FY2023 Annual Report

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Abstract

The genome contains all the genetic information of a given organism. Decoding the genome provides the molecular basis for understanding every biological phenomenon. Since 2009, the Marine Genomics Unit (MGU) has conducted research in the realm of genome-based biological sciences. By sequencing genomes of target marine organisms (mainly marine invertebrates), we wish to understand genetic and developmental mechanisms underlying evolution and diversification of marine organisms. The major research fields are (a) evolutionary and developmental genomics of marine invertebrates, (b) environmental genomics of coral reefs, and (c) functional genomics of marine organisms including pearl oyster and algae. To date, we have reported draft genomes of a coral in 2011, a pearl oyster in 2012, and coral-symbiotic dinoflagellate (*Breviolum*) in 2013. We further decoded genomes of hemichordates and a brachiopod in 2015; a brown alga (Okinawa-mozuku) in 2016; Crown-of-Thorns starfish in 2017; a nemertean, phoronid, and two dinoflagellate clades in 2018; jellyfish, dicyemids, acoel flatworm, siphonous macroalga (umi-budo), brown alga (ito-mozuku) in 2019; and hydra and four strains of “Okinawa mozuku” brown alga in 2020. In 2021 we have reported sequenced genome of 19 coral species (collaboration with Tokyo Univ.), the kuruma shrimp (collaboration with Tokyo U. of Marine Sci. Tech.), and nearly complete genome of the tunicate *Ciona* (collaboration with Kyoto U.). In this year, we reported haplotype-phased genome of a pearl oyster . In addition, we have advanced genome-based coral research, especially coral-specific eDNA projects, and one research result shall be reported below.

[Photo on June 7, 2023]

1. Staffs and Students

- Professor Noriyuki Satoh
- Staff Scientists
    - Eiichi Shoguchi (Group Leader)
    - Keisuke Nakashima
    - Takeshi Takeuchi
    - Takeshi Noda
- Technical Staffs
    - Kanako Hisata
    - Sakura Kikuchi
    - Haruhi Narisoko
    - Mayuki Suwa
- Research Assistants
    - Aya Koseki (COI-NEXT)
- Research Administrators
    - Tomomi Teruya

    - Kazuko Toyoda
- Students
    - Ph.D students (co-superviser)
        - Rio Kashimoto (Supervisor: Prof. Laudet, V.)

2. Collaborations

2-1 Genome scientific studies of chordate evolution

- Type of collaboration: Scientific collaboration
- Researchers: Prof. Daniel Rokshar, OIST

2-2 Genome sequencing of marine invertebrates at haplotype-resolution level

- Type of collaboration: Scientific collaboration
- Researchers: Prof. Gene Myers, OIST

2-3. Molecular biological study of COTS communications

- Type of collaboration: Scientific collaboration
- Researchers: Prof. Scott Cummins, Univ. Sunshine Coast, Australia

2-4. Genome scientific study of dinoflagellates

- Type of collaboration: Scientific collaboration
- Researchers: Prof. Pengchen Fu, Hainan University

2-5. Genome scientific study of coral-dinoflagellate symbiosis

- Type of collaboration: Scientific collaboration
- Researchers: Profs. Shigeki Fujiwara & Kaz Kawamura, Kochi University

2-6. Genome scientific study of left-right asymmetry of snails

- Type of collaboration: Scientific collaboration
- Researchers: Prof. Takehiro Asami, Shinshu University

2-7. Genome scientific study of amphioxus development

- Type of collaboration: Scientific collaboration
- Researchers: Dr. Hiroki Takahashi, National Institute for Basic Biology

2-8. Genome scientific study of hemichordate development

- Type of collaboration: Scientific collaboration
- Researchers: Profs. Kunifumi Tagawa, Asuka Arimoto & Tatsuya Ueki, Hiroshima University

3. Research activities and findings

Of several studies published in 2023, we report here an advance in scleractinian (stony, reef-building) corals, which was published in Proc. Roy. Soc. B, 290: 20230026 (2023).

