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Research Organization of Information and Systems
NATIONAL INSTITUTE OF GENETICS

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Introduction

The National Institute of Genetics (NIG) was established in 1949 as the central institute to study various aspects of genetics. It was reorganized in 1984 as an inter-university research institute to promote collaborations with researchers at universities. Since 1988, NIG has been participating in graduate education as the Department of Genetics of the Graduate University for Advanced Studies (SOKENDAI). NIG also serves as a center for various genetic resources such as mutant strains, clones and vectors, and houses DDBJ, the DNA Data Bank of Japan, and a DNA sequencing center.

The history of NIG overlaps the period of a revolution in the field of life science. Genetics is no longer a discipline to study the rules and mechanisms of heredity, but has become the basis for all fields of life science. Molecular techniques now allow us not only to decipher the entire genome sequence of organisms including humans, but also to understand the details of higher biological phenomena: cell differentiation, morphogenesis, brain function, and evolution --- the history of life itself. Currently, 36 research groups are actively performing pioneering and cutting-edge researches in these fields at NIG.

Recent generation of massive information on biological systems and their environment calls for new directions in life sciences, such as bioinformatics, system-level analysis, and theoretical approaches to extract knowledge from databases. To this end NIG and three other national institutes, the National Institute of Informatics, The Institute of Statistical Mathematics and the National Institute of Polar Research have formed a new organization, the Research Organization of Information and Systems (ROIS) since April 2004, as a part of the reform of national universities and research institutes in Japan. Inter-institutional collaborations within the new organization are in progress.

We welcome your comments and suggestions on our research activities and endeavors.

Yuji Kohara, Director-General

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Research Outline

Code	Division/Laboratory	Group name
A-a	Division of Molecular Genetics	Tatsuo Fukagawa
A-b	Division of Mutagenesis	Fumiaki Yamao
A-c	Molecular Mechanism Laboratory	Hiroaki Seino
B-a	Division of Cytogenetics	Tamotsu Yoshimori
B-a	Division of Cytogenetics	Takehiko Kobayashi
B-b	Division of Microbial Genetics	Hiroyuki Araki
B-b	Division of Microbial Genetics	Seiichi Yasuda
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C-b	Division of Gene Expression	Susumu Hirose
C-c	Division of Molecular and Developmental Biology	Koichi Kawakami
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D-a	Division of Population Genetics	Toshiyuki Takano
D-b	Evolutionary Genetics	Hiroshi Akashi
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E-b	Division of Agricultural Genetics	Tetsuji Kakutani
E-b	Division of Agricultural Genetics	Keiichi Shibahara
E-c	Division of Brain Function	Tatsumi Hirata
E-e	Division of Human Genetics	Itsuro Inoue
F-a	Mammalian Genetics Laboratory	Toshihiko Shiroishi
F-b	Mammalian Development Laboratory	Yumiko Saga
F-c	Mouse Genomics Resource Laboratory	Tsuyoshi Koide
F-d	Model Fish Genomics Resource	Noriyoshi Sakai
F-e	Plant Genetics Laboratory	Nori Kurata
F-f	Microbial Genetics Laboratory	Hironori Niki
F-g	Invertebrate Genetics Laboratory	Ryu Ueda
G-a	Genetic Informatics Laboratory	Yukiko Yamazaki
G-b	Genome biology Laboratory	Yuji Kohara
G-c	Comparative Genomics Laboratory	Asao Fujiyama
H-a	Biological Macromolecules	Kazuhiro Maeshima
H-a	Biological Macromolecules Laboratory	Makio Tokunaga
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H-d	Biomolecular Structure Laboratory	Yasuo Shirakihara
H-e	Gene Network Laboratory	Emiko Suzuki

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I-b	Laboratory for Gene-Product Informatics	Yasukazu Nakamura
I-c	Laboratory for Gene Function Research	Yoshio Tateno
I-d	Laboratory for Research and Development of Biological Databases	Toshihisa Takagi
I-d	Laboratory for Research and Development of Biological Databases	Hideaki Sugawara
I-e	Laboratory for Gene-Expression Analysis	Kousaku Okubo
J-a	Laboratory for Cell Lineage	Takako Isshiki
J-b	Neural Morphogenesis Laboratory	Emoto Kazuo
J-c	Cell Architecture Laboratory	Kimura Akatsuki
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L	EXPERIMENTAL FARM	EXPERIMENTAL FARM
M	Intellectual Property Unit	Intellectual Property Unit
N	Technical Section	Technical Section

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A. DEPARTMENT OF MOLECULAR GENETICS
A-a. Division of Molecular Genetics
Tatsuo Fukagawa

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1．Takami, Y., Ono, T., Fukagawa, T., Shibahara, K., and Nakayama, T.（2007）Essential Role of CAF-1-mediated Rapid Nucleosome Assembly for DNA Replication and Cell Division in Vertebrate Cells.，**Mol. Biol. Cell**，18，129 - 141
2．Kwon, M., Hori, T., Okada, M., and Fukagawa, T.（2007）CENP-C is involved in chromosome segregation, mitotic checkpoint function and kinetochore assembly.，**Mol. Biol. Cell**，18，2155 - 2168
3．Zuccolo, M., Alves, A., Galy, V., Bolhy, S., Formstecher, E., Racine, V., Sibarita, J., Fukagawa, T., Shiekhattar, R., Yen, T., and Doye, V.（2006）The human Nup107-160 nuclear pore subcomplex contributes to proper kinetochore functions.，**EMBO J.**，26，1853 - 1864
4．深川竜郎（2006）染色体分配制御に重要なキネトコア構造，遺伝，21，159 - 163

ORAL PRESENTATION

1．Fukagawa, T.　kinetochore assembly and organization in Vertrebrate cells　Department seminar of Wadswarth Center in SUNY　Wadswarth Center, Albany, NY　11/16

POSTER PRESENTATIONS

1．堀哲也、佐渡敬、深川竜郎「CENP-50ノックアウトマウスの染色体動態」，日本遺伝学会第79回大会，岡山市，9/
2．Fukagawa, T.「Functional role of CENP-H/I complex in the kinetochore」，BMB2007(第30回日本分子生物学会年会），横浜市，12/12
3．深川竜郎「キネトコアタンパク質複合体の機能解析と電子顕微鏡観察への展望」，生理学研究所研究会，岡崎，6/
4．深川竜郎「細胞構造とゲノム構造の進化ー染色体構造の機能と進化」，葉山高等研究センター研究会，葉山，12/6
5．Fukagawa, T.「Functional role of CENP-Q-class proteins in the kinetochore.」，16th International Chromosome Conference，Amsterdam，8/28
6．堀哲也, 真柳浩太, 前仲勝実, 保木裕子, 佐渡敬, 岡田聖裕,深川竜郎「クロマチン工学への応用に向けたキネトコアタンパク質複合体の再構成」，BMB2007(第30回日本分子生物学会年会），横浜市，12/15
7．堀哲也, ,真柳浩太,前仲勝実,保木裕子, 佐渡敬, ,岡田聖裕,深川竜郎「クロマチン工学への応用に向けたキネトコアタンパク質複合体の再構成」，BMB2007(第30回日本分子生物学会年会），横浜市，12/12

