



Rapid Estimation of Marine Benthos Abundance Using "sedimentary DNA": A Case Study of the Burrowing Decapod *Upogebia major* in Tidal Flats



Kiyosuke Kitabatake^{1*}, Kentaro Izumi², Natsuko Ito-Kondo³, Kenji Okoshi¹ (¹Toho University, ²Chiba University, ³National Institute for Environmental Studies)

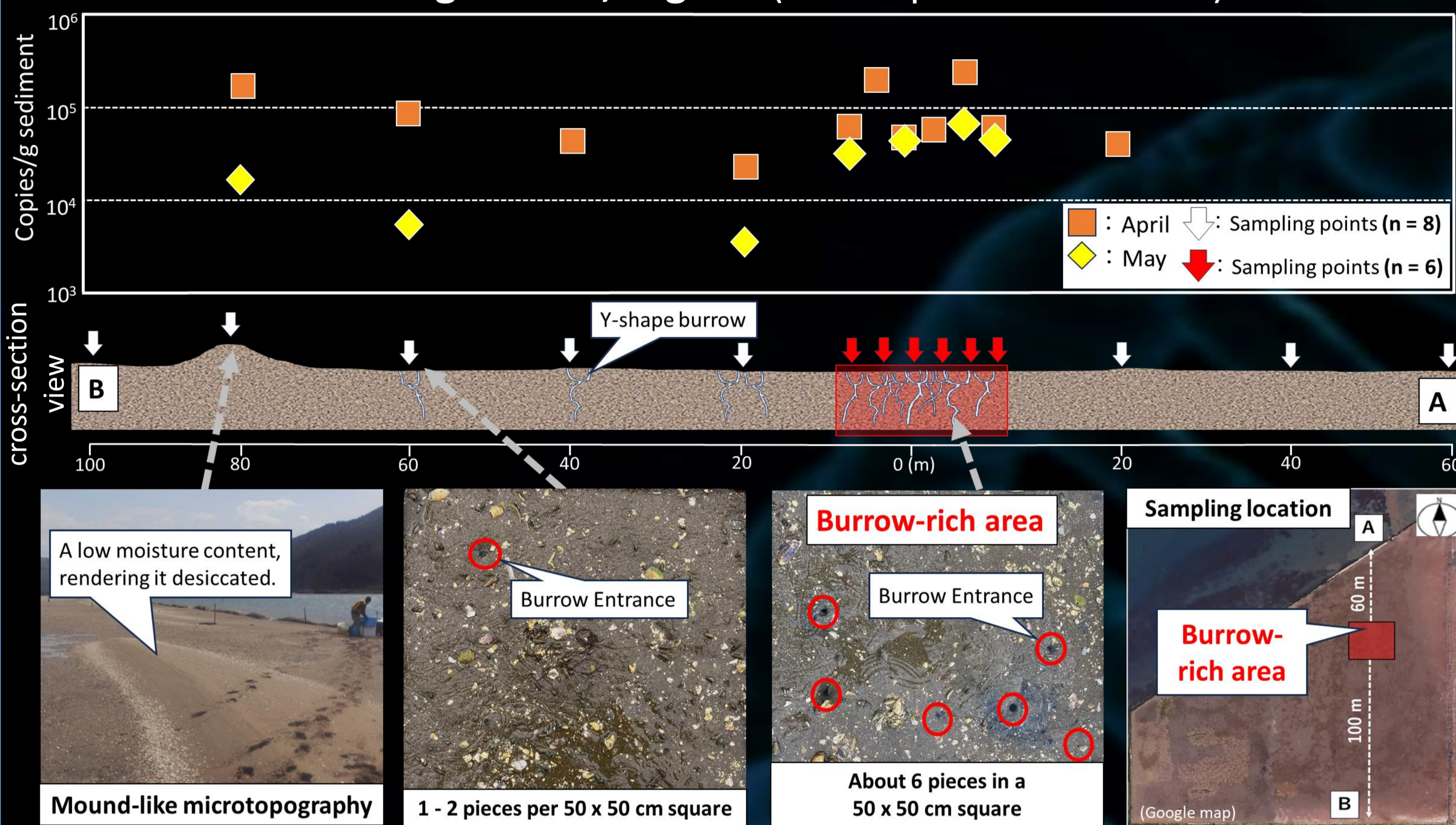
Summary

- A quantitative assessment of environmental DNA (sedimentary DNA; sedDNA) within sedimentary deposits originating from the **marine benthos**—a **pioneering study!**
- The concentration of sedDNA has the potential to reflect the extant biomass of benthos**, yet it is suggested to be subject to fluctuations due to **biological** and **physical factors**.
- Further accumulation of fundamental research is required to apply sedDNA analysis for estimating the current biomass of **fisheries resources**.