Coral reefs have the highest biodiversity of all marine ecosystems in tropical and subtropical oceans. However, scleractinian corals, keystone organisms of reef productivity, are facing a crisis due to climate change and anthropo- genic activities. A broad survey of reef-building corals is essential for worldwide reef preservation. To this end, direct observations made by coral-specialist divers might be supported by another robust method. We improved a recently devised environmental DNA (eDNA) metabarcoding method to identify more than 43 scleractinian genera by sampling 2 l of sur- face seawater above reefs. Together with direct observations by divers, we assessed the utility of eDNA at 63 locations spanning approximately 250 km near Okinawa Island. Slopes of these islands are populated by diverse coral genera, whereas shallow 'moats' sustain fewer and less varied coral taxa. Major genera recorded by divers included Acropora, Pocillopora, Porites and Montipora, the presence of which was confirmed by eDNA analyses. In addition, eDNA identified more genera than direct observations and documented the presence of previously unrecorded species. This scleractinian coral-specific eDNA method promises to be a powerful tool to survey coral reefs broadly, deeply and robustly.

In this study, together with direct observations by divers (a part of Monitoring Sites 1000 Project supported by the Ministry of the Environment of Japan), we assessed the utility of eDNA at 63 locations spanning ~250 km near Okinawa Island (Fig. 1). Of 63 monitoring sites, 51 were slopes (3-10m in depth), 8 were moats (1-3m in depth), and 4 sites were both slopes and moats.