8．鈴木應志, 朝長毅, 堀哲也, 岡田聖裕, 深川竜郎「 キネトコアを構成するCENP-H/I複合タンパク質の過剰発現は異数体細胞を誘導する 」, BMB2007(第30回日本分子生物学会年会）, 横浜市 , 12/14
9． Fukagawa, T. 「 KINETOCHORE ASSEMBLY AND ITS FUNCTIONS IN HIGHER VERTEBRATE CELLS 」, 国際シンポジウムFunctional Organization of the Nucleus , 淡路市 , 1/11
10．深川竜郎「 染色体安定性に本質的な役割を担うキネトコアタンパク質複合体 」, がん特定研究公開シンポジウム , 東京 , 2/23

EDUCATION

1．深川竜郎、原田昌彦　クロマチン研究会　−ゲノム・細胞核から個体発生まで−　遺伝研研究集会　三島　10/25, 26
2．日本遺伝学会　発生分化過程における細胞核ダイナミクス　日本遺伝学会シンポジウム　岡山　9／
3． Fukagawa, T., and Watanabe, Y.　Regulation and dynamics of chromosome segregation　日本分子生物学会年会シンポジウム　横浜　12/12

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A. DEPARTMENT OF MOLECULAR GENETICS
A-b. Division of Mutagenesis

Fumiaki Yamao

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．筒井康博、岩崎博史（2007）相同組換えと共役した複製フォークの再生研究の新展開，実験医学，25，718 - 726
2． Y. Akamatsu, Y. Tsutsui, T. Morishita, MD Shahjahan P Siddique, Y. Kurokawa, M. Ikeguchi, F. Yamao, B. Arcangioli, and H. Iwasaki （2007） Fission Yeast Swi5/Sfr1 and Rhp55/Rhp57 Deferentially Regulate Rhp51-dependent Recombination outcomes， **The EMBO J.**，26，1352 - 1362

POSTER PRESENTATIONS

1． Natsume, T.,Tsutsui, Y.,Iwasaki, H.,Yamao, F. 「 A DNA POLYMERASE α ACCESSORY PROTEIN, MCL1, IS REQUIRED FOR MAINTENANCE OF KINETOCHORE STRUCTURE 」, Fourth International Fission Yeast Meeting， Copenhagen, Denmark，6/11-6/16
2．筒井康博,黒川裕美子,菱田卓,森下卓,品川日出夫,山尾文明,岩崎博史 「 相同組換えに関与するF-boxヘリカーゼの生化学的解析 」, BMB2007，神奈川県横浜市，12/11-12/15
3．筒井 康博、夏目 豊彰、岩崎 博史、山尾 文明 「 DNAダメージ修復における分裂酵母Mcl1の機能解析 」, 第24回染色体ワークショップ，佐賀県唐津市，1/31-2/2
4．夏目 豊彰、筒井 康博、岩崎 博史、山尾 文明 「 分裂酵母Mcl1はセントロメアのクロマチン構造の維持に関与する 」, 第24回染色体ワークショップ，佐賀県唐津市，1/31-2/2

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A. DEPARTMENT OF MOLECULAR GENETICS
A-c. Molecular Mechanism Laboratory
Hiroaki Seino

RESEARCH ACTIVITIES

An in vitro ubiquitination assay of mitotic cyclin

Hiroaki Seino

Cell cycle events are regulated by sequential activation and inactivation of Cdk kinases. Mitotic exit is accomplished by the inactivation of mitotic Cdk kinase, which is mainly achieved by degradation of cyclins by a ubiquitin-proteasome system.

Previously we reported that two ubiquitin-conjugating enzymes, UbcP1/Ubc4 and UbcP4/Ubc11, were responsible for degradation of mitotic cyclin Cdc13 in fission yeast. Each of these two ubiquitin-conjugating enzymes is essential for cell viability and responsible for degradation of Cdc13. These results suggest that the functions of these two ubiquitin-conjugating enzymes are not redundant and they have distinct functions for ubiquitination of Cdc13. Furthermore, we found that ubiquitin chains of Cdc13 were totally reduced in ubc11 mutant cells, whereas ubiquitin chains were short and not reduced in ubc4 mutant cells. Thus, we proposed a hypothesis that Ubc11 might be involved in initiation of ubiquitination, and Ubc4 might be involved in elongation of ubiquitin chains of Cdc13. However, this hypothesis has not been elucidated yet.

To clarify the functional differences between Ubc4 and Ubc11 for degradation of Cdc13, development of an in vitro assay system for ubiquitination for Cdc13 by using fission yeast components is required. Currently, I am attempting to develop this assay system for Cdc13. A ubiquitin-activating enzyme, these two ubiquitin-conjugating enzymes and substrate Cdc13 were expressed as recombinant proteins in bacterial cells and purified. One component of Cdc13-specific ubiquitin ligase anaphase promoting complex/cyclosome (APC/C) was tagged and expressed in fission yeast cells, and APC/C was purified from fission yeast cells. Now I am examining the conditions for reconstitution of a ubiquitination reaction of Cdc13.

Regulation of DNA damage checkpoint by ubiquitin proteasome system

Hiroaki Seino

Cells defective in ubc11+ gene exhibit pleiotoropic phenotypes. One of the phenotypes is mitotic abnormality caused by stabilization and accumulation of mitotic cyclin Cdc13 and perhaps other mitotic regulators. Other phenotype is cell elongation that suggests delay in progression of interphase. This elongation phenotype was not well characterized. Because it seems that ubc11-deficient cells do not show the abnormality in DNA replication, G1 and S phase might be normal in ubc11-deficent cells. Thus, I focused on the relationship between Ubc11 function(s) and DNA damage and/or DNA replication checkpoint. Cell elongation phenotype exhibited by ubc11-deficient cells requires DNA damage checkpoint genes, rad3+, chk1+, crb2+ and rad9+ but does not require DNA replication checkpoint gene cds1+. Furthermore, effecter kinase Chk1 was phosphorylated in the ubc11-deficient cells. This suggests that DNA damage checkpoint is activated in ubc11-deficient cells. The cells defective in ubc11+ gene do not show hypersensitivity to genotoxic reagents. These

results suggest that the ubiquitin pathway involving Ubc11 regulates DNA damage checkpoint signaling pathway. Thus, Ubc11-pathway might function to recovery from cell cycle arrest by DNA damage checkpoint and/or to repress arrest signal in normal cell cycle. Furthermore, recently I found a candidate of the protein degraded by Ubc11-pathway that is involved in regulation of DNA damage checkpoint.

