

令和 3 年 6 月 15 日現在

機関番号：12102
 研究種目：若手研究(B)
 研究期間：2017～2020
 課題番号：17K17622
 研究課題名(和文) Understanding the Impacts of Ocean Acidification: from Biodiversity to Ecosystem Functioning
 研究課題名(英文) Understanding the Impacts of Ocean Acidification: from Biodiversity to Ecosystem Functioning
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 交付決定額(研究期間全体)：(直接経費) 2,500,000円

研究成果の概要(和文)：現在の海洋中のCO₂濃度は、海底生物が複雑な三次元的構造を作り出すのに適しており、それによって高い生物多様性が保たれています。一方、CO₂濃度が高くなり海洋が酸性化すると、生物群の構成が変化する過程(遷移過程)の初期段階において、環境の変化が激しい場所でも多くの子孫を残す生存戦略をとる、微細藻や小型の藻類(日和見種)が増え、他の大型藻類の加入が阻害されます。そのため、生態系における種の多様性は低いままとなり、構造的な複雑性を持つことができません。構造的複雑性は、様々な生物資源を創出するなど、生態系の機能的側面を支えており、その喪失は、人類が享受する生態系サービスの劣化を意味しています。

研究成果の学術的意義や社会的意義
 人間活動に伴い、沿岸の生態系の構造や機能が劇的に変化しています。特に、海藻の海中林やサンゴ礁がマット状の微細藻類に置き換わると、我々人類にとっての生態系の価値は著しく失われます。これから数十年で、多様で複雑性の高い環境が日和見種(短寿命で成長速度の大きな種)とされる微細藻類に置き換わるかもしれません。さらに、微細藻類が卓越すると他の生物種の加入が妨げられ、生態系の遷移が停止することも明らかとなりました。このようなフィードバックの仕組みは、様々なレベルでの環境変化に対して閾値を踏み越えた生態系の安定化を説明するものであり、沿岸生態系の価値を守るための適応戦略に組み入れることが必要です。

研究成果の概要(英文)：Long-term exposure to CO₂ can considerably alter community development, often resulting in simplified systems dominated by turf algae that possess reduced biodiversity and low ecological complexity. Current understanding of the underlying processes by which ocean acidification alters biological community development and stability remains limited, making the management of such shifts problematic. Here, we found that assemblages in reference pCO₂ conditions continued to gain species through time and had developed more structurally complex communities with clearly defined understory and canopy species. In contrast, the assemblages in the elevated pCO₂ became arrested in terms of their successional development due to competition for space by the turf algae, resulting in a highly simplified community. By understanding the ecological processes responsible for driving shifts in community composition, we can better assess how communities are likely to be altered by ocean acidification.

研究分野：Climate Change Marine Ecology

キーワード：Ocean Acidification Community Succession Biodiversity Climate Change Meta-barcoding Ecosystem Functioning

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様式 C-19、F-19-1、Z-19 (共通)

Title: Understanding the Impacts of Ocean Acidification: from Biodiversity to Ecosystem Functioning

1. 研究開始当初の背景

Marine ecosystems are currently under threat from ocean acidification, the change in seawater carbonate conditions associated with increasing levels of atmospheric CO₂. Although some species may benefit from elevated CO₂ (e.g., some fleshy macroalgae species) - under our current rate of CO₂ emissions, most marine organisms evaluated will have very high risk of negative impacts by 2100 and many by 2050 (Gattuso et al., 2015). This variety of responses within and between taxa mean that ocean acidification is likely to drive substantial change in marine ecosystems (Agostini et al., 2018; Hall-Spencer & Harvey, 2019). While these ecosystem changes are often gradual, they can reach tipping points, resulting in dramatic and abrupt regime shifts that change the structure and function of marine communities (Conversi et al., 2015; Möllmann et al., 2015). Regime shifts are particularly concerning because they can cause large losses of ecological and economic resources, and yet are often difficult to predict due to their non-linear nature (Hastings & Wysham, 2010). Presently, the next significant knowledge gap is to understand how ocean acidification will affect the structure and functioning of whole communities, with the long-term aim of informing on the implications for the ecosystem services that these communities provide (e.g. food, habitat provisioning, coastal defense, nutrient cycling).