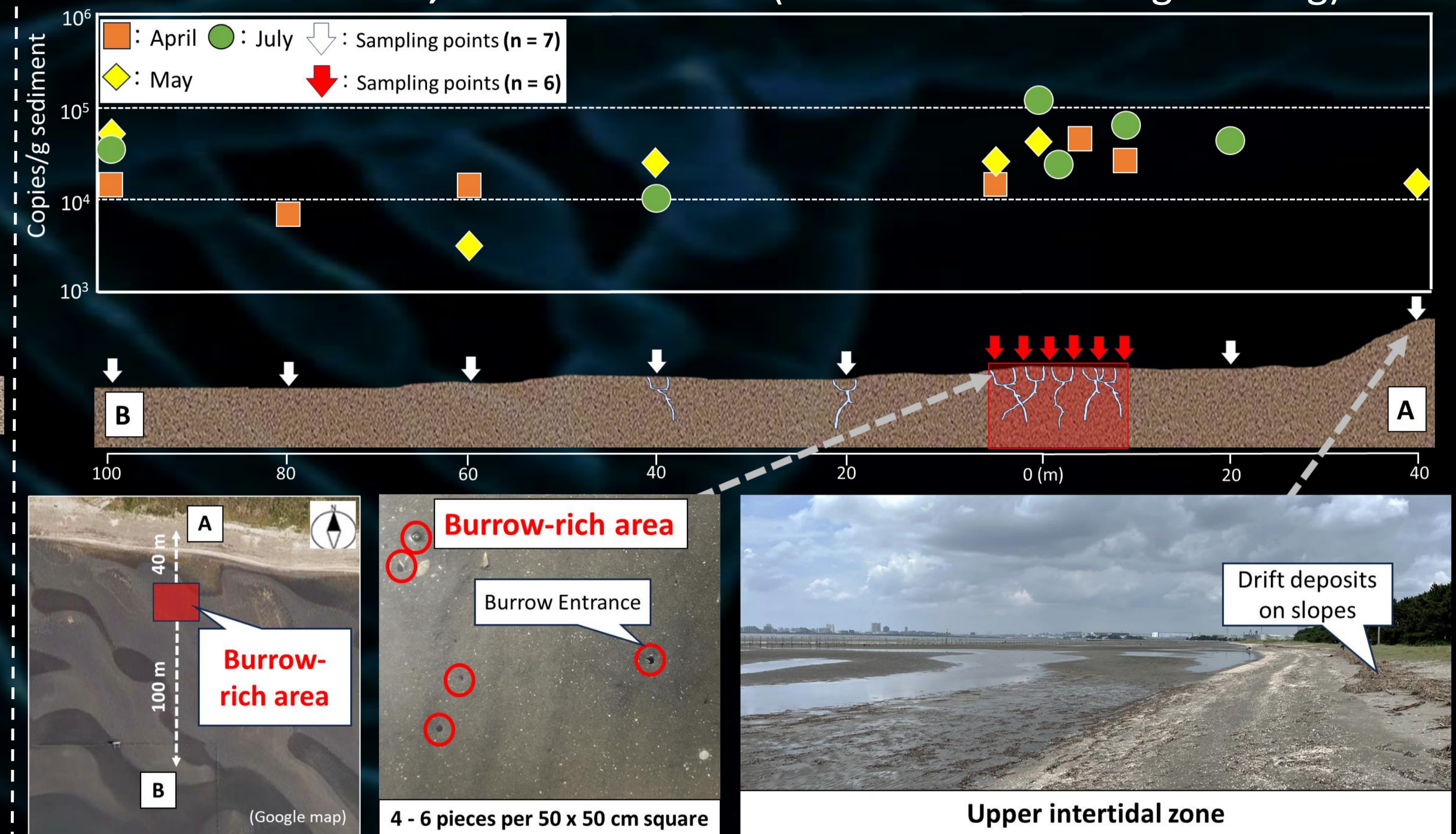
Results

Seasonal sedDNA concentration (copy numbers) of *Upogebia major* in lagoon and coastal tidal flat

Mangoku-ura, Lagoon (A tranquil environment)



Sanbanze, Coastal tidal flat (Waves about 1 m high hitting)



Discussion

① Difference in sedDNA concentration between the burrow-rich area and others

[Mangoku-ura]

F-test, $p > 0.05$

April: No significant difference. Detected in wide area.

