

Ecological Niche Changes of Microbial Communities in the Tasman Sea: the Interaction between Temperature and Diversity

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On January 24, 2024, Mark V. Brown, Martin Ostrowski, Lauren F. Messer, and others published a research paper titled "A marine heatwave drives significant shifts in polar microbiology" in the journal *Communications Biology*. Given the global trends and potential impacts of MHWs on marine ecosystems, this study analyzed the changes in microbial communities during the 2015/16 and 2017/18 Tasman Sea MHW events, revealing the impact of MHWs on microbial community structure, function, and niche status. Researchers used a large amount of microbial sample data from the southern hemisphere to systematically evaluate the selection pressure, community transformation, and diversity changes of MHWs on microbial communities through temperature index and niche indicators. The innovation and importance of this study lies in providing the world's first comprehensive framework for the impact of MHWs on microbial ecosystems, which helps to monitor, predict, and develop adaptation strategies for the future impact of MHWs on marine ecosystems.

1 Materials and Methods

The research team used thousands of samples from the southern hemisphere, covering the Tasman Sea and surrounding waters. The samples were mainly collected from the Maria Island National Reference Station (MAI NRS) of the Integrated Marine Observing System (IMOS) network and other sites. The sampling covers different depths, temperatures, and nutrient gradients from the surface to the deep layers, ensuring the representativeness of the data. The DNA in each sample is passed through DNeasy® PowerWater® Sterivex™ DNA Isolation Kit (Qiagen, Germany) extraction.

To identify and classify microbial communities, specific primers are used to amplify target gene regions, and the amplified products are sequenced using the Illumina high-throughput sequencing platform. The V1-V3 region of the 16S rRNA gene in bacteria was amplified using 27f and 519R primers, while the 16S rRNA gene in archaea was amplified using A2F and 519R * primers. The 18S rRNA gene in eukaryotic microorganisms was amplified using euk454FWD1 and TAReuk Rev3 primers. Subsequently, the sequencing data was processed using the DADA2 pipeline to remove low-quality and chimeric sequences, generating ASVs (Amplicon Sequence Variants). Bacteria and archaea ASVs are classified using the Genome Taxonomy Database (GTDB), while eukaryotic ASVs are classified using the PR2 database.

To evaluate the impact of marine heatwave events on microbial communities, this study calculated multiple niche indices, including species temperature index (STI) and community temperature index (CTI). STI is calculated using kernel density estimation to represent the optimal temperature preference for each ASV. CTI is based on the weighted average of STI for all ASVs in the sample, used to evaluate the average temperature preference of the entire microbial community. They also calculated other indices, including Salinity Index (CSI), Nutrient Index (CNI), and Oxygen Index (COI). Data analysis and chart drawing are conducted using R programming language.

2 Analysis of Experimental Data

Figure 1 shows the relationship between bacterial community temperature index (CTI) and environmental temperature. Figure 1a shows a significant positive correlation between CTI and temperature in marine navigation samples from the southern hemisphere (n=1 946). Samples from different depth ranges exhibit consistent trends, with surface to 100 m (light blue), 100 m to 1 000 m (black), and samples above 1 000 m (orange) all showing an increase in CTI with increasing temperature. Figure 1b shows that the relationship between CTI and temperature varies slightly among different stations in the time series station sample of the IMO National Reference Station (NRS) (n=1 660). Dark orange represents the MAI site, light blue represents the ROT site, green represents the PHB site, deep purple represents the NSI site, light purple represents the YON site, and green represents the DAR site. Overall, the CTI of each site is positively correlated with temperature, but shows different slopes in different temperature ranges, indicating that the bacterial communities of each site have different temperature adaptability and niche preferences within a specific temperature range.