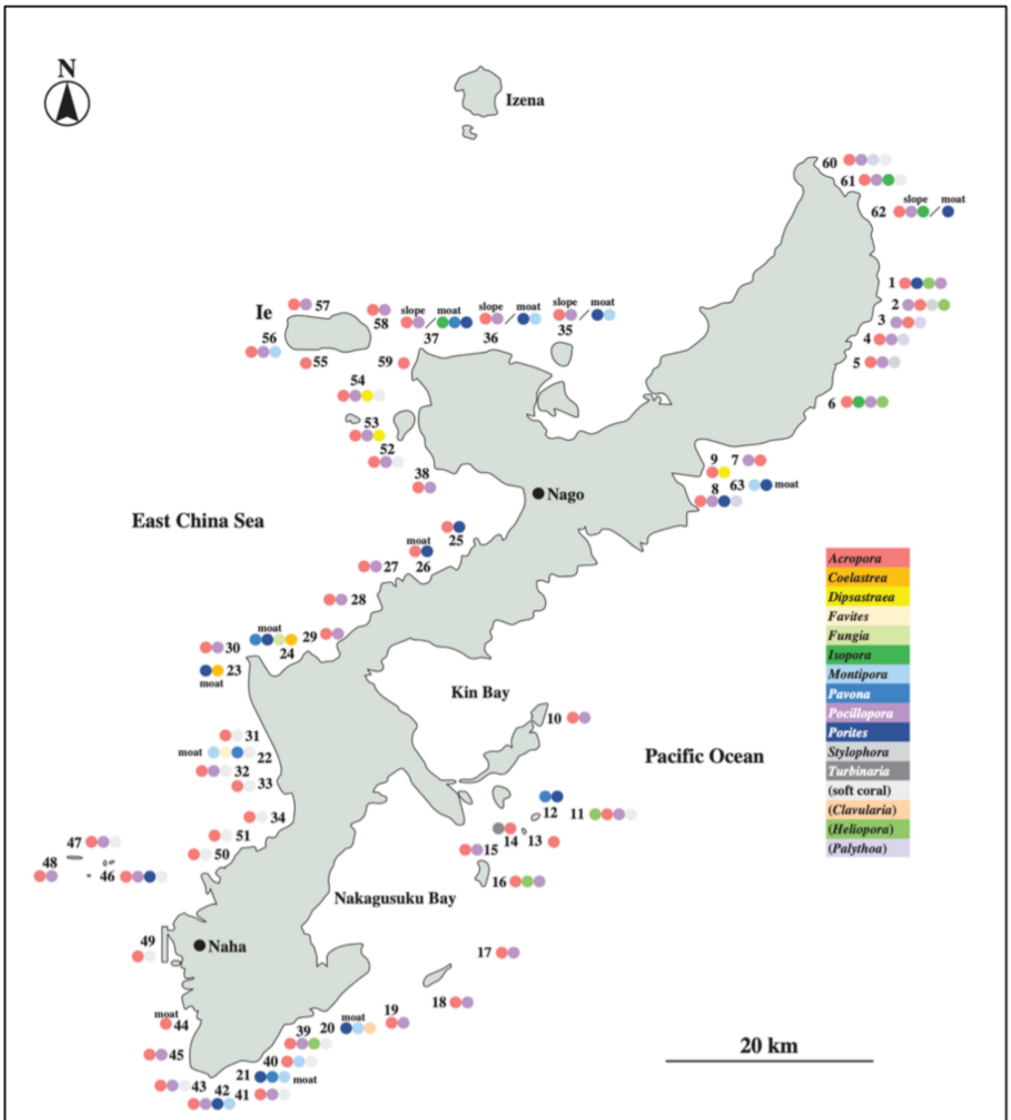

Figure 1. Sixty-three coral reef monitoring locations around Okinawa Island. Collections sites and representative coral genera are shown. Colour codes for genera are shown in the right corner. The order (from left to right) does not always indicate relative dominance of genera. Moats are indicated. Other locations are slopes. At locations #35, 36, 37 and 62, both slopes and moats were examined by diving, whereas only eDNA data were obtained from moats.

Major genera recorded by divers included *Acropora*, *Pocillopora*, *Porites*, and *Montipora* (Fig. 1). Simultaneously, scleractinian coral-specific eDNA barcoding analyses were carried out at 62 locations. We obtained amplicons from all samples at 62 sites, confirming that 2 L of surface seawater are enough for scleractinian-specific eDNA metabarcoding (Fig. 1). Results of the scleractinian coral-specific eDNA barcoding analyses confirmed genera recorded by direct observations by divers. To evaluate this scleractinian coral-specific eDNA method, we compared results of eDNA barcoding with direct observations (Table 1). As a result, 41 of 62 points were well matched (67%), 15 were moderately matched (24%), 4 were partially match (6%), and only 2 points showed no match (3%). In other words, at more than 91% (67%+24%) of monitored locations, eDNA results were confirmed by direct observations.

Table 1. Comparison of scleractinian corals called by direct diver obseration and coral-specific eDNA barcoding method

