

FY2011 Annual Report

Marine Genomics Unit

Professor Nori Satoh



Abstract

The genome contains all the genetic information of a given organism. Decoding the genome therefore provides the molecular basis for understanding every biological phenomenon. Since the turn of the 21st century, genomes of various metazoans have been sequenced, and consequently studies progressed efficiently in the fields of evolutionary biology, developmental biology, and environmental biology. The objective of the Marine Genomic Unit is to decode the genomes of target marine invertebrates so as to comprehensively elucidate the molecular mechanisms underlying the (a) environmental responses, (b) development, and (c) evolution of marine animals. In fiscal year 2011, we have decoded genome of the coral *Acropora digitifera* and that of the pearl oyster *Pinctada fucata*. We have published two papers in *Nature*. In addition, we have published 20 original papers of various research subjects. The major achievements were as follows.

(a) Environmental genomics:

The coral reefs of the Okinawa islands are amongst the most biologically diverse ecosystems in the world. The key organisms in their establishment, the scleractinian corals, increasingly

face a range of human-caused challenges including ocean acidification and seawater temperature rises. To understand better the molecular mechanisms underlying coral biology, in this year, we have finally succeeded in deciphering the 420-Mbp-long genome of the coral *Acropora digitifera*, which was published in *Nature*.

(b) Developmental genomics:

In spite of significant position of mollusks in developmental and evolutionary biology, so far no reports on genomes of this animal group appeared. We have decoded the pearl oyster genome this year, which was published in *DNA Research*.

(c) Evolutionary genomics:

We are interested in the origin and evolution of chordates. The notochord is the most prominent feature of chordates, and these organisms were named after this organ. Previously we revealed that a T-box transcription factor gene, *Brachyury (Bra)*, plays a pivotal role in the formation of the notochord in ascidian embryos. We have discussed the origin of chordates in relation to the innovation of *Bra* gene expression and function.

1. Staff

- Group Leader
 - Dr. Takeshi Kawashima
 - Dr. Eiichi Shoguchi
- Researcher
 - Dr. Mayuko Hamada
 - Dr. Tetsuro Ikuta
 - Dr. Ryo Koyanagi
 - Dr. Ken Maeda
 - Dr. Keisuke Nakashima
 - Dr. Takeshi Noda
 - Dr. Chuya Shinzato
 - Dr. Sutada Mungpakdee
 - Dr. Takeshi Takeuchi
- Technical Staff
 - Ms. Mayuki Fujiwara
 - Ms. Kanako Hisata
 - Ms. Sakura Kikuchi
 - Dr. Makiko Tanaka

- Research Administrator
 - Ms. Shoko Yamakawa
 - Ms. Tomomi Teruya

2. Collaborations

- Theme: Decoding of the coral genomes
 - Type of collaboration: Collaboration
 - Researchers:
 - Dr. David Miller, James Cook University, Australia
- Theme: Chip-sequence analysis of *Ci-Bra* target genes
 - Type of collaboration: Collaboration
 - Researchers:
 - Dr. Hiroki Takahashi, National Institute for Basic Biology, Japan
- Theme: Analysis of *Ciona* genes with transgenic lines
 - Type of collaboration: Collaboration
 - Researchers:
 - Dr. Yasunori Sasakura, Shimoda Marine Research Center, University of Tsukuba, Japan
- Theme: Analysis of the evolution of chordate genomes
 - Type of collaboration: Collaboration
 - Researchers:
 - Dr. Asao Fujiyama, National Institute of Genetics, Japan

3. Activities and Findings

3.1 Environmental genomics

To understand better the molecular mechanisms underlying coral biology, we decoded the approximately 420-megabase genome of *Acropora digitifera* using next-generation sequencing technology. This genome contains approximately 23,700 gene models. Molecular phylogenetics indicate that the coral and the sea anemone *Nematostella vectensis* diverged approximately 500 million years ago (Figure 1), considerably earlier than the time over which modern corals are represented in the fossil record. Despite the long evolutionary history of the endosymbiosis, no evidence was found for horizontal transfer of genes from symbiont to host. However, unlike several other corals, *Acropora* seems to lack an enzyme essential for cysteine biosynthesis (Table 1), implying dependency of this coral on its symbionts for this amino acid.

Corals inhabit environments where they are frequently exposed to high levels of solar radiation, and analysis of the *Acropora* genome data indicates that the coral host can independently carry out de novo synthesis of mycosporine-like amino acids, which are potent ultra- violet-protective compounds (Figure 2). In addition, the coral innate immunity repertoire is notably more complex than that of the sea anemone, indicating that some of these genes may have roles in symbiosis or coloniality (Figure 3). A number of genes with putative roles in calcification were identified, and several of these are restricted to corals. The coral genome provides a platform for understanding the molecular basis of symbiosis and responses to environmental changes.

We are now decoding the genome of a coral symbiont, *Symbiodinium minutum*.