2. 研究の目的

There has been extensive research into the effects of OA on single species (reviewed by Harvey et al., 2013, 2014), yet these experiments rarely investigate species interactions (such as habitat provisioning, competition, predation, or food limitation) and so it is difficult to assess how the results apply to natural ecosystems. By using natural *in-situ* CO₂ seeps, where CO₂ bubbles through the seabed due to nearby volcanoes, it is possible to provide insights into the future of marine ecosystems because they expose entire communities to the conditions we expect by the end of the century. This provides researchers with an avenue to assess the long-term development of communities and provides insights into whether resident species can cope or adapt to ocean acidification over their life span.

Previous work using CO₂ seeps across temperate, sub-tropical and tropical systems has shown profound shifts in the community due to ocean acidification (Hall-Spencer & Harvey, 2019), finding that ecosystems became increasingly simplified under ocean acidification with declines in biodiversity, habitat, and structural complexity. However, since these community assessments carried out to date having typically used traditional ecological methods, they have almost exclusively focussed on large and conspicuous species that represent only a minor fraction of marine diversity. Traditional approaches thereby highlight a limitation - how can we comprehensively quantify changes in biodiversity over time and understand the consequences of community shifts on ecosystem services if most species are unknown to science or cannot be easily surveyed? The purpose of this research was therefore to address this knowledge gap by using meta-barcoding approaches to characterise whole communities, link it to their ecosystem

functioning, and test how ocean acidification will influence biodiversity and ecosystem functioning.

3. 研究の方法

Recruitment tiles (150 x 150 mm volcanic rock tiles) were deployed in July 2016 in Shikine Island, being secured to the substrate using individual anchor bolts (8.5 mm width, 70 mm length) drilled into rock by SCUBA divers at ~6 m depth (Nemo Underwater Drill, Nemo Power Tools, CA, USA). Tiles were deployed within two zones: (i) near to the natural CO₂ seeps (High-CO₂, 900 ppm), and (ii) in a nearby bay for control conditions (Reference, 300 ppm). A total of 50 tiles were utilised ($n = 25$ per zone) with a subset of five tiles collected and analysed after 2, 4, 9, 18 and 24 months. These recruitment tiles allow us to analyse the biodiversity and abundance of species under different levels of CO₂ when substrate complexity and colonisation history are being held constant.

Upon collection, each tile was removed from the substrate and placed into plastic bags underwater and transported back to the laboratory. Within the laboratory, each recruitment tile was photographed (Nikon D7200, Nikon, Japan) to assess the total percentage cover of the tile, then each tile was measured for gross primary production and community respiration in a measure of the tiles community production rate, and finally each tile was stored at -20 °C until DNA extraction.

Community production and respiration of individual tiles were assessed by measuring, with an Orion 4-Star pH and dissolved oxygen meter (Thermo Scientific, USA), the changes in dissolved oxygen concentrations during an incubation within a 2.5 L seawater container (15 cm wide x 20 cm length x 10 cm height) in a temperature-controlled water bath. Magnetic stirrers (M-1 Controller and MS101A Stirrer, AS-One, Japan) were used to continuously mix the seawater within each container throughout measurements. Seawater for each treatment (pH_{NBS} ~8.10 vs. pH_{NBS} ~7.80) were acquired by bubbling with pure CO₂ (Fukurow pH Controller; Aqua Geek, Kawaguchi, Japan). Community production and respiration were measured over a 150-minute period; first determining oxygen production (60-minute light period, *ca.* 200 $\mu\text{mol m}^{-2} \text{s}^{-1}$), and after a 30-minute dark period, oxygen consumption (60-minute dark period). Net community production and community respiration were measured during the light and dark periods, respectively, with gross primary production calculated as the net community production minus community respiration.

The DNA was extracted from each tile using a Powermax Soil DNA Isolation Kit (MO-BIO) on homogenised tissue scraped from each tile. PCR assays were used to amplify universal primers of >300-bp, COI and 18S (eukaryotic organisms) and 16S (prokaryotic organisms) fragments - in each replicate sample before being sent for sequencing. Sequences were cleaned and processed using QIIME2 with DADA2, with downstream analysis carried out in the R environment. Comparisons were made between the 'Reference' and 'High-CO₂' sites, separately for the bacterial community composition (16S), algal community composition (18S) and fauna (COI).