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B. DEPARTMENT OF CELL GENETICS
B-a. Division of Cytogenetics
Takehiko Kobayashi

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1．Ide, S., Watanabe, K., Watanabe, H., Shirahige, K., Kobayashi, T., Maki, H.（2007）Abnormality in Initiation Program of DNA Replication Is Monitored by the Highly Repetitive rRNA Gene Array on Chromosome XII in Budding Yeast，**Mol. Cell. Biol.**，27，568 - 578
2．Kasahara K, Ohtsuki K, Ki S, Aoyama K, Takahashi H, Kobayashi T, Shirahige K, Kokubo T.（2007）Assembly of regulatory factors on rRNA and ribosomal protein genes in Saccharomyces cerevisiae.，**Mol. Cell. Biol.**，27，6686 - 6705
3．Ganley, A.R., Kobayashi, T（2007）Highly efficient concerted evolution in the ribosomal DNA repeats: total rDNA repeat variation revealed by whole-genome shotgun sequence data，**Genome Res.**，17，184 - 191
4．小林武彦（2007）複製フォークと組換えの共役による遺伝子増幅の制御，実験医学，25，63 - 69
5．小林武彦、Ganley, A.R.（2007）系統発生学的フットプリントによる機能性DNA配列の同定，生物の科学「遺伝」別冊，21，265 - 268

ORAL PRESENTATION

1．小林　武彦　リボソームRNA遺伝子の安定性と細胞の老化機構　理化学研究所公開セミナー　理化学研究所（和光）　7/27
2．小林武彦　基礎生物学概論「ゲノムの安定性と細胞老化及びがん化との関連について」基礎生物学研究所　10/27

POSTER PRESENTATIONS

1．小林　武彦「リボソームRNA遺伝子のゲノム維持における役割」，酵母遺伝学フォーラム第40回研究報告会，大阪，9/12
2．Kobayashi, T.「Strategies to maintain the stability of the ribosomal RNA gene repeats.」，Ribosomes: from structure to gene expression and beyond，Irvine, CA. USA，4/19
3．Kobayashi, T.「Extra-coding functions of ribosomal RNA gene repeats」，国際酵母遺伝学会，メルボルン　オーストラリア，7/3
4．小林　武彦「rDNAのコピー数調節機構とExtracoding function」，RNA若手の会，神戸，9/10
5．小林　武彦「リボソームRNA遺伝子の不安定性がもたらす細胞の老化機構」，第79回日本遺伝学会シンポジウム，岡山，9/19
6．Kobayashi, T.「Strategies to maintain the stability of the ribosomal RNA gene repeats」，RNA polymerase I transcription，レーゲンスブルグ　ドイツ，10/7

7．小林　武彦「リボソームRNA遺伝子のゲノム維持における役割」，第30回日本分子生物学会BMB2007，横浜，12/14
8．Kobayashi, T.「Extra-coding functions of ribosomal RNA gene repeats」，International Symposium “Genome Stability & Instability”，大阪，10/7
9．Ide, S.,Kobayashi, T.「Extra-coding functions of rDNA」，RNA polymerase I transcription meeting，Regensburg Germany，10/6
10．Austen R.D. Ganley, Pool, A., ,Kobayashi, T.「The function of TAR1」，RNA polymerase I transcription meeting，Regensburg Germany，10/6
11．Ganley, A.R.D.,Pool, A.,Kobayashi, T.「TAR1 is a suppressor of mitochondrial genetic conflict in Saccharomyces yeast: a hypothesis」，Evolution 2007，クリストチャーチ　ニュージーランド，6/18-23
12．Austen R.D. Ganley、井手聖、真木寿治、小林武彦「リボソームRNA遺伝子のExtra-coding機構」，日本分子生物学会 2006 フォーラム，名古屋市，12/6-8

EDUCATION

1．小林武彦、真木寿治　染色体の複製機構とゲノム安定性　第79回日本遺伝学会シンポジウム　岡山　9/19
2．小林武彦、太田邦史　ゲノムダイナミクスの制御中心としての重複DNA配列群　第30回日本分子生物学会ワークショップBMB2007　横浜　12/14

BOOK

1．Ganley, A.R.D. and Kobayashi, T.（2007）Phylogenetic footprinting to find functional DNA elements. **Comparative Genomics vol.1** 367 - 379

OTHERS

1．Kobayashi, T.，2，GGS Prize 2007
2．小林　武彦，1，日本遺伝学会　会計幹事

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B. DEPARTMENT OF CELL GENETICS
B-b. Division of Microbial Genetics

Hiroyuki Araki

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．Tanaka,S., Umemori,T., Hirai,K., Muramatsu,S., Kamimura,Y., and Araki,H. （2006） CDK-dependent phosphorylation of Sld2 and Sld3 initiates DNA replication in budding yeast , **Nature** , 445 , 328 - 332
2．Tanaka,S.,Tak,Y.-S., and Araki,H. （2007） The role of CDK in the initiation step of DNA replication in eukaryotes , **Cell Division** , 2 , 1 - 6