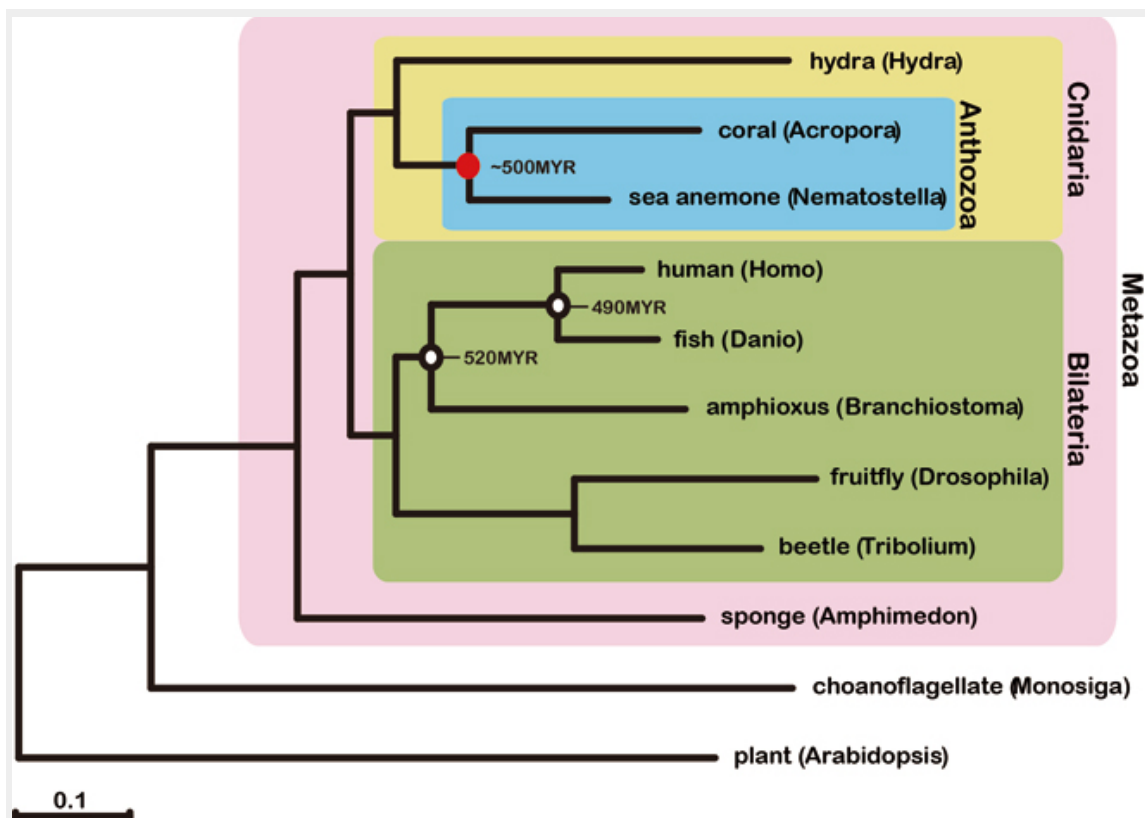


Figure 1: Molecular phylogeny of corals. 94,200 aligned amino acid positions of proteins encoded by 422 genes were obtained from the sponge *Amphimedon queenslandica*, from the cnidarians *A. digitifera*, *Nematostella vectensis* and *Hydra magnipapillata*, and from the triploblasts *Tribolium castaneum*, *Drosophila melanogaster*, *Branchiostoma floridae*, *Danio rerio* and *Homo sapiens*. The sequences were analysed using maximum likelihood methods, with the plant *Arabidopsis thaliana* and the choanoflagellate *Monosiga brevicollis* serving as outgroups. The scale bar represents 0.1 expected substitutions per site in the aligned

regions. The topology was supported by 100% bootstrap value. Approximate divergent times of the occurrence of basal chordates and divergence of vertebrates lineages are shown. This analysis indicates a deeper divergence of *Acropora* and *Nematostella*, approximately 500 million years (Myr) ago.

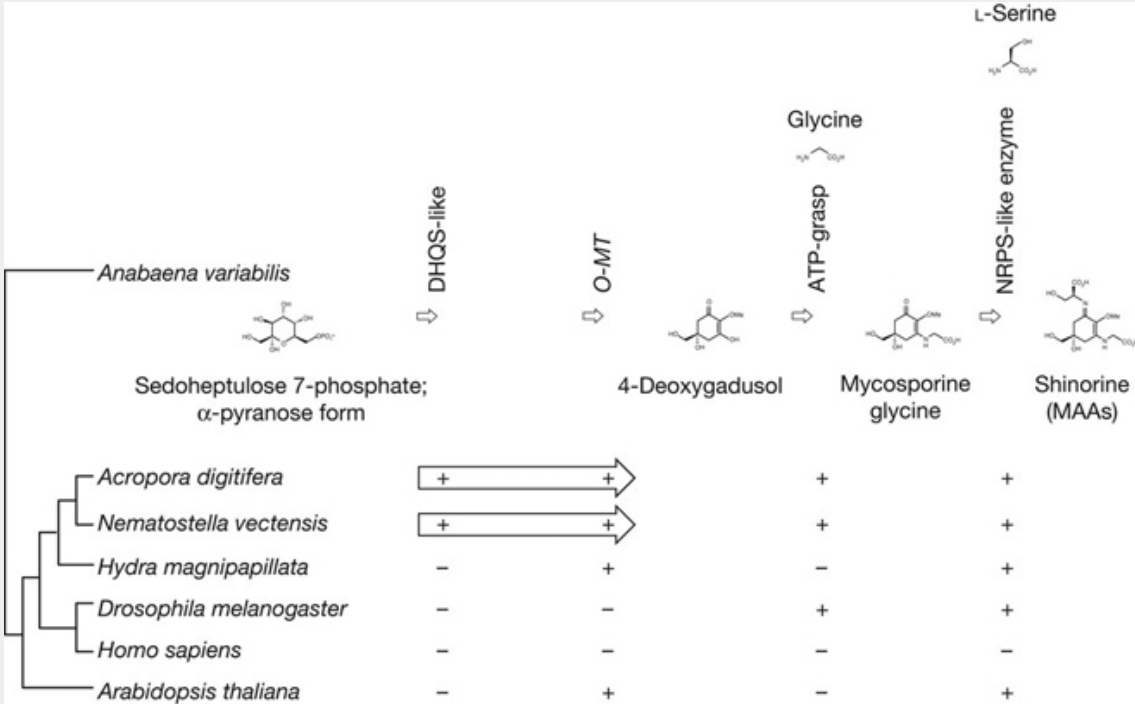


Figure 2: The genes required for the biosynthesis of shinorine are present in anthozoan cnidarians. Top, the organization of the gene cluster involved in the biosynthetic pathway of the photo-protective molecule shinorine, a mycosporine-like amino acid, in the cyanobacterium *Anabaena variabilis*. Bottom, the presence of corresponding genes in various organisms is indicated (+). The *Acropora* and *Nematostella* genomes contain homologues of each of the four genes, in which DHQS-like and O-MT are fused with each other.

