International symposia (IS-11 – IS-47)

IS–11 SAWA, Hitoshi[1,2] ([1]Center for Dev. Biol., Riken, [2]Dept. Biol., Grad. Sch. Sci., Kobe Univ.)

Regulation of asymmetric cell division by Wnt signaling in *C. elegans*

During animal development, Wnt signaling plays important roles in controlling cell polarity and gene expression. In *C. elegans*, Wnt signaling controls asymmetry of most cell divisions. In this process, Wnts first regulate cell polarity by localizing signaling components asymmetrically on the cell cortex. Then, the cortical polarity is converted to the nuclear differences between the daughter cells. For example, WRM-1/beta-cateinin localized on the anterior cortex before the divisions, whereas it localized to the posterior nucleus after the divisions. Cortical WRM-1 inhibits its own nuclear localization through the activity of APR-1/APC, thereby creating WRM-1 nuclear asymmetry. WRM-1 nuclear asymmetry leads to distinct activities of the transcription factor POP-1/TCF between the daughter cells. Because this mechanism operate in most cell divisions, it is mysterious how a single factor POP-1 regulates a variety of cell fates. We showed that, in a division of the T hypodermal cell, a Hox protein, NOB-1 cooperate with POP-1 to regulate expression of PSA-3/Meis in one of the daughter cells. Therefore, specificity of POP-1 target is determined by positional identity of the cells.

IS–12 MCGHEE, James D.[1] ([1]Dept. Biochem. and Molec. Biol., and Dept. Med. Genet., Univ. Calgary)

The ELT-2 GATA factor and the Global Regulation of Transcription in the *C. elegans* Intestine

The intestine (endoderm) of the nematode *C. elegans* is a simple tube with only 20 cells, all derived from a single cell of the eight-cell embryo. Yet, in spite of this simplicity, the *C. elegans* intestine has the same basic characteristics as intestines of higher organisms: polarized secretion, active vesicle trafficking, striking apical-basal polarity and elaborate microvillar brush border. We have used SAGE analysis to identify >4,000 different genes expressed in hand-dissected adult intestines and >5,000 different genes expressed in FACS-sorted cells of the embryonic intestine. The structure, function and development of the worm intestine must to a large degree reflect the regulated action of all of these genes.

Our primary interest is in the global regulation of intestinal gene transcription. We have used two different computational methods to search for over-represented sequence motifs in the 5'-flanking regions of ~80 intestine-specific/intestine-enriched genes identified in the adult library and in an independent set of ~80 such genes identified in the embryonic library. Both methods and both gene sets return the same over-represented site, namely an extended GATA-related sequence of the general form AHTGATAARR, which agrees with experimentally determined *cis*-acting control sequences identified in intestine genes over the past twenty years. I will present evidence that this sequence is the cognate binding sequence of the intestine-specific GATA-factor ELT-2 (the likely homolog of vertebrate GATA4, 5, 6) and that other GATA factors present in the differentiating intestine (ELT-4 and ELT-7) are dispensable. We thus propose that ELT-2 is the predominant transcription factor in the *C. elegans* intestine following endoderm specification and is directly involved in the transcription of **all** intestine genes, from the early embryo through to the dying adult.

IS–13 MOERMAN, Donald G.[1] ([1]Dept. Zoology, Univ. British Columbia)

The Embryonic Muscle Transcriptome of *Caenorhabditis elegans*

One of the fundamental features of metazoan development is myogenesis. *C. elegans* muscle cells are useful models for studies of myogenesis. We have used Serial Analysis of Gene Expression (SAGE) to generate a comprehensive profile of embryonic muscle gene expression. Our analysis is based on mRNA from 2 biological replicates of *myo-3*::GFP marked muscle cells isolated from dissociated embryos by Fluorescence Activated Cell Sorting (FACS). We have identified 7,810 genes with at least one tag from these two libraries. To verify expression of some of these genes in muscle we compared the expression of 572 genes found expressed in muscle with GFP::reporters to the genes identified in our SAGE library for muscle and identified 523 common genes. Using an RNAi feeding library (Kamath & Ahringer, 2003), we screened this muscle expressome for genes affecting viability as well as sarcomere assembly, stability and/or function. This approach proved to be a rapid and sensitive means to identify genes that affect muscle differentiation and sarcomere assembly, as we have identified over 100 new genes affecting muscle development in this organism. RNAi treated animals display an array of myofilament disruptions ranging from small aggregations of myo-3::GFP to large deposits, often accompanied by disorganization of the myofilaments. Many of the genes affecting sarcomere integrity have human homologs for which little or nothing is known. Our studies on these genes in the nematode may inform studies on these genes in more complex organisms.