May: **The burrow-rich area were significantly higher.**

May ⇒ There is a possibility that it **reflects abundance**

April ⇒ Is the **spawning period** involved?

Is April the peak spawning season?



[Sanbanze]

Every month: **No significant difference & widely detected.**

Is **wave action** involved?

Strong water flow → transported at the concentration at the time of generation.

Due to the effects of **wave action**...

Concentration differences ↓
Detection range ↑ ?

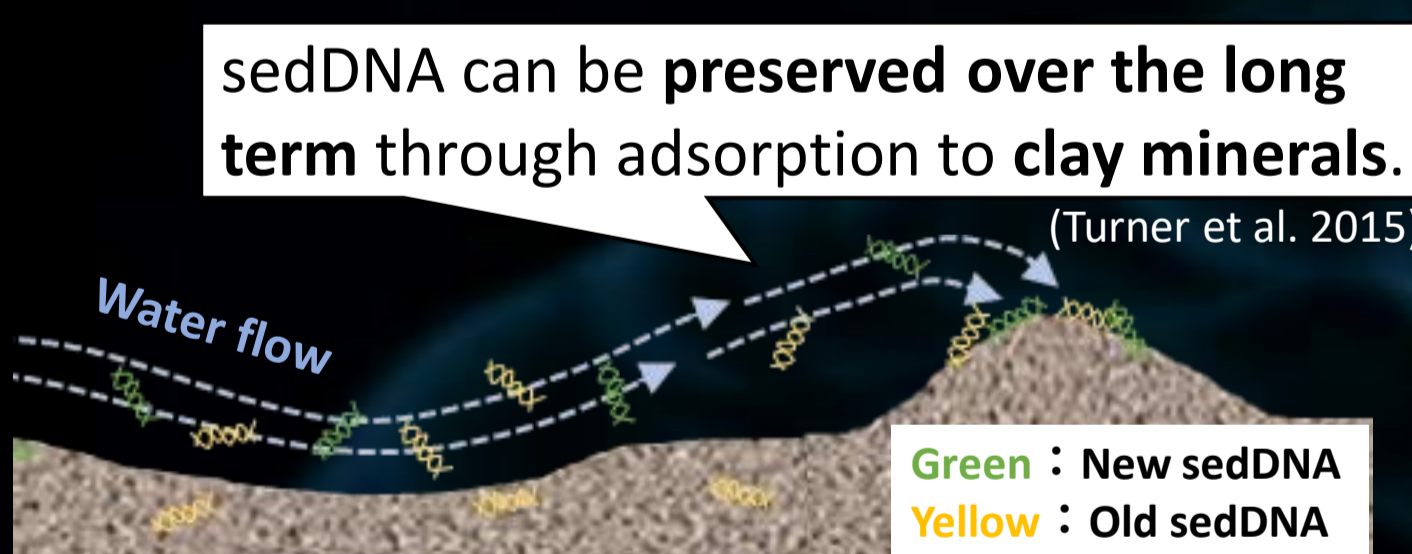
Did the eggs and larvae, among others, **disperse extensively**?

The diffusion of eDNA during the spawning period has also been reported for *Acanthopagrus schlegelii*.

② Relationship between microtopography and sedDNA

High concentrations of sedDNA were detected in raised sediments.

There is a possibility of being transported by water flow and subsequently **re-deposited**.