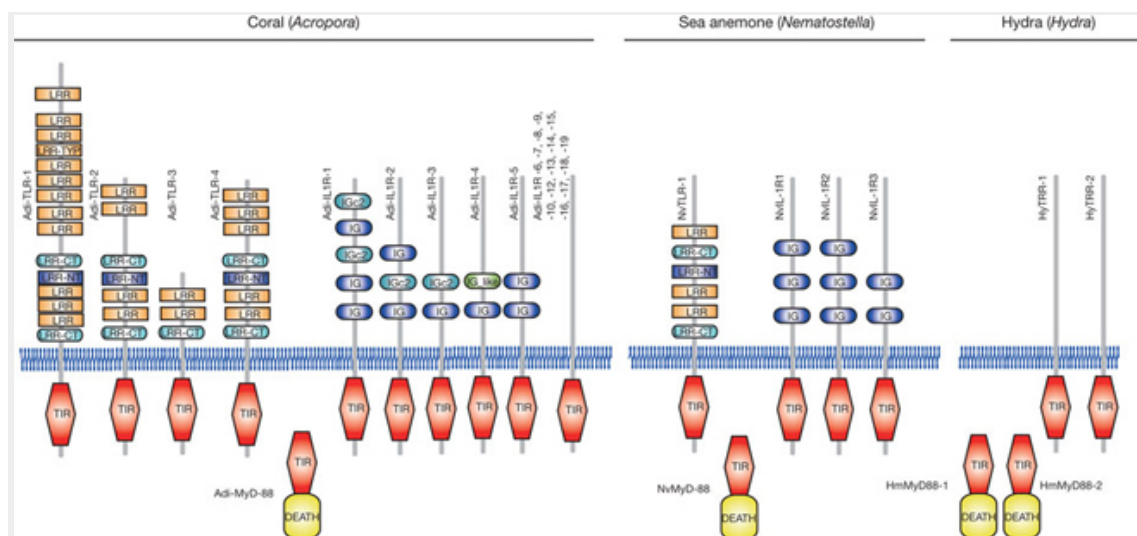


Figure 3: Repertoires of TIR-domain-containing proteins of three cnidarians. The schematic representation of the domain structures of TIR-domain-containing proteins identified in *A. digitifera*, alongside the corresponding complements from *Nematostella vectensis* and *Hydra magnipapillata*. The repertoire of Toll/TLR, IL-1R-like and TIR-only proteins is significantly more complex in the case of *A. digitifera* than in *N. vectensis* or *H. magnipapillata*. TIR, TIR domain. DEATH, DEATH domain. IG and IGc2, Ig domain. LRR, LRR-TRY, LRR-CT and LRR-NT, leucine-rich repeats.

	L-Homocysteine + L-Serine	Cbs	L-Cystathionine	Cth	L-Cysteine
<i>Hydra magnipapillata</i>		Yes*		Yes	
<i>Nematostella vectensis</i>		Yes*		Yes	
Complexa					
<i>Acropora digitifera</i>		No†		Yes	
<i>Acropora tenuis</i>		No‡		ND	
<i>Acropora millepora</i>		No§		Yes	
<i>Galaxea fascicularis</i>		Yes‡		ND	
Robusta					
<i>Montastraea faveolata</i>		Yes§		Yes	
<i>Favia lizardensis</i>		Yes‡		ND	
<i>Favites chinensis</i>		Yes‡		ND	
<i>Ctenactis echinata</i>		Yes‡		ND	

ND, not determined.

* Supported by sequenced genome and EST analyses.

† Supported by sequenced genome, EST and PCR amplification of genomic DNA.

‡ Supported by PCR amplification of genomic DNA.

§ Supported by EST analyses.

Table 1: The presence or absence of a gene encoding Cbs for L-cysteine biosynthesis

3.2 Developmental genomics

We have deciphered the pearl oyster genome with collaboration of various research groups of mollusk this year since the study of the pearl oyster *Pinctada fucata* is key to increasing our understanding of the molecular mechanisms involved in pearl biosynthesis and biology of bivalve mollusks (Figure 4). We sequenced ~1150-Mb genome at ~40-fold coverage using the Roche 454 GS-FLX and Illumina GAIIX sequencers. The sequences were assembled into contigs with N50 = 1.6 kb (total contig assembly reached to 1024 Mb) and scaffolds with N50 = 14.5 kb. The pearl oyster genome is AT-rich, with a GC content of 34%. DNA transposons, retrotransposons, and tandem repeat elements occupied 0.4, 1.5, and 7.9% of the genome, respectively (a total of 9.8%) (Figure 5). Version 1.0 of the *P. fucata* draft genome contains 23,257 complete gene models, 70% of which are supported by the corresponding expressed sequence tags. The genes include those reported to have an association with bio-mineralization (Table 2). Genes encoding transcription factors and signal transduction molecules are present in numbers comparable with genomes of other metazoans. Genome-wide molecular phylogeny suggests that the lophotrochozoan represents a distinct clade from ecdysozoans. Our draft genome of the pearl oyster thus provides a platform for the identification of selection markers and genes for calcification, knowledge of which will be important in the pearl industry.

In addition, in collaboration with Dr. Y. Sasakura's lab at Tsukuba University, we disclosed that ependymal cells of chordate larvae are stem-like cells that form the adult nervous system. Namely, in ascidian tunicates, the metamorphic transition from larva to adult is accompanied by dynamic changes in the body plan. For instance, the central nervous system (CNS) is subjected to extensive rearrangement because its regulating larval organs are lost and new adult organs are created. To understand how the adult CNS is reconstructed, we traced the fate of larval CNS cells during ascidian metamorphosis by using transgenic animals and imaging technologies with photoconvertible fluorescent proteins. We showed that most parts of the ascidian larval CNS, except for the tail nerve cord, are maintained during metamorphosis and recruited to form the adult CNS (Figure 6). We also show that most of the larval neurons disappear and only a subset of cholinergic motor neurons and glutamatergic neurons are retained. Finally, we demonstrate that ependymal cells of the larval CNS contribute to the construction of the adult CNS and that some differentiate into neurons in the adult CNS (Figure 6). An unexpected role of ependymal cells highlighted by this study is that they serve as neural stem-like cells to reconstruct the adult nervous network during chordate metamorphosis. Consequently, the plasticity of non-neuronal ependymal cells and neuronal

cells in chordates should be re-examined by future studies. This study was published in *Nature*.