ORAL PRESENTATION

1．荒木弘之　CDKによる染色体DNA複製の制御　医学共通講義　東京大学　大学院医学系研究科　1/23

POSTER PRESENTATIONS

1．Tanaka,S. and Araki,H.「 Cell cycle specific expression of Sld2 is important for the initiation of DNA replication 」, Eukaryotic DNA Replication and Genome Maintenance , NY, USA , 9/5-9/9
2．Tanaka,S., Muramatsu,S., Umemori,T., Hirai,K., Kamimura,Y. and Araki,H.「 CDK-Dependent Initiation of Chromosomal DNA Replication in Budding Yeast 」, eIMBL Workshop on DNA Replication , 東京 , 4/16
3．Araki,H.「 CDK-dependent initiation of chromosomal DNA replication in budding yeast 」, Eukaryotic DNA Replication and Genome Maintenance , NY, USA , 9/5-9/9
4．Li,Y., and Araki,H.「 The requirement of Sld3 for the assembly of replication initiation proteins ontopre-RC in budding yeast 」, Eukaryotic DNA Replication and Genome Maintenance , NY, USA , 9/5-9/9
5．Tanaka,T.,and Araki,H.「 The Sld7-Sld3 complex important for chromosomal DNA replication 」, Eukaryotic DNA Replication and Genome Maintenance , NY, USA , 9/5-9/9
6．平井和之, 坂本佐知子, 荒木弘之「 染色体DNAの複製開始時に形成されるタンパク質複合体の解析 」, 酵母遺伝学フォーラム第40回研究報告会 , 吹田 , 9/11-9/13
7．　田中誠司, 荒木弘之　「 CELL CYCLE SPECIFIC EXPRESSION OF Sld2 IS IMPORTANT FOR THE INITIATION OF DNA REPLICATION 」, 酵母遺伝学フォーラム第40回研究報告会 , 吹田 , 9/11-9/13
8．荒木弘之「 真核生物染色体DNAの複製開始機構 」, 日本遺伝学会第79回大会 , 岡山 , 9/19-9/21
9．平井和之, 坂本佐知子, 荒木弘之「 染色体DNAの複製開始時に形成されるタンパク質複合体の生化学的解析 」, BMB2007 , 横浜 , 12/11-12/15

10．　田中誠司，荒木弘之　「 CELL CYCLE SPECIFIC EXPRESSION OF Sld2 IS IMPORTANT FOR THE INITIATION OF DNA REPLICATION. 」，BMB2007，横浜，12/11-12/15
11．Li,Y., and Araki,H.「 Requirement of Sld3 protein for the formation of pre-CMG and the assembly to pre-RC 」，BMB2007，横浜，12/11-12/15
12．荒木弘之, 平井和之, 李燕, 坂本佐知子, 梅森稔子, 遠藤静子, 田中誠司「 真核生物染色体DNAの複製開始機構 」，BMB2007，横浜，12/11-12/15

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1．田中誠司，荒木弘之（2007）CDKによる染色体DNAの複製開始制御機構　実験医学 614 - 620

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C. DEPARTMENT OF DEVELOPMENTAL GENETICS
C-a. Division of Developmental Genetics

C. DEPARTMENT OF DEVELOPMENTAL GENETICS
C-a. Division of Developmental Genetics
Hiroshi Shimizu

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1 . Shimizu H, & Okabe, M. （ 2007 ） Evolutionary origin of autonomic regulation of physiological activities in vertebrate phyla. , **Comparative Biochemistry and Physiology** , 193 , 1013 - 1019
2 . 清水 裕、岡部 正隆（2007）消化管の進化的起源，蛋白質、核酸、酵素，52，0 - 0
3 . Shimizu, H., Takaku, Y., Zhang, X. and Fujisawa, T （ 2007 ） The aboral pore of hydra: evidence that the digestive tract of hydra is a tube not a sac. , **Development, Genes and Evolution** , 217 , 563 - 568

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1 . Shimizu, H. 「 Overturning the prejudices about hydra and metazoan evolution 」, Evolutionary Biology Meeting , Marseilles ,

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C. DEPARTMENT OF DEVELOPMENTAL GENETICS
C-a. Division of Developmental Genetics
Yasushi Hiromi

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1．Matsuno M, Kose H, Okabe M, Hiromi Y.（2008）TFIIH controls developmentally-regulated cell cycle progression as a holocomplex.，**Genes Cells**，12，1289 - 300
2．近藤周，岡部正隆，三浦正幸，広海健（2007）カスパーゼが誘導する増殖因子転写のメカニズム，実験医学，25，1575 - 1579
3．平本正輝，広海健（2007）ポスト化学走性仮説：拡散性濃度勾配を使わない軸索パターニング，細胞工学，26，1147 - 1152
4．Suto, F., Tsuboi, M., Kamiya, H., Mizuno, H., Kiyama, Y., Komai, S., Shimizu, M., Sanbo, M., Yagi, T., Hiromi, Y., Chedotal, A., Mitchell, K.J., Manabe, T. and Fujisawa, H.（2007）Interactions between Plexin-A2, Plexin-A4, and Semaphorin 6A control lamina-restricted projection of hippocampal mossyfibers.，**Neuron**，53，535 - 547

ORAL PRESENTATION

1．Hiromi, Y. Intra-axonal patterning: its mechanisms and implications Duke Univerisity 5/2
2．Yasushi Hiromi Intra-axonal patterning: its mechanisms and implications NCBS, Bangalore, India 2007.01.22
3．Yasushi Hiromi Patterning within a nerve cell: a new strategy to make a circuit Dept. Biotechnology, Anna University, Chennai, India 2007.01.24
4．Yasushi Hiromi Patterning within a nerve cell: a new strategy to make a circuit Dept. Biotechnology, IIT-Madras, Chennai, India 2007.01.25

POSTER PRESENTATIONS

1．Katsuki, T., DeFalco, T., Morita, M., Hiramoto, M., Hiromi, Y.「Intra-axonal Patterning In Drosophila Neurons Is Achieved By Compartmentalization Of The Axonal Membrane」, JDRC 8th，淡路島，7/2-4
2．Joshi, R., Katsuki, T., DeFalco, T., Hiromi, Y.「Intra-axonal patterning of axon guidance receptors in Drosophila」, International Symposium Celebrating Dr. David S. Hogness, Recipient of the 23rd International Prize for Biology，kyoto，11/21-22
3．広海健「海外経験をどう生かすか」，生命科学若手夏の学校シンポジウム「所変われば ラボ変わる -- 比べてわかる日本と世界 --」，埼玉県嵐山町，8/4
4．広海健「器官構築の発生遺伝学：個々の細胞は組織全体のためになにができるか？」，遺伝研公開講演会「生命科学の最前線」，東京，11/10
5．浅岡美穂, 広海健「ショウジョウバエ生殖巣における生殖幹細胞形成因子の探索」，第五