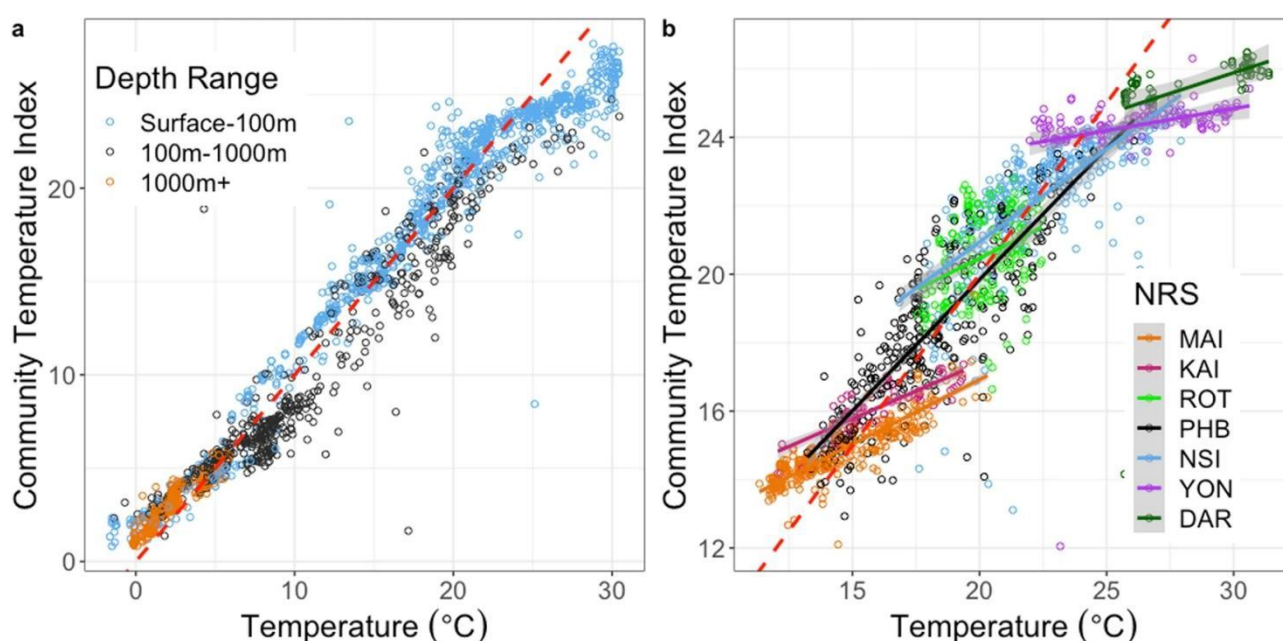


Figure 1 The relationship between bacterial community temperature index and in situ environmental temperature

Image caption: a: Samples collected spatially during oceanic voyages in the Southern Hemisphere (n = 1 946); b: Samples collected temporally at IMOS National Reference Stations (NRS) time-series sites around the Australian continental shelf (n = 1 660); Dashed red line represents a slope of one

Figure 6 shows the impact of marine heatwaves (MHW) on the composition and structure of microbial communities. Figure 6a shows the bacterial genera that caused the greatest difference in microbial community composition under MHW and non MHW conditions in the same month, with high-temperature adaptive genera such as *Synechococcus*, *Prochlorococcus*, and *Trichodesmium* significantly increasing under MHW conditions. Figure 6b and Figure 6c indicate that MHW altered the seasonal variation of bacterial diversity index. The Shannon index and inverse Simpson index generally rose during the MHW period, especially during the hot season from February to April. Figure 6d shows a significant increase in the number of "rare" bacterial groups in the samples during the MHW period, especially during the peak heatwave period from February to April. These results indicate that MHW significantly altered the diversity and composition structure of microbial communities.

3 Analysis of Research Results

The Tasman Sea marine heatwave (MHW) event in 2015/16 had a long duration and high intensity, while the MHW event in 2017/18 was relatively short and mild. In these two MHW events, there was a significant positive correlation between bacterial community temperature index (CTI) and in situ environmental temperature. In

samples of different depths and sites, CTI increases with increasing temperature. However, there are differences in the slope of the relationship between CTI and temperature among different sites, indicating differences in the adaptability of bacterial communities to temperature and niche preferences among different sites.