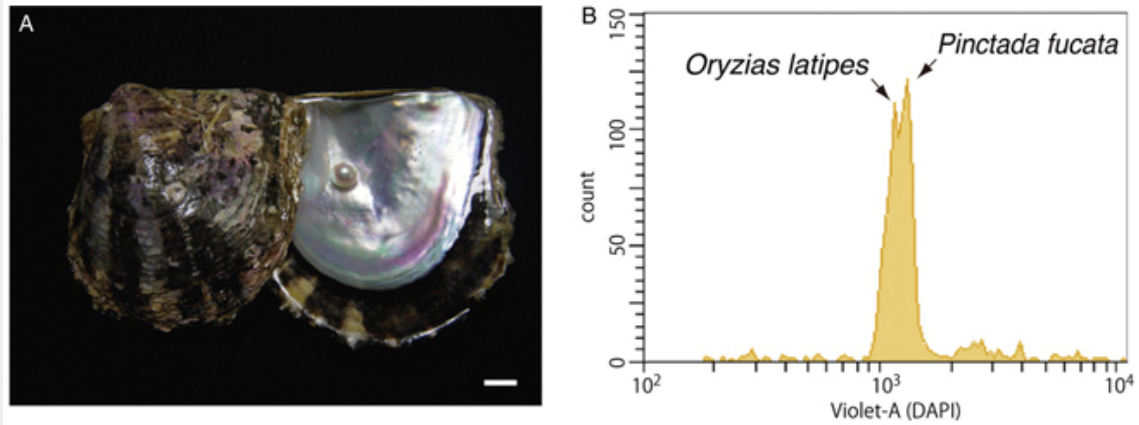


Figure 4: (A) The pearl oyster *P. fucata* and its pearl. Scale bar, 1 cm. (B) Flow cytometry of a mixture of sperm from *Pinctata* and *Oryzias*. The *Pinctata* genome, estimated to be ~1150 Mb in size, is slightly larger than the *Oryzias* genome (~1100 Mb).

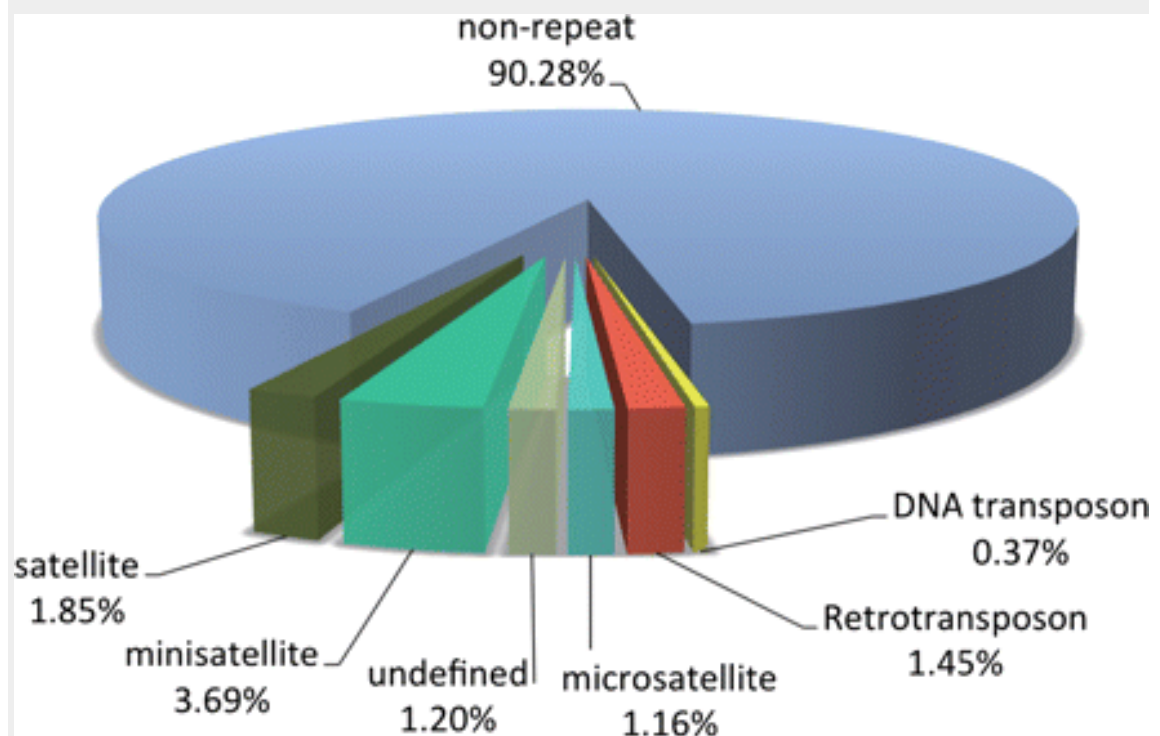
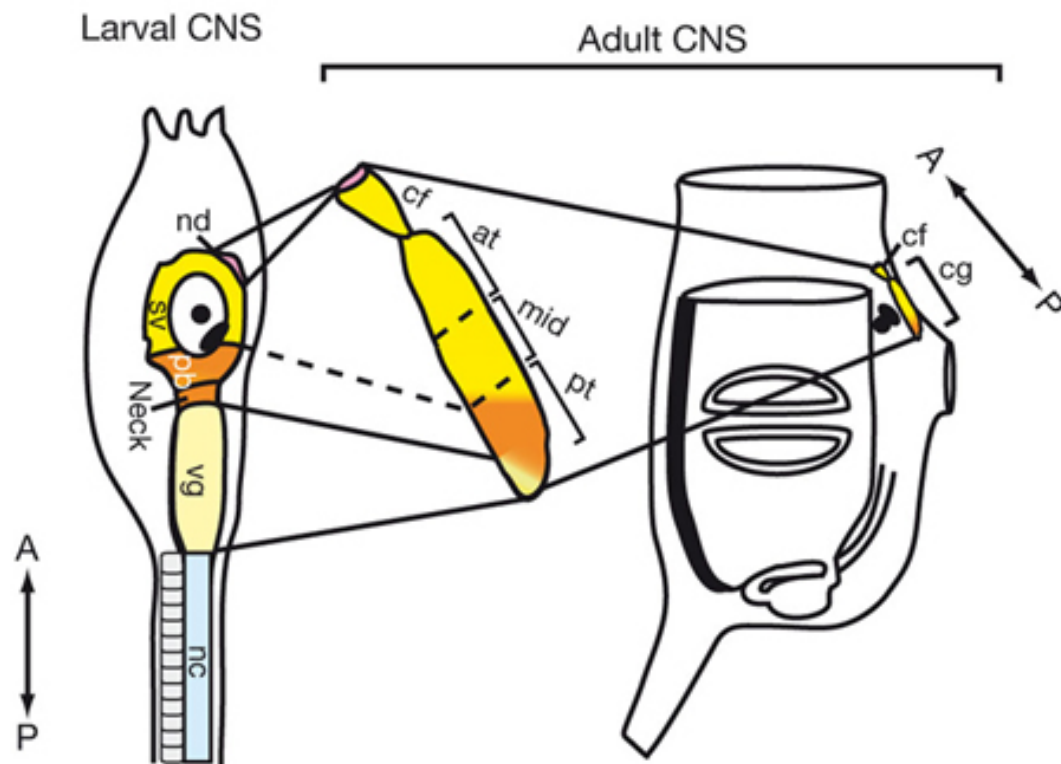