IS–14 MATSUNO, Kenji[1], HOZUMI, Shunya[1], MAEDA, Reo[1], TANIGUCHI, Kiichiro[1], OKUMURA, Takashi[1] ([1]Dept. Biol. Sci. Tech., Tokyo Univ. Sci.)

Left-right asymmetry in *Drosophila*

In animals, the internal organs often have left-right (LR) asymmetry. Although the formation of the anterior-posterior and dorsal-ventral axes is well understood, LR asymmetry has not been studied extensively in *Drosophila*. Here, we found that handedness of the embryonic gut and of the adult gut and testes was reversed, rather than randomized, in homozygous viable and fertile Myo31DF mutants. Myo31DF encodes an unconventional myosin, also called *Drosophila* MyoID, and is the first actin-based motor to be implicated in LR patterning. Myo31DF was required in the hindgut epithelium for normal embryonic handedness. Disruption of the actin filaments in the hindgut epithelium randomized the handedness of the embryonic gut, suggesting that the Myo31DF function requires the actin cytoskeleton. Myo31DF also colocalized with this cytoskeleton. Overexpression of Myo61F, another myosin I, reversed the handedness of the embryonic gut. These two unconventional myosin I proteins may have antagonistic functions in LR patterning. Our results suggest that the actin cytoskeleton and myosin I proteins may be crucial for creating the LR asymmetry of invertebrates.

IS-15 NAKAGOSHI, Hideki[1], MAKI, Yusuke[1], OTAKE, Yoshiaki[1] ([1]Grad. Sch. Natural Sci. Tech., Okayama Univ.)

Functional opsin patterning for *Drosophila* color vision

Vision is mainly based on two different tasks, object detection and color discrimination, through activities of photoreceptor (PR) cells. *Drosophila* compound eye consists of ~800 ommatidia. Every ommatidium contains eight PR cells; six outer cells (R1-R6) and two inner cells (R7 and R8) by which object detection and color vision are achieved, respectively. Expression of opsin genes in R7 and R8 is highly coordinated through the instructive signal from R7 to R8, and two major subtypes of ommatidium are distributed stochastically; pale type (~30%) expresses Rh3/Rh5 opsins, while yellow type (~70%) expresses Rh4/Rh6 opsins in R7/R8. The homeodomain protein Defective proventriculus (Dve) is expressed in yellow-type R7 and in all R1-R6. Surprisingly, *dve* mutant eyes exhibited atypical Rh3/Rh6 pairing in R7/R8, and the instructive signal was significantly blocked. Forced *dve* expression provides evidence that the functional opsin patterning for color vision is specified by two opposite functions of Dve in R1-R6 and R7.

IS-16 HIROMI, Yasushi[1,2] ([1]Natl. Inst. Genet., [2]Dept. Genet., SOKENDAI)

Intra-axonal patterning: pattern formation within a nerve cell

The essence of "development" is the precise control of gene expression in time and space. In order for the gene products to exert its proper function in the cell, they must be accurately positioned at particular intracellular "compartments" where they act. Such intracellular distribution of proteins can provide "positional information" not only inside the cell, but also to the surrounding environment, if the cell possesses long cellular processes — such as axon and dendrites of neurons. We are examining the role and the mechanism of localized distribution of membrane proteins to sub-segments of axons. We have shown that sub-axonal localization of a Drosophila axon guidance receptor can concentrate its ligands to strategic positions within the nervous system, thereby creating guiding information for other neurons. We further show that, in primary culture, Drosophila neurons have an intrinsic activity to subdivide their axon into multiple "compartments": distal and proximal; these compartments act as units of sub-axonal localization of membrane proteins. The genetic information for the compartment-specific localization is likely encoded within the protein sequence.

IS-21 UEDA, Hitoshi[1] ([1]Grad. Sch. Natural Sci. Tech., Okayama Univ.)