4. 研究成果

Overall community composition between the Reference and High-CO₂ sites at all time points were highly separated by nMDS for bacteria (Figure 1A-B), algae (Figure 1C-D) and fauna (Figure 1E-F). This highlights that across early-stage (2-m and 4-m), mid-stage (9-m), and late-stage (18-m and 24m) succession, communities entirely diverge and remain separated in terms of their composition. These differences in the community are also demonstrated by diversity, with the high-CO₂ showing reduced diversity compared to the Reference site. This is most clearly shown when looking at the latest stages of succession (24-m), where assemblages in reference *p*CO₂ conditions continued to gain species through time and had developed more structurally complex communities with clearly defined understory and canopy species (Figure 2). In contrast, the assemblages in the elevated *p*CO₂ became arrested in terms of their successional development due to competition for space by the turf algae, resulting in a highly simplified community (Figure 2).

The turf algae that were observed at 24 months in the High-CO₂ site, was also prevalent at other time points, and likely played a role in maintaining the species-poor state. The benefits of seawater acidification to opportunistic species, such as turf algae, over others (including calcareous species) is well established. It is likely that the enriched CO₂ environment had a positive effect on the fast-growing microalgae and turf algal species in the early stages of community

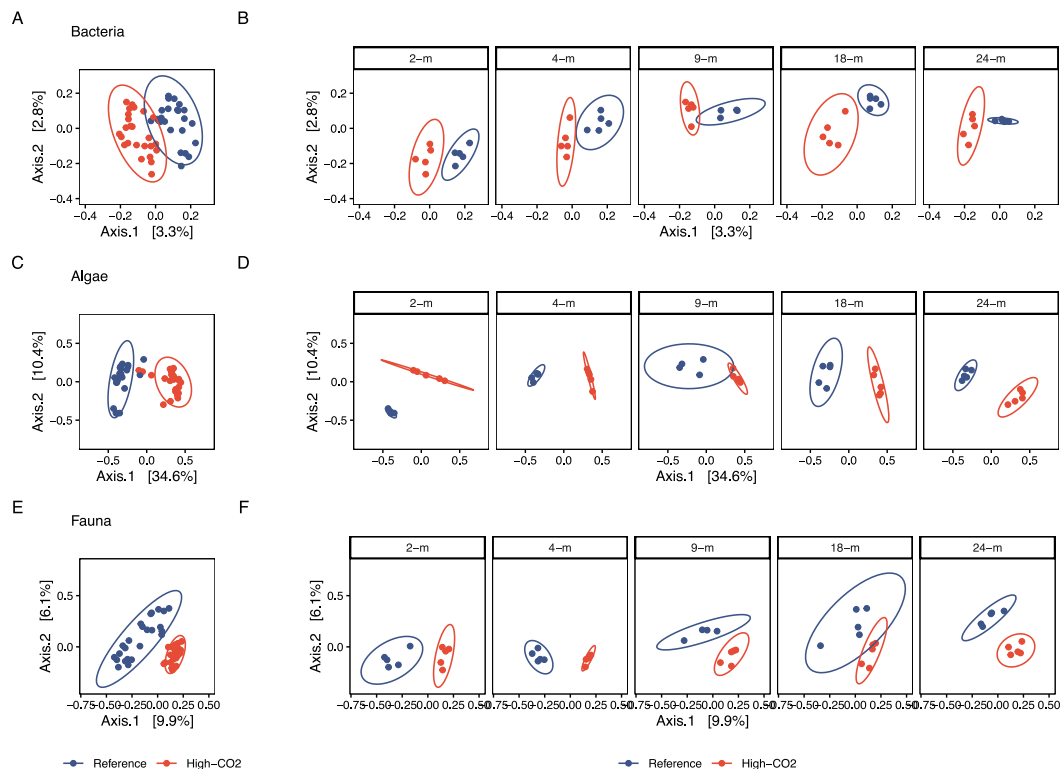


Figure 1: nMDS of community composition based on meta-barcoding between Reference (blue) and High-CO₂ (red) communities. Each point represents a community, with more similar communities closer to each other. Communities are separated as Bacteria by 16S (A-B), Algae by 18S (C-D), and Fauna by COI (E-F). Panels on the right (B, D and F) show the different durations of development before collection (2, 4, 9, 18 and 24 months).