Figure 5: Repeat elements in the *P. fucata* genome.

Protein	cDNA accession number	Scaffolds
Aspein	AB094512	sca03_465.1
Chitin synthase 1	AB290881	sca03_4962.1
KRMP-3(MSI7)	AF516712	sca03_229418.1
MSI60	D86074	sca03_523.1
N16	AB023067 (#1)	sca03_1834.1
N19	AB332326	sca03_2495.1
Nacrein	D83523	sca03_33972.1
PFMG1	DQ104255	sca03_72180.1
Pfty-1	AB254132	sca03_10251.1
Pfty-2	AB254133	sca03_21093.1
Pif177	AB236929	sca03_20175.1
Prisilkin-39	EU921665	sca03_12887.1
Prismalin-14	AB159512	sca03_15935.1
Prismin	AB368930	sca03_263.1
Shematrín-1	AB244419	sca03_24266.1
Shematrín-2	AB244420	sca03_89285.1
Shematrín-3	AB244421	sca03_72160.1
Shematrín-4	AB244422	sca03_16186.1
Shematrín-5	AB244423	sca03_3950.1
Shematrín-6	AB244424	sca03_14895.1
Shematrín-7	AB244425	sca03_411.1

Table 2: The gene location in the *P. fucata* genome for reported cDNAs or proteins that are associated with pearl oyster shell matrix formation

a Larval ependymal cells/neurohypophysial duct



b Larval neurons

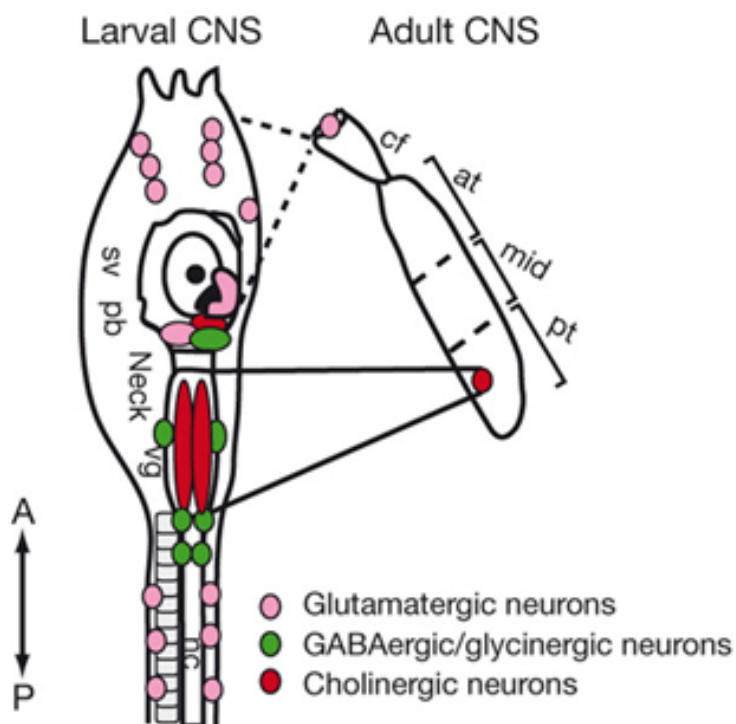


Figure 6: Adult CNS is constructed from the larval CNS. The relationship between the larval and adult CNS with respect to larval ependymal cells (**a**) and larval neurons (**b**); nd, neurohypophysial duct; sv, sensory vesicle; pb, posterior brain; vg, visceral ganglion; nc, nerve cord; cf, ciliated funnel; at, mid and pt, anterior, middle and posterior parts of the cerebral ganglion, respectively; cg, cerebral ganglion; A, anterior; P, posterior.