回幹細胞シンポジウム，淡路，5/17-5/19
6．浅岡美穂「ショウジョウバエ卵巣における生殖幹細胞形成機構」，2007年度 国立遺伝学研究所 研究会「生殖細胞と生殖腺形成の普遍性と多様性」，三島，7/23-24
7．浅岡美穂，広海健「ショウジョウバエ生殖巣における生殖幹細胞形成因子の探索」，BMB2007 (The 30th Annual Meeting of MSBJ)，横浜，12/11-12/15
8．Hiromi, Y.「Intra-axonal patterning: pattern formation within a nerve cell」，International Symposium “Gene Expression Control and Genome Evolution”，Okayama ，9/19-21
9．Hiromi, Y.「Intra-axonal patterning」，Visual Processing in Insects: From Anatomy to Behavior，Janelia Farm ，4/29-5/1
10．Hiromi, Y.「Intra-axonal patterning: its mechanisms and implications」，The Second Taiwan-Japan Bi-Lateral Symposium on Cellular and Developmental Biology， Taipei, Taiwan，2007.01.18-19
11．金井誠, 広海健「ショウジョウバエSeven-upによる神経幹細胞・遺伝情報発現の時間的制御」，遺伝情報デコード・冬のワークショップ，越後湯沢，2007.1.25-27
12．湯浅喜博, 広海健「Notch情報伝達系によるグリア細胞の終分化を規定する細胞内環境」，遺伝情報DECODE・転写研究会共催冬のワークショップ，越後湯沢，2007.01.25-27
13．Yuasa, Y., Hiromi, Y.「PROSPERO Regulates the Terminal Differentiation of Drosophila CNS Glia」，the UK-APDBN Joint Meeting "Development and theEmergence of Function in the Nervous System,"，神戸，2007.02.08-10
14．Morita, R., Katsuki, T., Hiromi, Y.「Relationship Between Sub-axonal Compartment and Axonal Turning in vitro」，UK-APDBN Meeting "Development and the Emergence of Function in the Nervous System"，神戸，2007.2.8-10
15．須藤文和、八木健、Alain Chedotal, Kevin J. Mitchell, 広海健, 藤澤肇「プレキシン／セマフォリンシグナルによる海馬神経回路形成の制御」，第112回日本解剖学会総会・全国学術集会，大阪，2007.3.27-29
16．Yoshihiro YUASA, Yasushi HIROMI「Subtype Specific Expression and Function of PROS in the Longitudinal Glia」，Annual Drosophila Research Conference，Philadelphia，2007.3.7-11
17．Takeo Katsuki, Masaki Hiramoto, Yasushi Hiromi「Sub-axonal membrane compartmentalization in Drosophila neuro」，第10回国際細胞膜研究フォーラム，京都，2007.2.27-3.2
18．Takeo Katsuki, Masaki Hiramoto, Yasushi Hiromi「Drosophila neurons form intra-axonal compartments through a cell-autonomous mechanism」，UK-APDBN Meeting "Development and the Emergence of Function in the Nervous System"，神戸，2007.2.8-10

OTHERS

1．Yasushi Hiromi，1，Dr. Hiromi served as an editor for Development, Growth and Differentiation.
2．Yasushi Hiromi，1，日本分子生物学会 男女共同参画委員会委員 Dr. Hiromi served as a memner of the Gender Equality Committee of The Molecular Biology Society of Japan.

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C. DEPARTMENT OF DEVELOPMENTAL GENETICS
C-b. Division of Gene Expression

Susumu Hirose

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．広瀬 進（0）ヘテロクロマチンの制御，実験医学，25，753 - 757
2． Nakayama, T., Nishioka, K., Dong, Y.-X., Shimojima, T., and Hirose, S. （0）*Drosophila* GAGA factor directs histone H3.3 replacement that prevents the heterochromatin spreading.，**Genes Dev.**，21，552 - 561

POSTER PRESENTATIONS

1．広瀬 進「non-coding RNAの新しい機能:転写干渉による空間特異的転写制御」，第5回転写研究会，湯沢，1/25-27
2． Petruck, S., Sedkov, Y., Riley, K., Hodgson, J., Schweisguth, F., Hirose, S., Janes, J., Brock, H., and Mazo, A.「Transcriptional elongation of non-coding RNAs promoted by the Trithorax TAC1 complex represses Ubx by a transcriptional repression mechanism」，47th Annual Drosophila Research Conference，Philadelphia，3/7-11

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C. DEPARTMENT OF DEVELOPMENTAL GENETICS
C-c. Division of Molecular and Developmental Biology

C. DEPARTMENT OF DEVELOPMENTAL GENETICS
C-c. Division of Molecular and Developmental Biology
Koichi Kawakami

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．Jeong, J.-Y., Einhorn, Z., Mathur, P., Chen, L., Lee, S., Kawakami, K., and Guo, S.（2006）Patterning the zebrafish diencephalon by the conserved zinc-finger protein Fezl，**Development**，134，127 - 136

2．Kawakami, K.（2007）Tol2: a versatile gene transfer vector in vertebrates，**Genome Biology**，8，7 - 0

3．Fan, X., Hagos, E.G., Xu, B., Sias, C., Kawakami, K., Burdine, R.D., and Dougan, S.T.（2007）Nodal signals mediate interactions between the extra-embryonic and embryonic tissues in zebrafish.，**Developmental Biology**，310，363 - 378

4．Seguchi, O., Takashima, S., Yamazaki, S., Asakura, M., Asano, Y., Shintani, Y., Wakeno, M., Minamino, T., Kondo, H., Furukawa, H., Nakamaru, K., Naito, A., Takahashi, T., Ohtsuka, T., Kawakami, K., Isomura, T., Kitamura, S., Tomoike, H., Mochizuki, N., and Kitakaze, M.（2007）A cardiac myosin light chain kinase regulates sarcomere assembly in the vertebrate heart.，**The Journal of Clinical Investigation**，117，2812 - 2824

5．浦崎明宏,川上浩一（2007）脊椎動物におけるトランスポゾンを用いた遺伝学的方法論，実験医学，25，2507 - 2512

6．Nakada, T.,Hoshijima, K.,Esaki, M.,Nagayoshi, S.,Kawakami, K.,Hirose, S.（2007）Localization of ammonia transporter Rhcg1 in mitochondrion-rich cells of yolk sac, gill, and kidney of zebrafish and its ionic strength-dependent expression.，**Am J Physiol Regul Integr Comp Physiol**，293，1743 - 1753

7．Shibano, T.,Takeda, M.,Suetake, I.,Kawakami, K.,Asashima, M.,Tajima, S.,Taira, M.（2007）Recombinant Tol2 transposase with activity in Xenopus embryos.，**FEBS letters**，581，4333 - 4336

8．浅川和秀, 川上浩一（2007）Tol2トランスポゾンを用いたゼブラフィッシュGaL4エンハンサートラップ法の確立，バイオテクノロジージャーナル，7，603 - 606