Future prospects

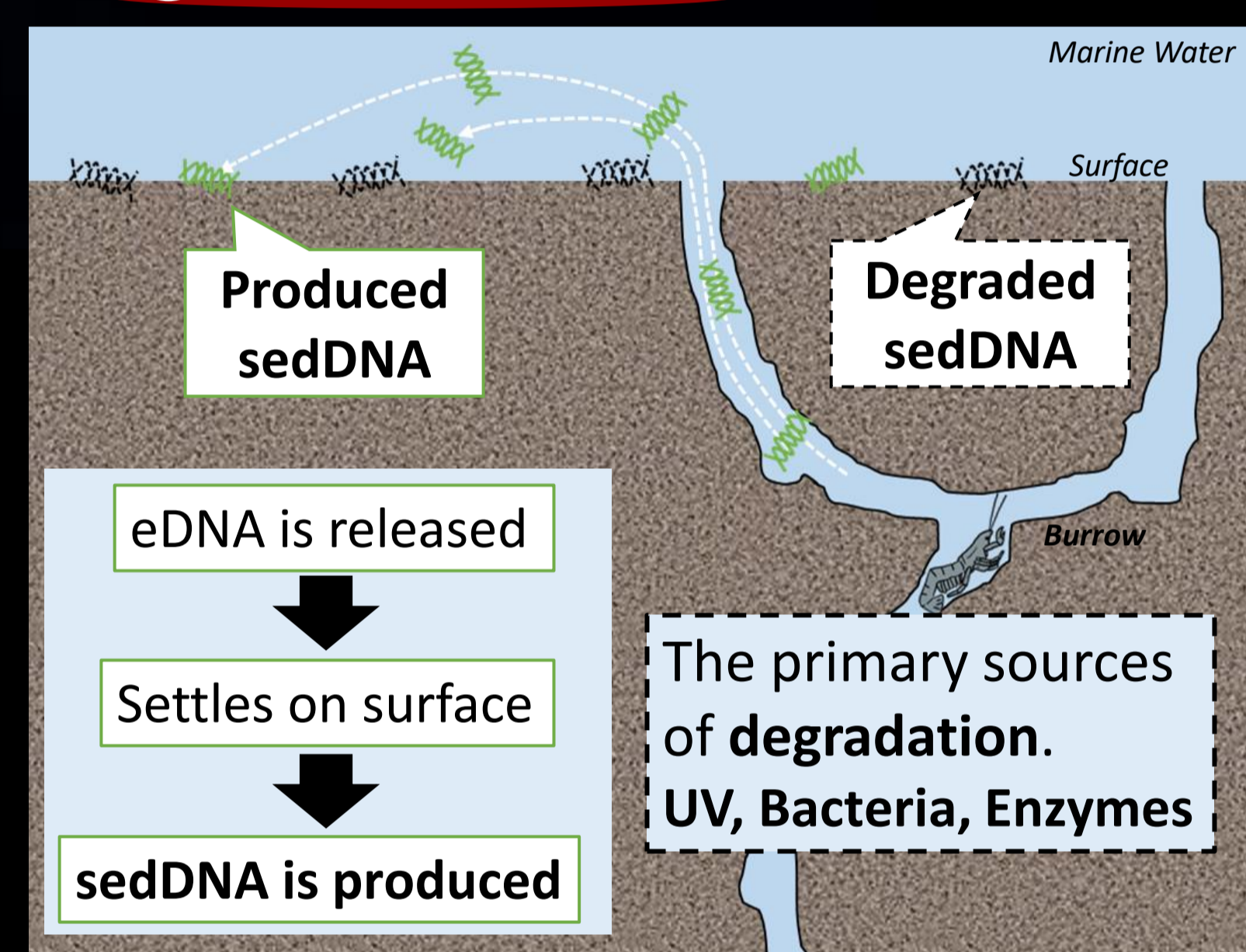
① Future tasks

To interpret concentration data ...

Estimation of **production** and **degradation rates** is necessary!

Through tank experiments, we are empirically measuring the production and degradation rates for each of

"Season", "Growth stage", "Particle size"



② Application to fisheries

sedDNA concentrations fluctuate depending on biological and physical factors... However, they may also reflect existing abundance!



Potential for application in **fisheries** if this novel method is established.

For example, Asari clams *Ruditapes philippinarum*, (an important fisheries resources both in France and in Japan)

The commonality between *U. major* and *R. philippinarum* is...

Low mobility **Filter-feeder** **Benthic infauna** → Knowledge of *U. major* can be applied to other species.