3.3 Evolutionary genomics

We have studied on the origin and evolution of chordates. More than 550 million years ago, chordates originated from a common ancestor shared with nonchordate deuterostomes by developing a novel type of larva, the “tadpole larva.” The notochord is the supporting organ of the larval tail and the most prominent feature of chordates; indeed, phylum Chordata is named after this organ. In a recent review, we discussed the molecular mechanisms involved in the formation of the notochord over the course of chordate evolution with a special emphasis on a member of T-box gene family, *Brachyury* (Figure 7). Comparison of the decoded genome of a unicellular choanoflagellate with the genomes of sponge and cnidarians suggests that T-box gene family arose at the time of the evolution of multicellular animals. Gastrulation is a morphogenetic movement that is essential for the formation of two- or three-germ-layered embryos. *Brachyury* is transiently expressed in the blastopore (bp) region, where it confers on cells the ability to undergo invagination. This process is involved in the formation of the archenteron in all metazoans. This is a “primary” function of *Brachyury*. During the evolution of chordates, *Brachyury* gained an additional expression domain at the dorsal midline region of the bp. In this new expression domain, *Brachyury* served its “secondary” function, recruiting another set of target genes to form a dorsal axial organ, notochord. The Wnt/ β -catenin, BMP/Nodal, and FGF-signaling pathways are involved in the transcriptional activation of *Brachyury*. We discuss the molecular mechanisms of *Brachyury* secondary function in the context of the dorsal–ventral (D–V) inversion theory and the aboral-dorsalization hypothesis. Although the scope of this review requires some degree of oversimplification of *Brachyury* function, it is beneficial to facilitate studies on the notochord formation, a central evolutionary developmental biology problem in the history of metazoan evolution.

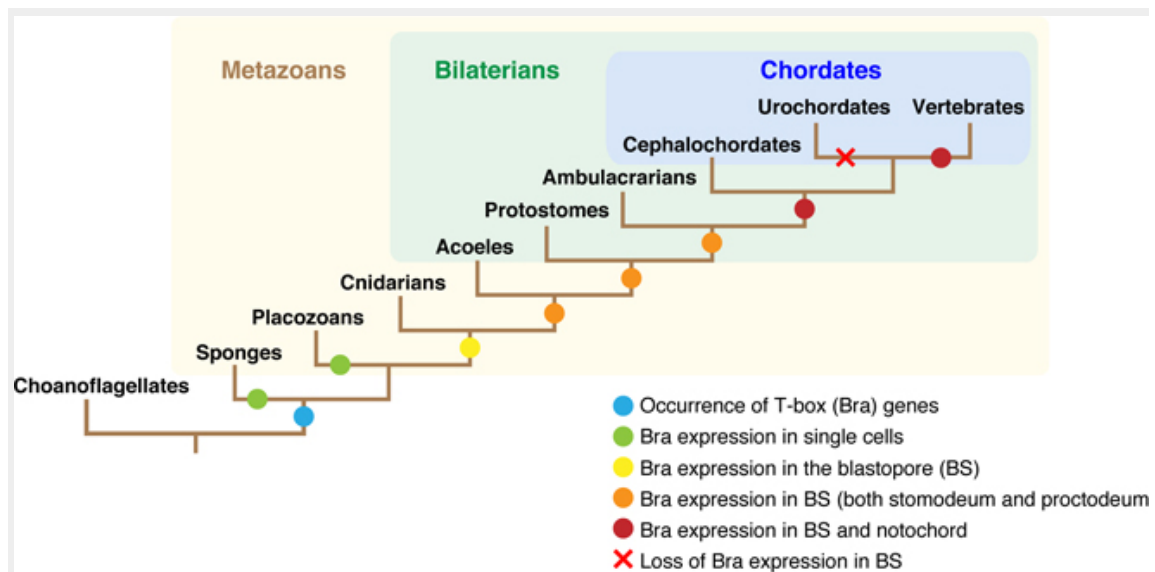


Figure 7: A schematic representation of the innovation in *Brachyury* expression and function during evolution of animals.

4. Publications

4.1 Journals

[2011]

Shinzato, C., Shoguchi, E., Kawashima, T., Hamada, M., Hisata, K., Tanaka, M., Fujie, M., Fujiwara, M., Koyanagi, R., Ikuta, T., Fujiyama, A., Miller, D. J., and Satoh, N. 2011. Using the *Acropora digitifera* genome to understand coral responses to environmental change. *Nature* 476: 320-323.

Horie, T., Shinki, R., Ogura, Y., Kusakabe, T. G., Satoh, N., and Sasakura, Y. 2011. Ependymal cells of chordate larvae are stem-like cells that form the adult nervous system. *Nature* 469: 525-528.

Ogura, Y., Sakaue-Sawano, A., Nakagawa, M., Satoh, N., Miyawaki, A., and Sasakura, Y. 2011. Coordination of mitosis and morphogenesis: role of a prolonged G2 phase during chordate neurulation. *Development* 138: 577-587.

Hamada, M., Shimosono, N., Ohta, N., Satou, Y., Horie, T., Kawada, T., Satake, H., Sasakura, Y., and Satoh, N. 2011. Expression of neuropeptide- and hormone-encoding genes in the *Ciona intestinalis* larval brain. *Developmental Biology* 352: 202-214.

