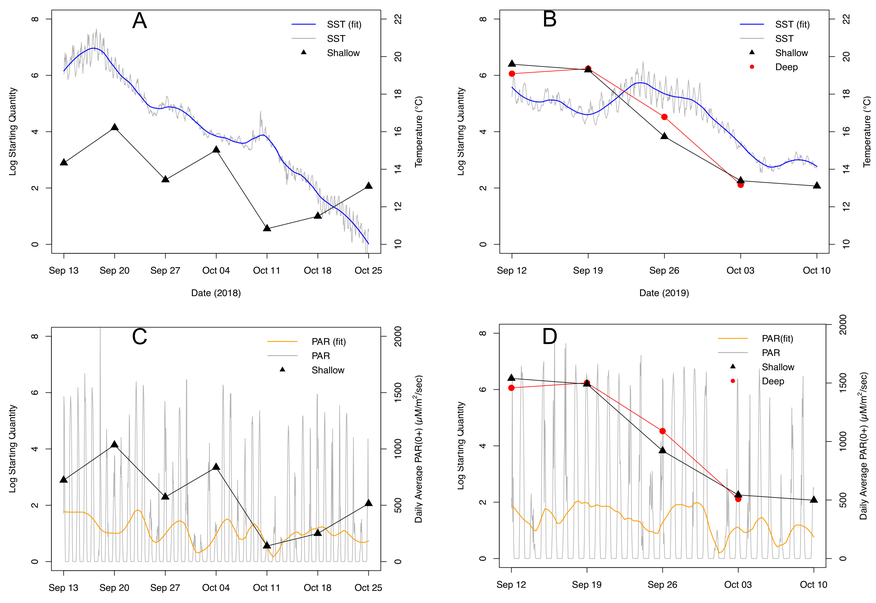


Figure 1. *K. mikimotoi* starting quantity (log10 scale) graphed against (A) temperature changes within 2018 sampling periods, (B) temperature changes within 2019 sampling periods, (C) radiation changes within 2018 sampling periods, and (D) radiation changes within 2019 sampling periods. A loess fitted curve for SST or PAR is shown as guidance for trend on each graph.

Figure 2

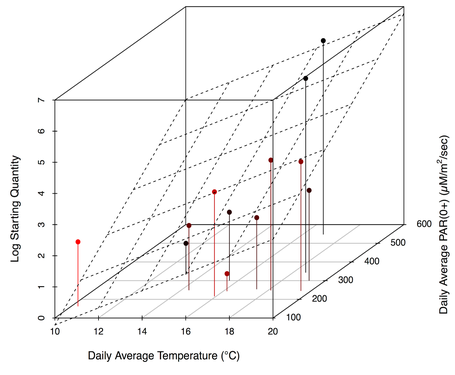


Figure 2. Model (dashed plane) of temperature and PAR covarying with *K. mikimotoi* concentrations. The data points (n = 12) are shown as red dots, highlighted by shorter distance to (0, 0, 0).

- On a 95% confidence level, there is no significant relationship between the *K. mikimotoi* gene concentration and the linear combination of SST and PAR ($F = 3.958$, $df = 2$ and 9, $p_{SST} = 0.141$, $p_{PAR} = 0.116$, $R^2 = 0.4651$).
- The coefficient for SST has an 85% confidence interval of (0.00521, 0.545) and the coefficient for PAR has an 85% confidence interval of (0.000943, 0.0160), where 0 is in neither of these.

Results

- *Karenia mikimotoi* was present in both 2018 and 2019, with a noticeable smaller temperature range and higher concentration observed in 2019 samples.
- The model expression is:

$$\log_{10}(Starting\ Quantity) = -3.82 + 0.27 * SST + 0.00849 * PAR$$

- At an 85% confidence level, there is evidence showing positive correlations between abundance and the linear combination of temperature and radiation.

Discussion

- Since *Karenia spp.* is thought to live over winter in low numbers as motile cells awaiting favorable bloom conditions (Gentien 1998), one reasonable explanation for the higher concentration in 2019 samples is that *K. mikimotoi* cumulated at a faster pace this year as there was a large amount from previous years available for reproduction.
- The environmental factor model shows that there is weak evidence of positive linear correlations between gene copy numbers and SST and PAR. Future studies can incorporate other abiotic factors that contributes to the ideal growth environment for *K. mikimotoi*, such as hydrology, low salinity, high nutritions, and low wind speed (Barnes et. al 2015). With more data, we hope to predict HAB events in advance.
- One source of imprecision could result from the data not taken at the sample location nor the exact location of the blooms, but instead from the nearest buoy.
- We recommend to encourage citizen scientists to use portable DNA extraction and qPCR kits to support the monitoring dataset in the future.

Acknowledgements

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