9．Sato, Y., Kasai, T., Nakagawa, S., Tanabe, K., Watanabe, T., Kawakami, K., and Takahashi Y.（2007）Stable integration and conditional expression of electroporated transgenes in chicken embryos，**Developmental Biology**，305，616 - 624

10．Esaki, M., Hoshijima, K., Kobayashi, S., Fukuda, H., Kawakami, K., and Hirose, S.（2006）Visualization in zebrafish larvae of Na+ uptake in mitochondria-rich cells whose differentiation is dependent on foxi3a，**Am J Physiol Regul Integr Comp Physiol**，292，470 - 480

11．Kosaka, K., Kawakami, K., Sakamoto, H., and Inoue, K.（2006）Spatiotemporal localization of germ plasm RNAs during zebrafish oogenesis，**Mechanism of Devlopment**，124，279 - 289

12． Scott, E.K., Mason, L., Arrenberg, A.B., Ziv, L., Gosse, N.J., Xiao, T., Chi, N.C., Asakawa, K., Kawakami, K., Baier, H（2007）Targeting neural circuitry in zebrafish using GAL4 enhancer trapping，**Nature Methods**，48，323 - 326

ORAL PRESENTATION

1． Kawakami, K.　Transposon-mediated gene and enhancer trapping in zebrafish　Department seminar　Seoul National University, Dr. Lee lab　9/13
2．Kawakami, K.　Transposon-mediated gene trapping and enhancer trapping in zebrafish　IITM　10/25
3．Kawakami, K.　Transposon-mediated gene and enhancer trapping in zebrafish　Seoul National University　9/13

POSTER PRESENTATIONS

1．辻田忠志,小林麻己人,川上浩一,山本雅之「Nrf2活性モニター用トランスジェニックゼブラフィッシュ系の開発」，第30回日本分子生物学会年会・第80回日本生化学会大会，横浜，12/11 ~15
2． Kawakami, K.,Asakawa, K.,Abe, G.,Urasaki, A., Kikuta, H., Kishimoto, Y., Mutou, A., Maximiliano, S.,「トランスポゾンを用いたGal4-UAS法による細胞の可視化と機能改変」，第30回日本分子生物学会年会・第80回日本生化学会大会，横浜，12/11 ~15
3．舟橋淳一，川上浩一，仲村春和「遺伝子トラップ系統を用いたゼブラフィッシュ三半規管形態形成の解析」，第30回日本分子生物学会年会・第80回日本生化学会大会，横浜，12/11 ~15
4．Tsujita, T.,Kobayashi, M.,Kawakami, K.,Yamamoto, M.「Nrf2活性モニター用トランスジェニックゼブラフィッシュ系の開発」，第30回日本分子生物学会年会・第80回日本生化学会大会，横浜，12/11 ~15
5． Kawakami, K.「Transposon-mediated gene trapping and enhancer trapping in zebrafish」，ISDB，Agra, India，10/18-19
6．Kawakami, K.「Transposon-mediated gene and enhancer trapping in zebrafish」，The 16th Korea Genome Organization Conference，Seoul，9/13-14
7．舟橋淳一, 川上浩一, 仲村春和「三次元タイムラプスによるゼブラフィッシュ三半規管形態形成の解析」，第13回小型魚類研究会，東京，9/16-17
8． 江嵜正浩, 星島一幸, 川上浩一, Eric S. Weinberg, 広瀬茂久「魚類の外部器官であるMitochondria-rich cells (MRCs) の複雑な発生分化機構」，第13回小型魚類研究会，東京，9/16-17
9． 岡本仁, 川上浩一, 東島眞一「ゼブラフィッシュバイオリソースII」，第13回小型魚類研究会，東京，9/16-17
10． Kishimoto, Y.,Koshida, S.,Furutani-Seiki, M.,Kawakami, A.,Reiss, J.,Kondoh, H.,Kawakami, K.「Molybdenum cofactor biosynthesis essential for heparan sulfate formation and fgf signaling during vertebrate embryogenesis」，5th European Zebrafish Genetics and Development Meeting，Amsterdam，7/12-15
11． Gebhart, N.,Kawakami, K.,Ono, F.「Insertion of RFP using gene trap results in a knockdown of the pax8 gene」，5th European Zebrafish Genetics and Development Meeting，Amsterdam，7/12-15
12． Esaki, M.,Hoshijima, K.,Kobayashi, S.,Fukuda, H.,Kawakami, K.,Hirose, S.「Visualization in zebrafish larvae of Na+ uptake in mitochondria-rich cells whose differentiation is dependent on foxi3A」，5th European Zebrafish Genetics and Development Meeting，Amsterdam，7/12-15
13． Komisarczuk, A.,Navratilova, P.,Kawakami, K.,Becker, T.「Analysis of conserved element regulating expression of fgf8 in zebrafish」，5th European Zebrafish Genetics and Development Meeting，Amsterdam，7/12-15
14． Asakawa, K.,Mizusawa, K.,Nagayoshi, S.,Kotani, T.,Urasaki, A.,Kishimoto, Y.,Hibi, M.,Kawakami, K.「Targeted gene expression by GAL4 gene and enhancer trapping in zebrafish defines subsets of neurons required for simple vetebrate behaviors」，5th European Zebrafish Genetics and Development Meeting，Amsterdam，7/12-15
15． Urasaki, A.,Asakawa, K.,Kawakami, K.「New genetic techniques by excision of the