Regulation of developmental timing by transcription factors in *Drosophila*

Each organism determines its developmental timing during the process of development, but the mechanism is not well understood. At the onset of metamorphosis in *Drosophila*, a large pulse of ecdysone triggers puparium fomation and followed by another small pulse of ecdysone triggering pupation at 12 hours after puparium formation, but the determination mechanism of the pupation timing is not known. During a process of regulation mechanism of the *ftz-f1* gene, which is induced by ecdysone pulse and expressed slightly before pupation, we found that dBlimp-1, an ecdysone inducible transcriptional repressor, binds to the promoter region of the *ftz-f1* gene and plays an important role in determining the precise timing of βFTZ-F1 expression. We further found that the prolonged dBlimp-1 expression significantly delayed the timing of pupation. Furthermore, when βFTZ-F1 was induced under control of the heat shock promoter at delayed timing in ftz-f1 mutant, pupation timing was delayed depending on the heat shock timing. These findings suggest that the pupation timing is at least determined through regulation of expression timing of dBlimp-1 and βFTZ-F1.

IS-22 LEE, Junho[1] ([1]Res. Cent. for Functional Cellulomics, Inst. Molec. Biol. and Genetics, Dept. Biol. Sci.s, Seoul National Univ.)

Differential tissue-specific regulation of a Runx gene mediated by distinct signaling pathways

The adoption of differential gene regulation modes for a single gene mediated by different signaling pathways can be used as a strategy for obtaining evolutionary novelty without adding too much burden on genomic complexity. Here we show that dual modes of expression regulation can be adopted by a single gene in different tissues for different physiological purposes. We found that RNT-1, the nematode RUNX transcription factor, attenuates its transcription in the hypodermis, which is critical for maintaining developmental integrity in this tissue, by binding to its own intronic sequences. Unlike in the hypodermis, RNT-1 was controlled at the protein stability level in the intestine. RNT-1 was rapidly stabilized by an environmental stress and *rnt-1* mutant animals were more sensitive to the stress, indicating that rapid RNT-1 stabilization can be an early step of defence against environmental stress. Distinct signalling pathways were required for RNT-1 repression and stabilization respectively, further exemplifying differential *in vivo* roles of distinct signalling pathways in regulating a single gene in different tissues.

IS-23 KATSURA, Isao[1] ([1]Natl. Inst. Genet. and SOKENDAI)

How do worms change their behavior by smelling environments?

Animals sense environmental cues and change behavior for their survival and proliferation. We are studying the molecular mechanism of such behavioral plasticity using the model-organism *Caenorhabditis elegans*. In this symposium I will briefly overview the olfactory system of *C. elegans* and review our study on "butanone enhancement," i.e., enhancement of chemotaxis to butanone by pre-exposure to butanone in the presence of food. *C. elegans* senses many odorants including butanone with a pair of olfactory neurons called AWC, which actually consist of slightly different neurons AWC^{ON} and AWC^{OFF}. Isolation and characterization of mutants revealed that this behavioral plasticity requires the AWC^{ON} neuron and the function of Bardet-Biedl syndrome genes in this neuron, which suggests that the sensory cilium is important for this plasticity. I will discuss how the AWC^{ON} sensory cilium may achieve this plasticity and how the difference between AWC^{ON} and AWC^{OFF} contributes to the high performance of the olfactory system. (Ichiro Torayama and Hiroshi Ichijo did a major part of the study on butanone enhancement.)

IS-24 SONG, Hyun-Ok[1], LEE, Gukgyu[1], AHNN, Joohong[1,2] ([1]Dept. Life Sci., GIST, [2]Dept. Life Sci., Hanyang Uinv.)

Studies on the calcium binding proteins in *C. elegans*

In our laboratory we have been studying functions of calcium binding proteins which are important for regulating development and behavior of *C. elegans*. For examples, **calcineurin** has been demonstrated to modulate many different behaviors including egg-laying, defecation and thermotaxis in *C. elegans*. We have previously reported that *cnb-1* mutants, null mutants of a regulatory B subunit, displayed pleiotropic defects including uncoordinated movement and delayed egg laying in *C. elegans*. Interestingly, gain-of-function mutants of a catalytic A subunit showed exactly opposite phenotypes to those of *cnb-1* mutants providing an excellent genetic model to define calcium-mediated signaling pathway at the organism level.
Another example of calcium-binding protein **calreticulin**, a Ca^{2+}-binding protein in the endoplasmic reticulumn (ER) membrane, has been implicated in various biological functions including chaperone activity, calcium homeostatis, phagocytosis and ER stress-induced apoptosis. The *crt-1* null mutants show temperature dependent reproduction defects and retarded growth under stress. Moreover, a double knockout mutant of calnexin and calreticulin exhibited more severe defects. Interestingly, *crt-1* transcript and protein levels are elevated under stress conditions, suggesting that CRT-1 may be important for stress-induced chaperoning functions in *C. elegans*.

