

technology team, Genome Core Technology Facilities, RIKEN Genomic Sciences Center, Suehiro-cho 1-7-22, W406, Tsurumi-ku, Yokohama city, Kanagawa 230-0045, Japan, <sup>6</sup>National Institute of Informatics, Tokyo 101-8430, Japan

We started the medaka genome sequencing project in 2002 and now this project reached the final step. For the genome wide comparison of nucleotide sequences in vertebrates, the sequence continuity must be at the chromosome size level. So, we have mapped the generated scaffolds with the single nucleotide polymorphism (SNP) using new typing panel consisting 93 Hd-r/HNI backcross progeny. Until now, we mapped over 2000 SNP markers and total length of scaffolds aligned on this SNP map reached nearly 600M bp, 75% of medaka genome. We are now analyzing the genome evolution among medaka, fugu, Tetraodon, zebrafish and human on the sequence level. We found that the most chromosomes between medaka and Tetraodon shows 1:1 relationship. This result suggests inter-chromosomal rearrangements are not major driving force of the teleost genome evolution in contrast with the mammalian genome evolution.

#### DIFFERENTIAL GENE EXPRESSION UNDERLYING DEVELOPMENTAL FATE DETERMINATION IN EMBRYOS OF THE ASCIDIAN *CIONA INTESTINALIS*

○Kenji Kobayashi<sup>1,2</sup>, Lixy Yamada<sup>1</sup>, Yutaka Satou<sup>1</sup>, Nori Satoh<sup>1,2</sup>

<sup>1</sup>Department of Zoology, Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan, <sup>2</sup>CREST, Japan Science and Technology Agency, Kawaguchi, Saitama 330-0012, Japan

Embryogenesis is a process in which a unicellular egg with pluripotency gives rise to a multicellular organism. During cleavages, the developmental fate of embryonic cells is gradually restricted until eventually they are destined to give rise to one type of tissue. A general interpretation of fate determination is that it is initiated with the activation of one or a few genes with the critical function of triggering the differentiation pathway. Using blastomere isolation, microarray and whole-mount *in situ* hybridization, the present study of the ascidian, *Ciona intestinalis*, showed that fate determination is accompanied by the expression of a complex set of developmentally relevant genes.

#### A GENOMEWIDE ANALYSIS OF ZINC FINGER GENES IN THE ASCIDIAN, *CIONA INTESTINALIS*

○Kyoko Miwata, Takuto Chiba, Reiko Horii, Lixy Yamada, Nori Satoh, Yutaka Satou

Department of Zoology, Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan

More than a half of transcription factor genes in the animal genomes decoded so far are predicted to encode a zinc-finger protein, while not all of the zinc-finger proteins work as transcription factors. In spite of their potential significant roles, these genes for the zinc finger proteins have not been analyzed systematically in any animals. In the present study, we comprehensively identified about 600 zinc-finger genes in the draft genome sequence of *Ciona intestinalis*, and then examined their embryonic expression patterns by whole-mount *in situ* hybridization. The present study will become an important milestone for future functional analyses of the ascidian genome as well as for comparative evolutionary genome studies.

#### SPERM MITOCHONDRIAL TRANSMISSION TO MALE AND FEMALE IN BLUE MUSSEL, *MYTILUS GALLOPROVINCIALIS*

○Mayu Obata, Kouichi Kawamura, Akira Komaru

Department of Faculty of Bioresources, Mie University, Kurimamachiya 1577, Tsu, Mie prefecture 514-8507, Japan

In blue mussel, paternal mitochondrial DNA (M type mtDNA) from sperm is known to be inherited to offspring. The phenomenon is called doubly uniparental inheritance (DUI). In DUI, it was reported that female mussel generally transmit only maternal mtDNA (F type mtDNA). In this study, we examined the mode of mtDNA transmission in *Mytilus galloprovincialis* using M and F type mtDNA specific primer sets. The ratio of M and F type mtDNA were measured in each sample by SNaPshot. M type mtDNA was detected in adductor muscle and ovary of all females. In 84.6% of unfertilized eggs (22/26), M type mtDNA was also detected. F type mtDNA was more abundant than M type mtDNA in all females. Although the ratio of M type mtDNA in females was very low, all females contained M type mtDNA. From these results, we propose three suggestions about DUI system. 1) Sperm M type mtDNA are not eliminated in females. In females, M type mtDNA are not selectively duplicated. Thus F type mtDNA dominated in females. 2) M type mtDNA are selectively duplicated only in testis. 3) The presence of M type mtDNA in unfertilized eggs indicates the hypothesis that egg's M type mtDNA contributes to M type mtDNA inheritance.