Tol2 transposon: isolation of revertants and creating frame shift mutations」, 5th European Zebrafish Genetics and Development Meeting , Amsterdam , 7/12-15
16．川上浩一「 ゼブラフィッシュにおける新しい遺伝学的方法論の確立 」, 東洋紡バイオ財団設立25周年記念シンポジウム「次世代へのメッセージ」, 大阪 , 6/14-18
17． Yoshiko Takahashi,Emi Ohata,Tadayoshi Watanabe,Teruaki Takahashi,Koichi Kawakami,Jun Kohyama,Hideyuki Okano,Yuki Sato「 Somitic contribution to the formation of dorsal aorta involves cell migration regulated by Notch and ephrin 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
18．原田英斉,松田佳昌,田中順,鈴木一平野明日香,川上浩一,高橋淑子,仲村春和「 ニワトリ胚視蓋極性形成におけるEnとFgfシグナルの役割 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
19． 浅川和秀,水澤寛太,永吉さおり,小谷友也,浦崎明宏,岸本康之,日比正彦,川上浩一 「 ゼブラフィッシュGAL4トラップ法を用いた行動制御に関与する神経細胞の探索 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
20．浦崎明宏,浅川和秀,川上浩一「 ゼブラフィッシュにおけるJump starterトランスポゾンシステムの開発 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
21． 柴野卓志,武田正利,末武勲,川上浩一,浅島誠,田嶋正二,平良眞規 「 Xenopus胚において活性をもつ組換えTol2移転酵素の精製 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
22．江崎正浩,星島一幸,小林さや子,福田英一,川上浩一,広瀬茂久 「 ゼブラフィッシュ幼生におけるNaイオン吸収細胞の同定とその発生分化機構の解析 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
23．舟橋淳一,川上浩一,仲村春和「 遺伝子トラップ系統を用いたゼブラフィッシュ三半規管形態形成の解析 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
24．岸本康之,越田澄人,古谷-清木誠,川上厚志,Joechen Reiss,近藤寿人,川上浩一「 モリブデン補酵素生合成は、硫酸イオン生成を通じて脊椎動物胚発生におけるFgfシグナル伝達に必須の役割を果たす 」, 第40回日本発生生物学会 第59回日本細胞生物学会 合同大会 , 福岡 , 5/28-30
25． Titus, T.A., Asakawa, K., Nagayoshi, S., Kawakami, K., Montgomery, K.L., Murphy, J., Rodriguez-Mari, A., Song, H., Starks, A.M., Wilson, C., Yan, Y.-L., Postlethwait, J.H. 「 Zebrafish Models for Fanconi Anemia 」, Second strategic conference of zebrafish investigators , Asilomar, USA , 2/2-2/6
26． Kawakami, K.「 Transposon-mediated GAL4 gene and enhancer trap methods and its application to inihibition of synaptic function in zebrafish 」, Second strategic conference of zebrafish investigators , Asilomar, USA , 2/2-2/6

EDUCATION

1．小椋利彦, 川上浩一　脊椎動物の器官形成と生体内バイオイメージング　第30回日本分子生物学会年会ワークショップ4W21　横浜　12/11-15
2．竹田潤二, 川上浩一　テクニカルセッション（座長）　第40回日本発生生物学会 第59回日本細胞生物学会 合同大会　福岡　5/28-30
3．川上浩一　脊椎動物の器官形成とバイオイメージング　国立遺伝学研究所研究会　三島　3/15-3/16
4． Kawakami, K., Evans, T., Chien, C.B.　Manipulation of gene function　2nd Strategic Conference of Zebrafish Investigators　Asilomar, USA　2/2-2/6

DB SOFT

1． Kawakami, K. , zTrap:zebrafish gene trap and enhancer trap database http://kawakami.lab.nig.ac.jp/

OTHERS

1． Kishimoto, Y.,Koshida, S.,Furutani-Seiki, M.,Kawakami, A.,Reiss, J.,Kondoh, H.,Kawakami, K. , 2 , Best Poster at 5th European Zebrafish Genetics and Development

Meeting
2 . Asakawa, K.,Mizusawa, K.,Nagayoshi, S.,Kotani, T.,Urasaki, A.,Kishimoto, Y.,Hibi, M.,Kawakami, K. , 2 , Best Poster at 5th European Zebrafish Genetics and Development Meeting

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D. DEPARTMENT OF POPULATION GENETICS
D-a. Division of Population Genetics

Naruya Saitou

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．Tamura, M., Tanaka, S., Fujii, T., Aoki, A., Komiyama, H., Ezawa, K., Sumiyama, K., Sagai, T., and Shiroishi, T.（2007）Members of a novel gene family, Gsdm, are expressed exclusively in the epithelium of the skin and gastrointestinal tract in a highly tissue-specific manner.，**Genomics**，89，618 - 629
2．Takahashi, H., Kamiya, A., Ishiguro, A., Suzuki, A. C., Saitou, N., Toyoda, A., and Aruga, J.（2007）Conservation and Diversification of Msx Protein in Metazoan Evolution，**Molecular Biology and Evolution.**，25，69 - 82
3．Matsuya, A., Sakate, R., Kawahara, Y., Koyanagi, K.O., Sato, Y., Fujii, Y., Yamasaki, C., Habara, T., Nakaoka, H., Todokoro, F., Yamaguchi, K., Endo, T., Oota, S., Makalowski, W., Ikeo, K., Suzuki, Y., Hanada, K., Hashimoto, K., Hirai, M., Iwama, H., Saitou, N., Hiraki, A.T., Jin, L., Kaneko, Y., Kanno, M., Murakami, K., Noda, A.O., Saichi, N., Sanbonmatsu, R., Suzuki, M., Takeda, J., Tanaka, M., Gojobori, T., Imanishi, T., Itoh, T.（2007）Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees，**Nucleic Acids Research**，36，787 - 792
4．斎藤成也（2007）遺伝学と進化学，シリーズ**21**世紀の動物科学1　日本の動物学の歴史，1，88 - 97
5．Kitano T., Umetsu K., Tian W., Yamazaki K., and Saitou N.（2007）Tempo and mode of evolution of the Rh blood group genes before and after gene duplication，**Immunogenetics**，59，427 - 431
6．Yuasa I., Umetsu K., Harihara S., Kido A., Miyoshi A., Saitou N., Dashnyam B., Jin F., Lucotte G., Chattopadhyay P. K., Henke L., and Henke J.（2007）Distribution of two Asian-related coding SNPs in the MC1R and OCA2 genes，**Biochemical Genetics**，45，535 - 542
7．Yuasa I., Umetsu K., Harihara S., Miyoshi A., Saitou N., Park K. S., Dashnyam B., Jin F., Lucotte G., Chattopadhyay P. K., Henke L., and Henke J.（2007）OCA2 481Thr, a hyofunctionl allele in pigmentation, is characteristic of northeastern Asian populations，**Journal of Human Genetics**，52，690 - 693
8．斎藤成也（2007）生物はなぜ変化するのか？新･進化論，**Newton**，，0 - 0
9．斎藤成也（2007）遺伝子データから日本列島人の成立を考える，生物の科学　遺伝，61，34 - 38
10．斎藤成也（2007）DNAの基礎知識，**BAN**，AUGUST，22 - 24

ORAL PRESENTATION

1．斎藤　成也　Comparative genomics of various mammalian species with special

reference toward human evolution　lecture　Seoul National University Department of Statistics　11/6
2．斎藤　成也　人類への進化を遺伝子からたどる　講義　お茶の水女子大学　2/27,2/28
3．斎藤成也　比較ゲノム学　講義　東京大学大学院理学系研究科　7/14
4．斎藤成也　分子進化学　集中講義　関西学院大学理工学部　8/28, 8/29
5．斎藤成也　人類遺伝学　講義　京都大学大学院理学系研究科　10/4.10/5
6．斎藤成也　分子進化学　講義　山形大学　1/18
7．斎藤成也　DNAから見た人類進化-自然淘汰と中立進化　特別講義　京都大学　3/20
8．斎藤成也　極保存配列の比較ゲノム解析　セミナー　東海大学　医学部　5/8
9．斎藤成也　分子進化学　講義　東京大学理学部　5/16,5/30,6/13,6/20
10．隅山健太　cis-elementの分子進化　分子進化学講義　東京大学理学部　6/6