No	point name	geomorphic classification	direct observation			number of genus detected	eDNA method				number of genus detected	match	Overlap coefficient
25	Busenamisaki west	slope	*Acropora*	*Porites*		2	*Acropora*	*Porites*	*Pocillopora*		3	◎	1
27	Onna	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*	*Montipora*		3	◎	1
28	Onnason Akasaki west	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Montipora*	*Pocillopora*		3	◎	1
29	Maedamisaki west	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*	*Montipora*		3	◎	1
30	Zanpamisaki west	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*	*Dipsastraea*		3	◎	1
31	Toguchi west	slope	*Acropora*			1	*Acropora*	*Montipora*	*Pocillopora*		3	◎	1
32	Mizugama	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Porites*	*Dipsastraea*		3	○	0.5
33	Sunabe	slope	*Acropora*			1	*Acropora*	*Montipora*	*Plesiastrea*		3	◎	1
34	Isa	slope	*Acropora*			1	*Acropora*	*Pocillopora*	*Goniastrea*		3	◎	1
38	Shiokawa Port south	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Montipora*	*Porites*		3	○	0.5
49	Oominezaki Oose	slope	*Acropora*			1	*Acropora*	*Montipora*	*Pocillopora*		3	◎	1
50	Karasuzaki west	slope	*Acropora*			1	*Acropora*	*Porites*	*Goniastrea*		3	◎	1
51	Janase	slope	*Acropora*			1	*Acropora*	*Goniastrea*	*Dipsastraea*		3	◎	1
52	Sesokojima south	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*	*Montipora*		3	◎	1
53	Minnajima east	slope	*Acropora*	*Pocillopora*	*Dipsastraea*	3	*Acropora*	*Pocillopora*	*Porites*	*Dipsastraea*	4	◎	1
54	Nakanshi east	slope	*Acropora*	*Pocillopora*	*Dipsastraea*	3	*Acropora*	*Pocillopora*	*Porites*		3	○	0.666666667
55	Iejima Funazubaru south	slope	*Acropora*			1	*Porites*	*Acropora*	*Goniastrea*		3	◎	1
56	Iejima West	slope	*Acropora*	*Pocillopora*	*Montipora*	3	*Acropora*				1	◎	1
57	Ieijma Waji north	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Montipora*	*Pocillopora*		3	◎	1
58	Iejima Isharabaru east	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*			2	◎	1
59	Aquarium west	slope	*Acropora*			1	*Acropora*	*Pocillopora*	*Montipora*		3	◎	1
45	Kyan Port west	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Dipsastraea*	*Porites*	*Pocillopora*	4	◎	1
1	Adagashima north	slope	*Acropora*	*Porites*		2	*Acropora*	*Porites*	*Montipora*		3	◎	1
2	Adagashima south	slope	*Pocillopora*	*Acropora*	*Stylophora*	3	*Plesiastrea*	*Acropora*	*Montipora*	*Pocillopora*	4	○	0.666666667
3	Ishikinazaki southwest	slope	*Pocillopora*	*Acropora*		2	*Acropora*	*Montipora*	*Porites*	*Pocillopora*	4	◎	1
4	Katsusenozaki south	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pavona*	*Porites*	*Pocillopora*	4	◎	1
5	Aha south	slope	*Acropora*	*Pocillopora*	*Stylophora*	3	*Acropora*	*Pavona*	*Porites*	*Dipsastraea*	4	△	0.333333333
6	Pumped Storage Hydropower Station southeast	slope	*Isopora*	*Pocillopora*	*Acropora*	3	*Acropora*	*Montipora*	*Pocillopora*		3	○	0.666666667
7	Higashison Miyagi Unse south	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Montipora*	*Pocillopora*		3	◎	1
8	Gesashi Uppama east	slope	*Acropora*	*Pocillopora*	*Porites*	3	*Acropora*	*Montipora*	*Porites*	*Pocillopora*	4	◎	1