#### FEEDING ECOLOGY OF FOUR SPECIES OF SEA URCHINS (GENUS *ECHINOMETRA*) ON THE OKINAWAN CORAL REEFS

○Yuji Hiratsuka, Tsuyoshi Uehara

Graduate School of Engineering and Science, University of the Ryukyus, 1 Senbaru, Nishihara, Okinawa 903-0213, Japan

Distribution pattern, food availability and gut content of four genetically diverged species of sea urchins (Genus *Echinometra*) were studied at five different sites on the Okinawan coral reefs. Distribution pattern showed the habitat preference that *Echinometra* sp. A was common in the subtidal and submerged areas, *E. mathaei* occurred in a excavated burrow on the subtidal and intertidal rock platform, and *Echinometra* sp. C and *E. oblonga* inhabited deep burrows on the reef margin or upper intertidal areas exposed to wave action. Although diets of *Echinometra* four species typically depended on the food available at particular habitat, gut contents were commonly composed of vegetal food items, indicating that Okinawan *Echinometra* spp. were herbivorous in nature. On the other hand, the most widespread species *Echinometra* sp. A utilized more variety of diets than other three species distribution of which was generally restricted around the intertidal area. In this study, it was suggested that the difference in feeding habits of Okinawan *Echinometra* spp. was closely related to their ecological distribution pattern characterized by the distinct habitat segregation.

#### DO TROPICAL OCTOPUSES LIVE GROUPED OR SOLITARY?

○Natsumi Kaneko<sup>1</sup>, Yuzuru Ikeda<sup>2</sup>

<sup>1</sup>Department of Chemistry, Biology and Marine Science, University of the Ryukyus, Nishihara-city, Okinawa 903-0213, Japan, <sup>2</sup>Department of Chemistry, Biology and Marine Science, University of the Ryukyus, Nishihara-city, Okinawa 903-0213, Japan

We investigated distribution pattern of nine octopus species at the intertidal zone (500 square-meters area) in southern coast of Okinawa Island through October, 2004 to February 2005. Small sized octopus species (e.g. *Octopus laqueus*) showed high density distribution pattern (IE=2.77: Eberhardt index test), while large sized octopus species (e.g. *O. ornatus*) occurred almost alone in studied area. Although benthic octopuses had been considered as solitary animal, possibility of clumped aggregation in octopus at tropical waters was indicated.

#### HABITAT OF AMPHIOXUS FOUND IN THE WHALE FALL OFF NOMAMISAKI IN KAGOSHIMA

○Kaoru Kubokawa<sup>1</sup>, Tomoko Yamamoto<sup>2</sup>, Masaru Kawato<sup>3</sup>, Yoshihiro Fujiwara<sup>3</sup>

<sup>1</sup>Center for Advanced Marine Research, Ocean Research Institute, University of Tokyo, Minamidai, Nakano, Tokyo 164-8639, Japan, <sup>2</sup>Kagoshima University, Shimoarata, Kagoshima 890-0056, Japan, <sup>3</sup>Japan Agency for Marine-Earth Science and Technology, Yokosuka, Kanagawa 237-0061, Japan

In 2003, the new species of amphioxus was collected in whale fall community created among the sulfide rich environment of decaying dead whale in underwater. Nishikawa (2004) named the amphioxus as *Asymmetron inferum*. The whale fall in Kagoshima has been studied by the team of Japan Agency for Marine-Earth Science and Technology (JAMSTEC) and other scientists from 2003. In the depth of 230 m, the fallen whale carcass was quickly decayed, and deep-sea chemosynthesis-based community such as hydrothermal vent and seep which was characteristics as the unique ecosystems of whale falls in deep sea, have not found in the whale bone in Kagoshima. In 2004, the amphioxus also collected in the sulfur-laden ooze and whale wax, and the population occupied a large part of the community of whale fall. The distribution of body length demonstrated the three generations. Amphioxus possibly reproduces in the whale fall community. The sulfide-rich environment and the sediment composition of very fine sand and silt are not fit for the habitat of other species of amphioxus. The habitat and morphology between *Branchiostoma belcheri* and the *Asymmetron* species is compared and discussed.

#### STRESS TOLERANCE AND ZOOXANTHELLA GENOTYPES OF *PAVONA DIVARICATA* AND *P. DECUSSATA*

○Ryota Suwa<sup>1</sup>, Mamiko Hirose<sup>2</sup>, Michio Hidaka<sup>3</sup>

<sup>1</sup>Department of Science and Engineering, University of Ryukyus, Nishihara, Okinawa 903-0126, Japan, <sup>2</sup>21st century COE program, Department of Science and Engineering, University of Ryukyus, Nishihara, Okinawa 903-0126, Japan, <sup>3</sup>Department of Chemistry, Biology and Marine Science, University of Ryukyus, Nishihara, Okinawa 903-0126, Japan

It is believed that different genotypes of zooxanthellae show different stress tolerance and when corals recover from bleaching they may acquire more stress tolerant algae. Coral bleaching thus provides the host with an opportunity to adapt to new environment by changing the algal partner. The objective of this study is to investigate how changes in the algal composition affect the stress tolerance of corals. We found that most colonies of *Pavona divaricata* from Okinawa harbored clade D zooxanthellae while some others harbored clade C. *P. decussata* was associated with clade C. Fragments of both corals were exposed to high temperature stress and damage to photosystem II (PSII) was estimated from measurements of photochemical efficiency (Fv/Fm) of PSII. Both clade C and D algae in *P. divaricata* suffered similar but less damage than clade C algae in *P. decussata*. Present results suggest that physiological diversity of zooxanthellae belonging to the same clade is large and that the host plays a major role in determining stress tolerance. We are planning to study why dominant genotypes were different between the sympatric two species of *Pavona*.