- Noda, T. 2011. The maternal genes Ci-p53/p73-a and Ci-p53/p73-b regulate zygotic ZicL expression and notochord differentiation in *Ciona intestinalis* embryos. *Developmental Biology* 360: 216-229.
- Onimaru, K., Shoguchi, E., Kuratani, S., and Tanaka, M. 2011. Development and evolution of the lateral plate mesoderm: Comparative analysis of amphioxus and lamprey with implications for the acquisition of paired fins. *Developmental Biology* 359: 124-136.
- Yoshida, M. A., Ishikura, Y., Moritaki, T., Shoguchi, E., Shimizu, K. K., Sese, J., and Ogura, A. 2011. Genome structure analysis of molluscs revealed whole genome duplication and lineage specific repeat variation. *Gene* 483: 63-71.
- Shoguchi, E., Hamada, M., Fujie, M., and Satoh, N. 2011. Direct examination of chromosomal clustering of organ-specific genes in the chordate *Ciona intestinalis*. *Genesis* 49: 662-672.
- Yamada, S., Ueno, N., Satoh, N., and Takahashi, H. 2011. *Ciona intestinalis* Noto4 contains a phosphotyrosine interaction domain and is involved in the midline intercalation of notochord cells. *Int J Dev Biol* 55: 11-18.
- Shoguchi, E., Fujie, M., and Hamada, M. 2011. No chromosomal clustering of housekeeping genes in the marine chordate *Ciona intestinalis*. *Mar Genomics* 4: 151-157.
- Asakura, T., Koyanagi, R., Nishiyama, N., Kuboyama, N., Kiba, H., and Abiko, Y. 2011. Bone regeneration on the epicondyle of the femur supported by silk fibroin-based scaffold: a model system for dental surgery. *Journal of Insect Biotechnology and Sericology* 80: 25-30.
- Hirose, E., Nakashima, K., and Nishino, A. 2011. Is there intracellular cellulose in the appendicularian tail epidermis? A tale of the adult tail of an invertebrate chordate. *Communicative & Integrative Biology* 68: 1623-1631.
- Iguchi, A., Shinzato, C., Foret, S., and Miller, D. J. 2011. Identification of Fast-Evolving Genes in the Scleractinian Coral *Acropora* Using Comparative EST Analysis. *PLoS One* 6: e20140.
- Ikuta, T. 2011. Evolution of Invertebrate Deuterostomes and Hox/ParaHox Genes. *Genomics, Proteomics & Bioinformatics* 9: 77-76.
- Katayama, T., Wilkinson, M. D., Vos, R., Kawashima, T., Kawashima, S., Nakao, M., Yamamoto, Y., Chun, H. W., Yamaguchi, A., Kawano, S., Aerts, J., Aoki-Kinoshita, K. F.,

Arakawa, K., Aranda, B., Bonnal, R. J., Fernandez, J. M., Fujisawa, T., Gordon, P. M., Goto, N., Haider, S., Harris, T., Hatakeyama, T., Ho, I., Itoh, M., Kasprzyk, A., Kido, N., Kim, Y. J., Kinjo, A. R., Konishi, F., Kovarskaya, Y., von Kuster, G., Labarga, A., Limviphuvadh, V., McCarthy, L., Nakamura, Y., Nam, Y., Nishida, K., Nishimura, K., Nishizawa, T., Ogishima, S., Oinn, T., Okamoto, S., Okuda, S., Ono, K., Oshita, K., Park, K. J., Putnam, N., Senger, M., Severin, J., Shigemoto, Y., Sugawara, H., Taylor, J., Trelles, O., Yamasaki, C., Yamashita, R., Satoh, N., and Takagi, T. 2011. The 2nd DBCLS BioHackathon: interoperable bioinformatics Web services for integrated applications. *J Biomed Semantics* 2: 4.

Maeda, K., Mukai, T., and Tachihara, K. 2011. Newly collected specimens of the sleeper *Eleotris acanthopoma* (Teleostei: Eleotridae) from French Polynesia indicate a wide and panmictic distribution in the West and South Pacific. *Pacific Science* 65: 257–264.

Maeda, K., Saeki, T., and Tachihara, K. 2011. New record of a freshwater terapontid fish, *Mesopristes cancellatus* (Teleostei: Terapontidae) from Okinawa Island in the Ryukyu Archipelago. *Biogeography* 13: 45-50.

Miller, D. J., Ball, E. E., Foret, S., and Satoh, N. 2011. Coral genomics and transcriptomics — Ushering in a new era in coral biology. *Journal of Experimental Marine Biology and Ecology* 408: 114-119.

Nakashima, K., Nishino, A., and Hirose, E. 2011. Forming a tough shell via an intracellular matrix and cellular junctions in the tail epidermis of *Oikopleura dioica* (Chordata: Tunicata: Appendicularia). *Naturwissenschaften* 98: 661-669.

Nakashima, K., Nishino, A., Horikawa, Y., Hirose, E., Sugiyama, J., and Satoh, N. 2011. The crystalline phase of cellulose changes under developmental control in a marine chordate. *Cell Mol Life Sci* 68: 1623-1631.

[2012]

Satoh, N., Tagawa, K., and Takahashi, H. 2012. How was the notochord born? *Evolution & Development* 14: 56-75.

Takeuchi, T., Kawashima, T., Koyanagi, R., Gyoja, F., Tanaka, M., Ikuta, T., Shoguchi, E., Fujiwara, M., Shinzato, C., Hisata, K., Fujie, M., Usami, T., Nagai, K., Maeyama, K., Okamoto, K., Aoki, H., Ishikawa, T., Masaoka, T., Fujiwara, A., Endo, K., Endo, H., Nagasawa, H.,

Kinoshita, S., Asakawa, S., Watabe, S., and Satoh, N. 2012. Draft Genome of the Pearl Oyster *Pinctada fucata*: A Platform for Understanding Bivalve Biology. *DNA Res* 19: 117-130.

4.2 Books and other one-time publications

Satoh, N. 2011. *Tunicate embryos and cell specification*, *Encyclopedia of Life Sciences*.

4.3 Oral and Poster Presentations

Hamada, M. 2011. An unexpected diversification of NOD-like receptor system in the coral *Acropora digitifera*. In International Workshop on Marine Evolutionary and Environmental Genomics. Academia Sinica, Taipei, Taiwan.

Kawashima, T. 2011. Haplotype SNPs in coral genome: examples from GPCR family genes. In 14th Meeting of Open Bio Japan. Nomi, Ishikawa, Japan.

Koyanagi, R., Fujie, M., Usami, T., and Ikuta, T. 2011. De novo genome assembly using next-generation sequencers: optimization of data amount. In 14th Meeting of Open Bio Japan. Nomi, Ishikawa, Japan.

Mungpakdee, S. 2011. Genetic variation between individuals of *Acropora digitifera* from Okinawa. In International Workshop on Marine Evolutionary and Environmental Genomics. Academia Sinica, Taipei, Taiwan.

Satoh, N. 2011. On the origin and evolution of chordates: Lessons from their genomes. In Searching for eve: Basal metazoans and the evolution of multicellular complexity. Tutzing, Germany.