9	Gesashi north	slope	*Acropora*	*Dipsastraea*		2	*Acropora*	*Porites*	*Montipora*		3	○	0.5
10	Ikeijima east	slope	*Acropora*	*Pocillopora*		2	*Montipora*	*Acropora*	*Pocillopora*		3	◎	1
11	Ukibaru Yokobishi east	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pavona*	*Pocillopora*		3	◎	1
12	Ukibaru Yokobishi south	slope	*Pavona*	*Porites*		2	*Montipora*	*Acropora*	*Palythoa*		3	X	0
13	Minamiukibaru southeast	slope	*Acropora*			1	*Acropora*	*Montipora*	*Porites*		3	◎	1
14	Minamiukibaru south	slope	*Turbinaria*	*Acropora*		2	*Acropora*	*Pavona*	*Montipora*		3	○	0.5
15	Ginogiiwa northeast	slope	*Acropora*	*Pocillopora*		2	*Porites*	*Acropora*	*Montipora*		3	○	0.5
16	Tsukenjima Agihama east	slope	*Acropora*	*Pocillopora*		2	*Montipora*	*Acropora*	*Pachyseris*	*Pocillopora*	4	◎	1
17	Uganiwa south	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Porites*			2	○	0.5
18	Kudakajima Erabuiwa east	slope	*Acropora*	*Pocillopora*		2	*Montipora*	*Acropora*	*Pocillopora*		3	◎	1
19	Kumakajima south	slope	*Acropora*	*Pocillopora*		2	*Montipora*				1	X	0
39	Ohjima south	slope	*Acropora*	*Pocillopora*		2	*Montipora*	*Acropora*	*Porites*		3	○	0.5
40	Mabuni south	slope	*Acropora*	*Montipora*		2	*Acropora*	*Montipora*	*Goniastrea*		3	◎	1
41	Ohdo	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Montipora*	*Porites*		3	○	0.5
43	Arasaki west	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*	*Montipora*		3	◎	1
46	Chiibishi Kamiyama south	slope	*Acropora*	*Pocillopora*	*Porites*	3	*Acropora*	*Pocillopora*	*Porites*		3	◎	1
47	Chiibishi Nagannu north	slope	*Pocillopora*	*Acropora*		2	*Pocillopora*	*Acropora*	*Montipora*		3	◎	1
48	Chiibishi Nagannu west	slope	*Acropora*	*Pocillopora*		2	*Acropora*	*Pocillopora*	*Montipora*		3	◎	1
60	Usahama east	slope	*Acropora*	*Pocillopora*		2	*Isopora*	*Acropora*	*Dipsastraea*	*Pocillopora*	4	◎	1
61	Oku Port north	slope	*Acropora*	*Pocillopora*	*Isopora*	3	*Acropora*	*Porites*	*Goniastrea*		3	△	0.333333333
26	Afuso north	moat	*Acropora*	*Porites*		2	*Acropora*	*Porites*	*Turbinaria*		3	◎	1
35	Kourijima Tokeihama	moat	*Porites*	*Montipora*		2	*Montipora*	*Acropora*	*Porites*		3	◎	1
36	Nakijinson Nagahama	moat	*Porites*	*Montipora*		2	*Montipora*	*Acropora*	*Porites*		3	◎	1
37	Bisezaki east	moat	*Isopora*	*Pavona*	*Porites*	3	*Astreopora*	*Pavona*	*Porites*		3	○	0.666666667
44	Itoman Port Kurantogai north	moat	*Acropora*			1	*Acropora*	*Montipora*	*Pocillopora*		3	◎	1
20	Ohjima south	moat	*Porites*	*Montipora*		2	*Montipora*				1	◎	1
21	Ohdo east	moat	*Porites*	*Pavona*	*Montipora*	3	*Pavona*	*Montipora*	*Acropora*	*Porites*	4	○	0.666666667
22	Mizugama	moat	*Montipora*	*Favites*	*Pavona*	3	*Montipora*	*Goniastrea*	*Porites*	*Pavona*	4	△	0.333333333
23	Zanpamisaki west	moat	*Porites*	*Coelastrea*		2	*Montipora*	*Porites*	*Dipsastraea*	*Goniastrea*	4	○	0.5
24	Maedamisaki west	moat	*Pavona*	*Porites*	*Fungia*	3	*Dipsastraea*	*Pavona*	*Porites*		3	△	0.333333333
62	Kunigamison Akasaki north	moat	*Porites*			1	*Acropora*	*Montipora*	*Pocillopora*	*Porites*	4	◎	1
63	Gesashi Uppama east	moat	*Montipora*	*Porites*		2	*Acropora*	*Montipora*	*Pocillopora*		3	○	0.5