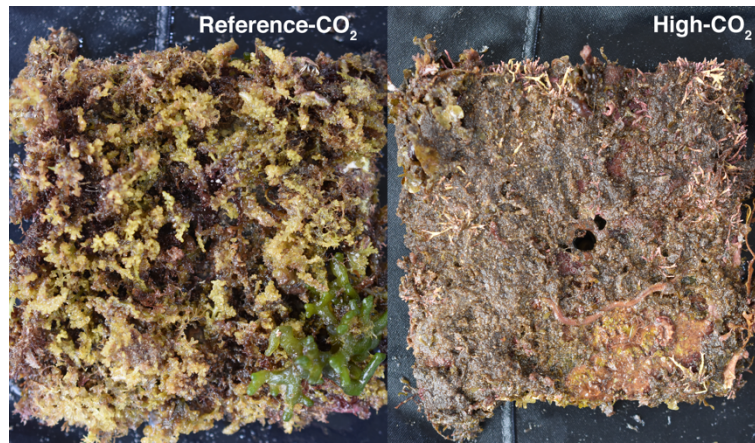


Figure 2: Example photographs from the laboratory of the recruitment tiles after 24-months. Communities on the tiles were visually distinct from each other.

development, which are then locked-in, leaving a species-poor, low complexity community. The simplification of the marine ecosystem, such as by systems shifting to turf dominance, likely leads to functional-biodiversity loss in the system with implications for functioning of the system under future ocean acidification

When assessing the community production rates a clear pattern emerged. Communities within the Reference site consistently demonstrated higher levels of gross primary production (Figure 3A) and community respiration (Figure 3B) compared to the High-CO₂ site. This was driven by the greater biomass, diversity, and complexity of the community. The hindered development of the High-CO₂ community, i.e. the state of being turf-dominated from early to late succession, was also mirrored in the production rates with the rates showing far less change over time (Figure 3A-B).

In conclusion, ocean acidification can set the course of successional development and lead to communities dominated by turf algae, causing reduced algal biomass, diversity and complexity.

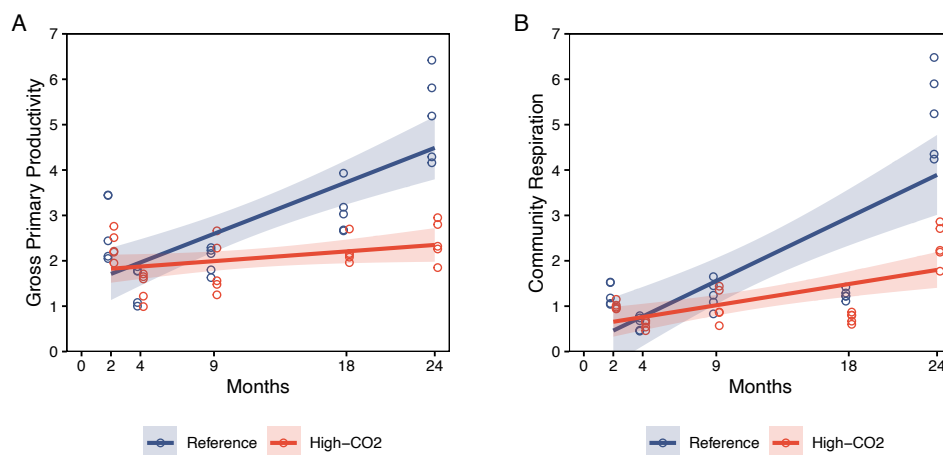


Figure 3: Community production rates of the recruitment tiles for gross primary production (A), and community respiration (B).

5. 主な発表論文等

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〔図書〕 計0件

〔産業財産権〕

〔その他〕

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6. 研究組織

氏名 (ローマ字氏名) (研究者番号)	所属研究機関・部局・職 (機関番号)	備考
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7. 科研費を使用して開催した国際研究集会

〔国際研究集会〕 計0件

8 . 本研究に関連して実施した国際共同研究の実施状況

共同研究相手国	相手方研究機関
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