IS-25 DEMIRBAG, Zhini[1], INCE, I. A.[1], AKTURK, Y.[1], VLAK, J. M.[2], OERS, M.M. van[2], NALCACIOGLU, R.[1] ([1]Karadeniz Technical Univ., Faclt. Arts and Sci.s, Dept. Biol., [2]Wageningen Univ. Lab. Virology Binnenhaven)

Potential promoter regions and transcriptional analysis of immediate early, delayed early and late genes of *Chilo iridescent* virus (CIV)

Chilo iridescent virus (CIV), the type species of the genus *Iridovirus*, a member of the *Iridoviridae*, is highly pathogenic for a variety of insect larvae. In this study we demonstrated that *exonuclease*, *dnapol*, and *mcp* are immediate early, delayed-early and late genes, respectively. Transcription initiated at position -30 for *exonuclease*, -35 for *dnapol* and position -15/-16 for *mcp*, relative to the translational start sites of these genes. Dual luciferase assay results indicated that *DNApol* sequences between positions -27 and -6, and *mcp* sequences between -67 and -43 relative to the transcriptional start site, were essential for promoter activity. A series of increasing deletions and mutations were made, starting at the 5' end of this upstream region and extending towards the RNA start site of *DNApol*. When the size of the upstream element was reduced from position -19 to -15 relative to the transcriptional start site, the luciferase activity was reduced to almost zero. Point mutations showed that each of the five nucleotides (AAAAT) located between -19 and -15 were equally essential for promoter activity. Mutations at individual bases around the transcription initiation site showed that the promoter extended till position -2 upstream of the transcription start site.

IS-31 TAKAHASHI, Taku[1] ([1]Grad. Sch. Natural Sci. Tech., Okayama Univ.)

The uORF-mediated gene expression control in higher plants

Disruption of the *Arabidopsis thaliana ACAULIS5* (*ACL5*) gene, which has recently been shown to encode thermospermine synthase, results in a severely dwarfed phenotype. To elucidate *ACL5*-mediated regulatory pathways of the stem growth, we have isolated extragenic suppressor mutants of *acl5* (*sac*) that reverse the *acl5* phenotype. The gene responsible for the dominant *sac51-d* mutant, which almost completely restores the stem elongation of *acl5-1*, encodes a basic helix-loop-helix (bHLH) transcription factor. The *sac51-d* allele disrupts a short upstream open reading frame (uORF) of *SAC51*, suggesting that premature termination of the uORF in *sac51-d* results in the increased transcription and translation of the downstream main ORF. The gene responsible for the semi-dominant *sac52-d* mutant encodes a ribosomal protein L10 (RPL10A), which is highly conserved among eukaryotes and implicated in translational regulation. GUS reporter activity under the control of the *SAC51* promoter with its uORFs was higher in *acl5-1 sac52-d* than that in *acl5-1*. Our results suggest that *ACL5* plays a role in translational activation of *SAC51* and that the suppression of the *acl5* phenotype by *sac52-d* is attributable, at least in part, to the enhanced translation of *SAC51*.

IS–32 SAKAMOTO, Wataru[1] ([1]Res. Inst. Biores., Okayama Univ.)

Genetic dissection of leaf variegation in *Arabidopsis*

Leaf variegation is derived from a formation of sectors that contain either normal chloroplasts or abnormal plastids. Variegated mutations have been reported in many plant species after the re-discovery of Mendelian law. Despite this, their responsible genes remained uncharacterized at the molecular levels. Recent studies by us and others demonstrated that leaf variegation occurs through various functions. We focus on yellow variegated in Arabidopsis, and discuss about possible mechanisms leading to green and white sector formations in these mutants.