In the future, **fundamental research will be indispensable** for the application of sedDNA analysis in **fisheries!**

Introduction

Upogebia major × sedimentary DNA (sedDNA)



Upogebia major

- Filter-feeder** → Contributes to **water purification** (Dworschak, 1981)
- Forms Y-shaped burrows** more than 2 m deep → Hosts a variety of **symbionts** in its burrows and body (e.g. Seike & Goto, 2020)
- Dominant species** in parts of **Japan and Korea** (Hong, 2013)

Conventional methods of quantification are... Collection & counting of burrows

We aimed to develop a novel method utilizing **environmental DNA** (eDNA).

The detection of American bullfrog DNA in the water of a pond in **France** served as the **inception of eDNA analysis**.



The concentration of eDNA is... **Sediment** > **Water** (e.g. Sakata et al. 2020)

Estimating presence/absence with a sample of about **1 g** → **distribution area** can be estimated with high accuracy! (Sakata et al. 2021)



In order to quantitatively assess the impact of the presence and behaviour of *U. major* on the coastal environment... → **distribution** and **abundance** needs to be determined!

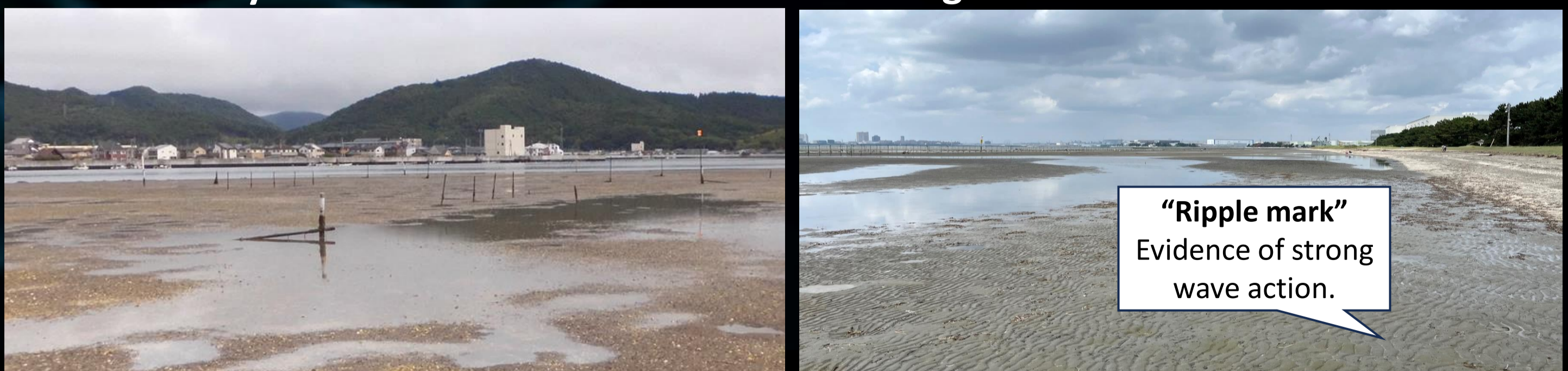
The purpose of this study

To estimate current **abundance** from sedDNA... → **Verification of the concordance between the abundance of *U. major* (Burrow Density) and the concentration of sedDNA!**

Materials & Methods

① Sampling sites

- Mangoku-ura, Lagoon (Miyagi)** Less variability in the benthic environment.
- Sanbanze, Coastal tidal flat (Chiba)** Strong waves lash the tidal flats.



② Sampling of sediments

- 6 samples** from high-abundance areas (burrow-rich areas).
- Within 100 m of the burrow-rich area, **1 sample** was collected every 20 m.

③ sedDNA analysis

Sampling → **sedDNA extraction** → **Quantification of copy numbers using qPCR**

Acknowledgements

We appreciate the Ishinomaki Bay Branch of the Miyagi Prefecture Fisheries Cooperative Association for their understanding of the field survey and cooperation in transporting the samples. This study was partly funded by the Sasakawa Scientific Research Grant from The Japan Science Society and The Research Institute of Marine Invertebrates.

References

Kitabatake, K. (2023). The biology of Japanese burrowing decapods (Decapoda, Thoracostraca). *Journal of the Marine Biological Association of Japan*, 93(1), 1-14.

Species-specific primers and probes were designed based on the molecular phylogenetic data of the *U. major* (Kitabatake et al., in press).