Satoh, N. 2011. Genes involved in cell fate determination in a chordate, *Ciona intestinalis*. Cold Spring Harbor Asia Conference on "Developmental control of sex, growth & cellular fate".

Satoh, N. 2011. The Genome Science: the Past and Future. In Faculty of Science Lecture Series, Shizuoka University. Shizuoka, Japan.

Satoh, N. 2011. Ongoing genome projects in Marine Genomics Unit of OIST. In International Workshop on Marine Evolutionary and Environmental Genomics. Academia Sinica, Taipei, Taiwan.

Satoh, N. 2012. An evo-devo note on the origin and evolution of chordates. Institute of

Cellular and Organismic Biology, Academia Sinica, Taiwan.

Satoh, N., Tagawa, K., and Takahashi, H. 2011. How was the notochord born? In 6th international tunicate meeting. McGill University, Montreal, Canada.

Shinzato, C. 2011. Coral genome: a platform for understanding coral responses to environmental change. In Asia-Pacific Youth Science Exchange Forum in Okinawa. Okinawa, Japan.

Shinzato, C. 2011. Genome sequencing of the coral *Acropora digitifera*. In International Workshop on Marine Evolutionary and Environmental Genomics. Academia Sinica, Taipei, Taiwan.

Shinzato, C., Shoguchi, E., Kawashima, T., Hamada, M., Hisata, K., Fujie, M., Fujiwara, M., Koyanagi, R., Ikuta, T., Fujiyama, A., Miller, D. J., and Satoh, N. 2011. Genome sequencing of the coral *Acropora digitifera*. In Searching for Eve: basal metazoans and the evolution of multicellular complexity. Tutzing, Germany.

Takeuchi, T., Koyanagi, R., Kawashima, T., and Satoh, N. 2011. The genome of the Japanese pearl oyster, *Pinctada fucata*. In The International Symposium on Pearl Research. Tokyo, Japan.

Hamada, M. 2011. Transcriptome analysis of heat stress response in *Ciona intestinalis*. In 6th international tunicate meeting. McGill University, Montreal, Canada.

Kawashima, T., Koyanagi, R., Shinzato, C., Shoguchi, E., Hamada, M., Hisata, K., Tanaka, M., Fujie, M., Fujiwara, M., Ikuta, T., Fujiyama, A., Miller, D. J., and Satoh, N. 2011. Coral genome decoded. In DOE Joint Genome Institute Microbial Genomics & Metagenomics Workshops. Walnut Creek, California.

Kawashima, T., Koyanagi, R., Takeuchi, T., Shinzato, C., Shoguchi, E., and Satoh, N. 2011. The structures and general features of genomes viewed from the three non-model marine animals: coral, pearl oyster and acornworm. In SMCB 2011 Annual Meeting. Kyoto University, Japan.

Kondo, M., Maeda, K., Hanahara (Yamasaki), N., and Tachihara, K. 2011. Early development

and upstream activity of three amphidromous *Rhinogobius* species from Okinawa Island. In The 8th International Workshop on the Oceanography and Fisheries Science of the East China Sea. Okinawa, Japan.

Maeda, K., Saeki, T., and Tachihara, K. 2011. Larval fish fauna on a sandy beach and an estuary along the coast of Oh-ura Bay, Okinawa Island. In The 8th International Workshop on the Oceanography and Fisheries Science of the East China Sea. Okinawa Japan.

Shoguchi, E., Kawashima, T., Yu, J. K., N., I., Kuroki, Y., Fujiyama, A., Putnam, N. H., Rokhsar, D. S., and Satoh, N. 2011. Chromosomal mapping of amphioxus genome and rearrangement of chromosomes in the cephalochordate lineage. In The Biology of Genomes 2011. Cold Spring Harbor, USA.

5. Intellectual Property Rights and Other Specific Achievements

Nothing to report

6. Meetings and Events

6.1 OIST Marine Genomics Seminar

- Title: Evolution of chloroplasts in dinoflagellates - tertiary endosymbioses and kleptochloroplasts.
- Date: Apr 22, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Takeo Horiguchi (Department of Natural History Sciences Faculty of Science Hokkaido University)
- Co-organizers: Dr. Holger Jenke-Kodama (OIST, Japan)

6.2 OIST Marine Genomics Seminar

- Title: Ecological regulation of larval settlement: a functional genomics approach using the tropical abalone *Haliotis asinina*.
- Date: May 20, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Sandie Degnan (University of Queensland)

6.3 OIST Marine Genomics Seminar

- Title: The genome of the demosponge *Amphimedon queenslandica* and the origin of the pan-metazoan toolkit.
- Date: Apr 22, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Bernie Degnan (University of Queensland)

6.4 OIST Marine Genomics Seminar

- Title: From genes to shells: how molluscs form their exoskeletons?
- Date: June 1, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Kazuyoshi Endo (University of Tokyo)

6.5 OIST Marine Genomics Seminar

- Title: Origin and evolution of novel bodyplan – lessons from marine invertebrates: molluscs and hemichordates.
- Date: June 1, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Hiroshi Wada (University of Tsukuba)

6.6 OIST Marine Genomics Seminar

- Title: What happened to the genome of vertebrate closest relatives?
- Date: Aug 10, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Daniel Chourrout (Director of the Sars International Centre for Marine Biology, University of Bergen, Norway)

6.7 OIST Marine Genomics Seminar

- Title: Gene coexpression analysis to explore real gene network.
- Date: Sep 3, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Takeshi Obayashi (Assistant Professor of the Tohoku University, Japan)

6.8 OIST Marine Genomics Seminar

- Title: Retinoic acid and the chordate evolution.
- Date: Nov 22, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Shigeki Fujiwara (Professor in Kochi University, Japan)

6.9 OIST Marine Genomics Seminar

- Title: Genomics and the Origin and Diversification of Animals.
- Date: Dec 14, 2011
- Venue: OIST Campus Lab1
- Speaker: Dr. Daniel Rokhsar (UC Berkeley/ DOE-JGI, USA)

7. Other

Nothing to report.