IS–33 ARAKI, Takashi[1] ([1]Div. Integr. Life Sci., Grad. Sch. BioStud., Kyoto Univ.)

Regulation of gene expression by long-distance signaling during flowering in plants

In many plants, timing of initiation of flower development (flowering) is controlled by day-length, whose perception occurs in leaves by the action of circadian clock. A long-distance signal (florigen) is generated in leaves under inductive day-length conditions and is transported via phloem to the shoot apex where it triggers flower development. *FLOWERING LOCUS T* (*FT*), which encodes a protein with similarity to mammalian Raf kinase inhibitor protein (also known as phosphatidylethanolamine binding protein), is a well-conserved regulator of flowering in variety of plants and its protein product plays a role of the long-distance signal. *FT* is expressed in the phloem tissues of cotyledons and leaves with a peak in the late evening. FT protein is transported to the shoot apex and acts together with a bZIP transcription factor FD to activate transcription of target genes such as floral meristem identity gene *APETALA1* (*AP1*) in subsets of cells in the shoot apical meristem. Recent progress in our understanding of the long-distance and local signaling underlying the flowering process will be discussed.

IS–34 ZHAO, Yanmei[1,2], JUN, Lu[1], SUN, Hui[1], XIA, Chen[1,3], BAIQU, Huang[1] ([1]The Inst. Genet. and Cytology, Northeast Normal Univ., [2]Natl. Lab. Protein Eng. and Plant Genet Eng., Peking Univ, [3]Dept. Pharmacology, Sch. Basic Med. Sci.s, Jilin Univ)

Correlation between acetylation modification and *hsp* gene regulation in *D. melanogaster*

The promoter of the *Drosophila hsp26* gene contains two DNase I-hypersensitive (DH) sites and a positioned nucleosome, and this open chromatin structure is required for heat-inducible expression. Histone acetylation modification participates in transcriptional regulation of genes by affecting the status of chromatin remodeling. We investigated the roles of histone acetylation modification on *hsp26* expression in *Drosophila*. We showed that the histone deacetylase inhibitor (HDI) treatments of *Drosophila* larvae induced the histone H3 hyperacetylation at the promoter DH sites, which facilitated the binding of heat shock factor (HSF) to heat shock element (HSE). This resulted in a promoted transcription of *hsp26* gene following the heat shock, and further increased the inducible expression of *hsp26* gene. On the contrary, the HDI-induced histone H3 hyperacetylation in the middle nucleosome decreased the basal expression of *hsp26* gene under the normal growth conditions. In addition, by following up the heat-shock time course, we showed that the histone acetylation level at the DH sites exhibited a drop-raise-drop change, while that at the positioned nucleosome underwent a raise-drop-raise-drop switchover. These results demonstrated the distinct roles played by histone acetylation modification in *hsp26* gene basal and inducible expression regulation in *D. melanogaster*.

Key words: *hsp26*; histone deacetylase inhibitor; Chromatin remodeling

IS–35 HORIKOSHI, Masami[1] ([1]The Inst. Molec. Cell. BioSci.s, The Univ. Tokyo)

Semi-conservative replication model of nucleosome

Despite the long-believed idea that histone H3-H4 tetramer is rather stable, we showed that CIA (CCG1-interacting factor A), the most conserved histone chaperone among the eukaryotes (1), has an activity to disrupt the histone H3-H4 tetramer into H3-H4 dimers (2). We also solved the crystal structure, at 2.7 angstrom resolution, of CIA in complex with histones H3 and H4 (2). The structure shows the histone H3-H4 dimer's mutually exclusive interactions with another histone H3-H4 dimer and CIA. These findings suggest that the semi-conservative replication of a nucleosome is possible like DNA semi-conservative replication (3). It also implies that epigenetic information can be inherited through the nucleosome semi-conservative replication because histones hold the epigenetic information as a variety of modification obtained from the inside and outside of the cell. Therefore, CIA and its putative regulator(s) CIA activity play a key role in regulating nucleosome semi-conservative replication.