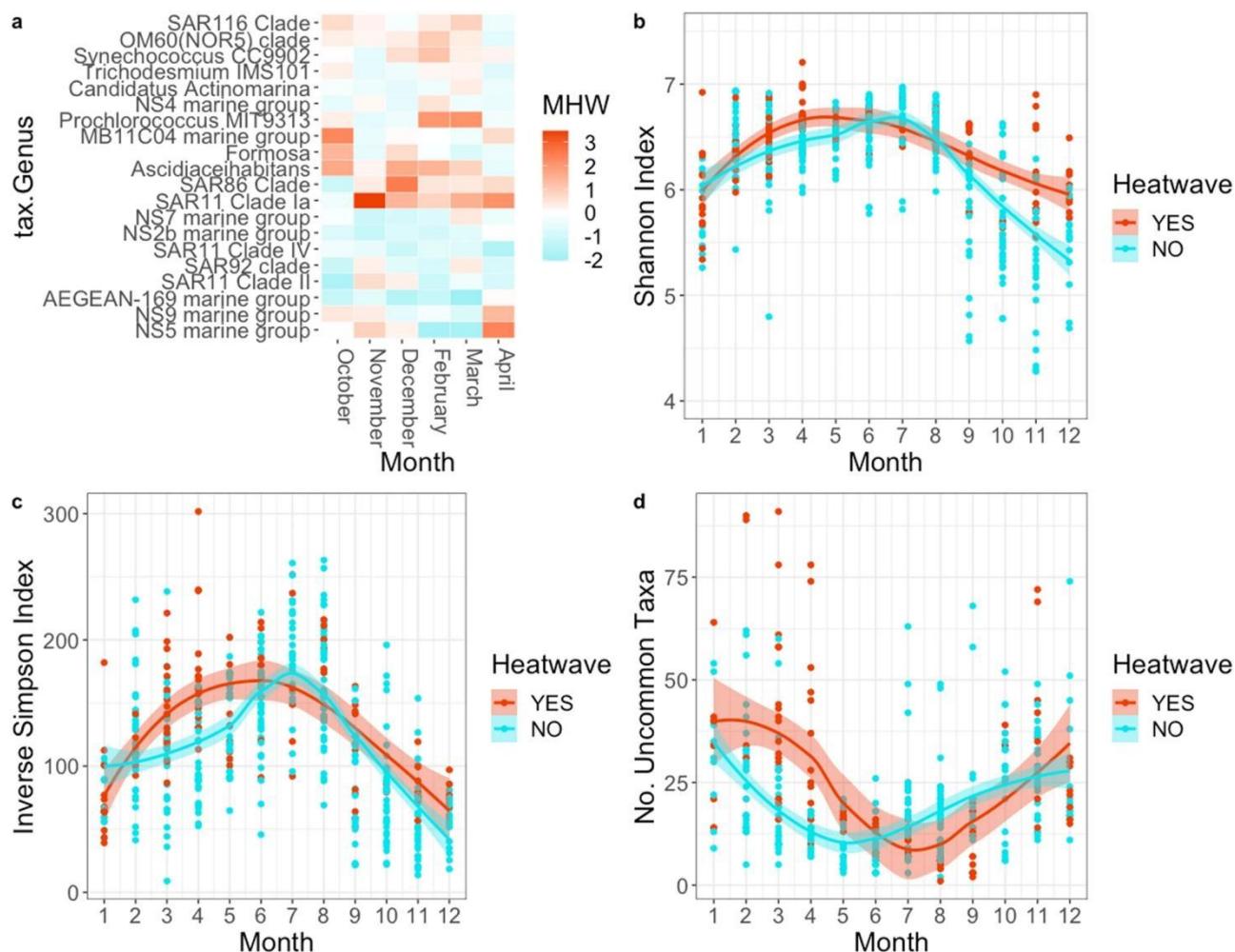


Figure 6 Marine heatwaves lead to compositional and structural changes in microbial assemblages

Image caption: a: Heatmap detailing the bacterial genera contributing most to the compositional difference between surface samples collected in equivalent months during MHW and non-MHW conditions; b: The seasonal cycle of bacterial Shannon diversity, (c) Inverse Simpsons diversity and (d) the number of "uncommon" bacterial taxa in each sample are all modulated by MHW condition; Samples collected during MHW conditions (n = 121) are in red and those collected during non-MHW conditions (n = 378) are in blue

During MHW, the bacterial genera that caused the greatest difference in microbial community composition included high-temperature adaptive genera such as *Synechococcus*, *Prochlorococcus*, and *Trichodesmium*, with a significant increase in relative abundance, while bacteria such as NS2b, NS5, and NS7 that preferred particle attachment decreased. Similar changes were observed in the Marine Group II archaea and Mamiellophytaecae green algae groups. This reflects the transformation of microbial communities towards high temperature and low nutrient niches due to high temperature and low nutrient conditions. This shift towards high-temperature and low nutrient niches may be a fundamental characteristic of warming in temperate oceans. Due to significant differences in the rate and fate of carbon fixation between smaller photosynthetic organisms and larger photosynthetic organisms, this change may have a profound impact on the entire food web.

During the MHW event, the Shannon index and inverse Simpson index significantly increased, leading to a significant increase in the number of "rare" taxa. During the peak period of MHW from February to April,

bacterial diversity reached its highest level throughout the year. This may be due to the emergence of new warm adaptive groups under MHW conditions, forming new microbial combinations.

4 Research Evaluation

This study revealed the profound impact of MHW on microbial community structure and function by analyzing microbial community data during two major marine heatwave (MHW) events in the Tasman Sea. The importance of the study lies in its first revelation of microbial niche and functional changes caused by MHW, providing a new perspective for understanding the response mechanisms of marine ecosystems in the context of global climate change. Research has found that microbial community diversity increases during MHW, leading to an increase in "rare" groups and enriching our understanding of diversity changes. The scientific calculation and application of indicators such as bacterial community temperature index (CTI) are of great innovation in the study of marine microbial niches.

5 Conclusion and Inspiration

The research results indicate that MHW events may occur more frequently in the future, with greater impacts on marine microorganisms and ecosystems. Therefore, it is particularly important to strengthen the monitoring and prediction of MHW and develop adaptation strategies. Future research can expand the regional scope, further reveal the response mechanisms of different marine microbial communities to MHW, and conduct in-depth studies on the specific effects of MHW on microbial functions through metabolomics, gene function analysis, and other means, in order to develop more effective protection and adaptation strategies.

6 Original Text Reading

Brown M.V., Ostrowski M., Messer L.F., Bramucci A., van de Kamp J., Smith M.C., Bissett A., Justin Seymour, Hobday A.J., and Bodrossy L., 2024, A marine heatwave drives significant shifts in pelagic microbiology, *Communications Biology*, 7: 125. DOI: 10.1038/s42003-023-05702-4

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