◎, strong match; ○, moderate match; △, partial match; X, no match

Therefore, we concluded that this scleractinian coral-specific eDNA method promises to be a powerful tool to survey coral reefs broadly, deeply, and robustly.

4. Publications

(a) Developmental and Evolutionary Genomics

1. Tominaga, H., Nishitsuji, K., Satoh, N. **A single-cell RNA-seq analysis of early larval cell-types of the starfish, *Patiria pectinifera* : Insights into evolution of the chordate body plan.** Developmental Biology, 496:52-62 (2023). PUBMED

2. Li, K., Nakashima, K., Hisata, K., Satoh, N. **Expression and possible functions of a horizontally transferred glycosyl hydrolase gene, *GH6-1*, in *Ciona* embryogenesis** EvoDevo, 14:11 (2023) PUBMED

3. Arimoto, A., Nishitsuji, K., Hisata, K., Satoh, N., Tagawa, K. **Transcriptomic evidence for *Brachyury* expression in the caudal tip region of adult *Ptychodera flava* (Hemichordata).** DGD, 65: 370-480 (2023) PUBMED LINK

4. Noda, T., Satoh, N., Gittenberger, E., Asami, T. **Left-right reversals recurrently evolved regardless of diaphanous-related formin gene duplication or loss in snails** Journal of Molecular Evolution, 91:721-729 (2023) PUBMED LINK

(b) Environmental Genomics

5. Nishitsuji, K., Nagata, F., Narisoko, H., Kanai, M., Hisata, K., Shinzato, C., Satoh, N. **An environmental DNA metabarcoding survey reveals generic-level occurrence of scleractinian corals at reef slopes of Okinawa Island.** Proc. Royal Soc. B.290:20230026 **(2023).**
6. Hillberg, A., Smith, M., Lausen, B., Suwansa-ard, S., Johnston, R., Mitu, S., MacDonald, L., Zhao, M., Motti, C., Wang, T., Elizur, A., Nakashima, K., Satoh, N., Cummins, S. **Crown-of-thorns starfish spines secrete defense proteins** PeerJ 11:e15689 (2023) LINK

7. Davies, S.W., Gamache, M.H., Howe-Kerr, L.I., Kriefall, N.G., Baker, A.C., Banaszak, A.T., Bay, L.K., Bellantuono, A.J., Bhattacharya, D., Chan, C.X., Claar, D.C., Coffroth, M.A., Cunning, R., Davy, S.K., del Campo, J., Díaz-Almeyda, E.M., Frommlet, J.C., Fuess, L.E., González-Pech, R.A., Goulet, T.L., Hoadley, K.D., Howells, E.J., Hume, B.C.C., Kemp, D.W., Kenkel, C.D., Kitchen, S.A., LaJeunesse, T.C., Lin, S., McIlroy,

S.E., McMinds, R., Nitschke, M.R., Oakley, C.A., Peixoto, R.S., Prada, C., Putnam, H.M., Quigley, K., Reich, H.G., Reimer, J.D., Rodriguez-Lanetty, M., Rosales, S.M., Saad, O.S., Sampayo, E.M., Santos, S.R., Shoguchi, E., Smith, E.G., Stat, M., Stephens, T.G., Strader, M.E., Suggett, D.J., Swain, T.D., Tran, C., Traylor-Knowles, N., Voolstra, C.R., Warner, M.E., Weis, V.M., Wright, R.M., Xiang, T., Yamashita, H., Ziegler, M., Correa, A.M.S., Parkinson, J.E. **Building consensus around the assessment and interpretation of Symbiodiniaceae diversity.** PeerJ 11:e15023 (2023)

8. Kawamura, K., Shioguchi, E., Nishitsuji, K., Sekida, S., Narisoko, H., Zhao, H., Shu, H., Fu, P., Yamashita., H., Fujiwara, S., Satoh, N. ***In vitro* Phagocytosis of Different Dinoflagellate Species by Coral Cells.** Zoological Science, 40:444-454 (2023).

(c) Functional Genomics

9. Smith, M.K., Rotgans, B.A., Lang, T., Johnston, R., Wang, T., Suwansa-Ard, S., Bose, U., Satoh, N., Egertova, M., Hall, M.R., Bryne, M., Elphick, M.R., Motti, C.A., Cummins, S.F. **Structure and proteomic analysis of the crown-of-thorns starfish (*Acanthaster* sp.) radial nerve cord.** Sci Rep. 13(1):3349. doi: 10.1038/s41598-023-30425-1 (2023).

5. Seminar: no seminar due to COVID problem.