(1) Munakata et al., Genes Cells, 5, 221-233 (2000)
(2) Natsume et al., Nature, 446, 338-341 (2007)
(3) Watson & Crick, Nature, 171, 737-738 (1953)

IS–41 GENGYO-ANDO, Keiko[1,2], MITANI, Shohei[1,2] ([1]Dept. Physiology, Tokyo Women's Med. Univ. Sch. Med., [2]CREST, JST)

Functional genomics on the Sec1/Munc18 family in membrane trafficking of *C. elegans*

The Sec1/Munc-18 (SM) proteins are essential for membrane trafficking in various eucaryotic cells. Alterations of SM genes have been implicated in causing human diseases, but their precise roles are still unclear. To elucidate the physiological roles for SM proteins in a multicellular organism, we have systematically isolated deletion mutations of the *C. elegans* SM genes. We found that the mutations result in various phenotypes, such as small brood size, embryonic or larval lethality and reduction of neurotransmission. To investigate which trafficking pathways are impaired in these mutants, transgenic analyses using fluorescent reporters were performed. In the mutants of vps-33.1 and vps-45, both fluid-phase and receptor-mediated endocytosis pathways were affected. We showed that these endocytic defects are linked to abnormal morphologies of endosomes or lysosomes in the mutant cells. The mutation of the neuron-specific gene, unc-18, resulted in the defect of secretion of synaptic vesicles. Genetic and biochemical approaches using these mutants revealed that SM proteins are key molecules of membrane trafficking on both the exo-and endocytic pathways in a multicellular organism.

IS–42 HOPE, Ian[1] ([1]Inst. Integrative & Comparative Biol., Faclt. Biol. Sci.s, Univ. Leeds)

Systematic studies of gene expression patterns in *C. elegans*

Gene expression patterns link directly the genetic information and the biology we observe. The fully described developmental cell lineage of the nematode *Caenorhabditis elegans* means gene expression patterns can be determined completely to the cellular level. My laboratory has used a series of approaches to reveal gene expression patterns in *C. elegans*. First, shotgun cloning of genomic DNA fragments upstream of reporters was combined with junction sequencing to identify plasmids bearing translational fusions. A low frequency of reporter expression, specifically for recently duplicated genes, suggested a high proportion of non-processed pseudogenes existed in the *C. elegans* genome. Second, the Promoterome allowed specific reporter gene fusions to be generated by Gateway recombinational cloning. The high success rate implied a resistance of genes in certain transcription factor families to local gene duplication. Third and currently, reporter genes are inserted into large genomic DNA fragments by recombineering; expression patterns are more likely to reflect accurately the expression of the endogenous gene because regulatory elements at considerable distances will be included. As procedures are developed to allow automatic determination of reporter gene expression in terms of the cell lineage, a global understanding of the mechanisms controlling expression of the *C. elegans* genome will emerge.

IS–43 BOAKYE, Daniel A.[1], SOUZA, Dziedzom K. de[1], BROWN, Charles A.[1], WILSON, Michael D.[1] ([1]Parasitology Dept., Noguchi Memorial Inst. Med. Res., Univ. Ghana)

DNA barcode analysis of the M and S molecular forms of the *Anopheles gambiae* complex, vectors of lymphatic filariasis

Molecular methods aimed at diagnosing the five chromosomal forms ("Bamako", "Mopti", "Savanna", "Forest" and "Bissau") within the *Anopheles gambiae* s.s. resulted in two molecular forms designated M and S forms. The M and S forms correspond in some areas to the Mopti and Savanna chromosomal forms respectively but unfortunately, this correspondence does not exist in all areas. There are other indications that the S form and M form may represent two species subsumed under *An. gambiae* s.s. Considering the importance of this species in the transmission of malaria and lymphatic filariasis we define the operational taxonomic units in the *Anopheles gambiae* s.s. from different ecological zones in Ghana, West Africa, by using the DNA barcode approach of analyzing the sequence variations in the cytochrome oxidase 1 gene. The hierarchical cluster analysis of data on the M and S forms from four sites in Southern Ghana are presented.

IS–44 ASADA, Nobuhiko[1], ITOH, Michiaki[1], SUN, Hui[2], EVIATAR, Nevo[3] ([1]Biol. Lab., Faclt. Sci., Okayama Univ. Sci., [2]Sch. Life Sci., Northeast Normal Univ., [3]Inst. Evolution, Univ. Haifa)

Biodiversity of mtDNA in *D. melanogaster*

The enigma of biodiversity of genomes and phenomes is central research at the Lower Nahal Oren micro site, "Evolution Canyon", in Israel since 1975. This site is constructed opposite slopes with different climate: south-facing slope (SFS, "African" dry) setting stations 1 (top), 2, 3 (bottom) and north-facing slope (NFS, "Euroasian" humidity) including stations 5 (bottom), 6, 7 (top). The canyon floor (CF) is represented by station 4. Drosophila melanogaster iso-female strains, SFS 2-1 and NFS 6-1, were examined on PCR-based mtDNA diversity. MtDNA was extracted from adult flies and conducted PCR method within the cytochrome oxidase I gene region. PCR products were purified, and determined the partial nucleotide sequences. Band patterns of PCR products and partial nucleotide sequence after alignment of mtDNA was different between both in strains derived from the opposite and microclimatic different slopes. The origin under and evolution of adaptation and spatiotemporal diversities at the micro geographic environment is discussed.

IS-45 VENKATESH, Byrappa[1] ([1]Inst. Molec. and Cell Biol. (IMCB))

Elephant shark (*Callorhinchus milii*) genome analysis

The living jawed vertebrates (Gnathostomes) are represented by two major lineages, the cartilaginous fishes (Chondrichthyes) and bony fishes (Osteichthyes). Whole genome sequences of several bony fishes including human, mouse, chicken, frog and teleost fishes have been generated. However, very few cartilaginous fishes have been targeted for large scale genome sequencing. Cartilaginous fishes (comprising sharks, rays, skates and chimaeras) are the oldest phylogenetic group of living jawed vertebrates that shared a common ancestor with bony fishes about 450 million years ago. Thus, they constitute an important group for reconstructing the evolutionary history of vertebrate genomes. We recently showed that the genome of the elephant shark (*Callorhinchus milii*, a chimaera) is the smallest among known cartilaginous fishes and proposed it as a model cartilaginous fish genome. We have now carried out survey sequencing (~1.4× coverage) of the elephant shark genome and compared it with the human and other bony vertebrate genomes. The comparison has identified several ancient genes that have been independently lost in the human and teleost fish genomes, and noncoding sequences and syntenic blocks of genes that have been highly conserved in the elephant shark and human genomes but divergent in the teleost genomes.

IS-46 NIIMURA, Yoshihito[1] ([1]Dept. Bioinform., Med. Res. Inst., Tokyo Med. and Dental Univ.)

Evolutionary Dynamics of Olfactory Receptor Genes in Mammals

Odor perception in mammals is mediated by a large multigene family of olfactory receptor (OR) genes. The number of OR genes varies extensively among different species of mammals, and most species have a large number of pseudogenes. To gain some insight into the evolutionary dynamics of OR genes, we identified the entire set of OR genes in platypuses, opossums, cows, dogs, rats, and macaques and analyzed them together with those of humans and mice. We found that platypuses and primates have <400 functional OR genes while the other species have 800-1,200 genes. We then estimated the numbers of gains and losses of OR genes for each branch of the phylogenetic tree of mammals. This analysis showed that (i) gene expansion occurred in the placental lineage each time after it diverged from monotremes and from marsupials and (ii) hundreds of gains and losses of OR genes have occurred in an order-specific manner, making the gene repertoires highly variable among different orders. The number of OR genes appear to be determined primarily by the functional requirement for each species, but once the number reaches the required level, it fluctuates by random duplication and deletion of genes.

IS-47 SAITOU, Naruya[1], KIM, Hyung-Cheol[2], SUMIYAMA, Kenta[1,2], TAKAHASHI, Mahoko[2], MASUYAMA, Waka[2] ([1]Div. Popul. Genet., Natl. Inst. Genet., [2]Dept. Genet., Sch. Life Sci., Grad. Univ. Adv. Stud., [3]Dept. Biol. Sci.s, Grad. Sch. Sci., Univ. Tokyo)

Evolutionary Genomic Analysis of Primates and Mammals

We determined ca. 200 non-exnonic UCE (Ultra-Conserved Elements) sequences for six mammalian species, and evolutionary rate of ~100-fold lower than that for genomic average was observed, while some UCEs accumulated significant number of changes only at some lineages. Another analysis dealt with evolutionary change of protein domain combination changes though mutiple genomic analysis. Using Pfam and GTOP databases, we compared many genome data of primates and mammals.