POSTER PRESENTATIONS

1．斎藤成也，江澤潔，河合洋介「遺伝子変換による重複遺伝子の均質化」，第30回日本分子生物学会年会，第80回日本生化学会大会合同大会，横浜市，12/14
2．隅山 健太, Frank H. Ruddle「Identification and evolutionary origin of a limb enhancer in the Dlx3-7 bigene cluster.」，日本進化学会第9回大会，京都，8/31
3．隅山健太、Frank Ruddle「Dlx3-7遺伝子クラスターの四肢エンハンサーの同定およびその進化的起源」，第40回日本発生生物学会大会，福岡，5/30
4．斎藤　成也「Evolutionary analysis on primates」，the 79th Annual Meeting of the Genetics Society of Japan，岡山市，9/21
5．鈴木留美子，江澤潔，斎藤成也「哺乳類・魚類・昆虫における同義置換とタンパク質ドメインの関係」，日本遺伝学会第79回大会，岡山市，9/19
6．斎藤　成也「ヒトゲノムの遺伝的個人差と遺伝的集団差」，第13回日本法科学技術学術集会，東京，11/8
7．斎藤　成也「ゲノム解読から見えて来た哺乳類を中心とする脊椎動物の進化と今後の展望」，第2回学際科学実験センターシンポジウム，金沢市，11/9
8．河合洋介，斎藤成也「類人猿ミトコンドリアDNAの塩基組成動態の解析」，日本進化学会第9回大会，京都市，8/31
9．河合洋介，太田聡史，斎藤成也「ヒトゲノムにおけるGC含量の時間的変化」，日本遺伝学会第79回大会，岡山市，9/19
10．斎藤成也「現代によみがえったベルツのアイヌ沖縄同系論」，アイヌ・先住民センター講演会，札幌市，9/7
11．斎藤成也「ダーウィンからキムラへゲノム進化の原動力とは」，生物学オリンピックハイスクールフォーラム，東京，7/28
12．斎藤成也「Neccessity of Non-Tree Structure in Nuclear DNA Phylogeny」，A tree of life constructed by genome-wide information，tibet，6/8
13．斎藤成也「比較ゲノムに基づく進化メカニズム研究」，特定領域研究「ゲノム」4領域2007年度合同班会議，神戸市，6/25
14．斎藤成也「Evolution of ultra-conserved elements in mammals」，SMBE Annual Meeting 2007，Hallifax，6/27
15．斎藤成也「ヒトとチンパンジーの違い-ゲノム比較解析を中心に」，第27回日本医学総会，大阪市，4/6
16．斎藤成也「近縁多種生物の同時比較による進化的保全度から見たゲノム階層構造の推定」，比較ゲノム情報解析研究会，京都市，4/26
17．Sumiyama, K. Ruddle, FH「Identification and evolutionary origin of a limb enhancer in the Dlx3-7 bigene cluster.」，Annual Meeting of the Society for Molecular Biology and Evolution，Halifax, Nova Scotia, Canada，6/27
18．斎藤成也「21世紀の新しい人間観を探る」，第11回KOSMOSフォーラム，東京，2/3
19．斎藤成也「ゲノムからみた生物進化」，電力館科学ゼミナール，東京，3/10

BOOK

1．隅山健太、斎藤成也（2007）脊椎動物の比較ゲノム：遺伝子間領域の比較解析　細胞工学別冊：比較ゲノム学から読み解く生命システム　50 - 55
2．藤山秋佐夫，服部正平，森下真一，斎藤成也（2007）微生物からネアンデルタール人ま

で　ゲノムはここまで解明された　87 - 179
3．斎藤成也（2007）ゲノムの塩基配列に刻まれた生命の歴史を人間までたどる　ゲノムはここまで解明された　15 - 33
4．斎藤成也（2007）ゲノム進化学入門　ゲノム進化学入門　0 - 0
5．斎藤　成也（2007）2006年大会をふりかえる　進化でどこまでわかるか　250 - 251
6．斎藤　成也（2007）研究で用いる言語　学術月報　102 - 102
7．斎藤成也（2007）類人猿と人類はどれほど近いか　ヒトはどのようにしてつくられたか　81 - 93
8．斎藤成也（2007）ゲノム進化を考える一系統樹の数理から脳神経系の進化まで一　臨時別冊　数理科学　0 - 0
9．斎藤成也（2007）霊長類ゲノムにひそむ網状の系統関係　ゲノムは何をどのように決めているのか　198 - 1208

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D. DEPARTMENT OF POPULATION GENETICS
D-a. Division of Population Genetics
Toshiyuki Takano

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1．Kawabe, A.,Fujimoto, R.,and Charlesworth D.（2007）High diversity due to balancing selection in the promoter region of the Medea gene in Arabidopsis lyrata.，**Curr Biol.**，17，1885 - 1889
2．Takahashi, A., Takahashi K., Ueda, R., and Takano-Shimizu, T.（2007）Natural variation of *ebony* gene controlling thoracic pigmentation in *Drosophila melanogaster*.，**Genetics**，177，1233 - 1237
3．Noro, Y, Takano-Shimizu, T, Syono, K, Kishima, Y, and Sano, Y.（2007）Genetic variations in rice in vitro cultures at the *EPSPs-RPS20* region.，**Theor. Appl. Genet.**，114，705 - 711

POSTER PRESENTATIONS

1．高橋文「分化した自然集団間の比較ゲノム機能解析によるショウジョウバエ種多様化メカニズムの解明」，第1回昆虫ゲノム研究会，東京，2/27-28
2．Takahashi, A.,Takano-Shimizu, T.「Polymorphism in the expression level of an enzymatic gene affecting cuticle pigmentation and mating preference in natural populations of Drosophila」，The Fifth Okazaki Biology Conference ，Kakegawa，3/6-7
3．Kawabe, A.「Arabidopsis lyrata における Medea 遺伝子の種内変異」，The 79th Annual Meeting of the Genetics Society of Japan，Okayama，9/19
4．Kawabe, A.「Petterns of DNA variation among three centromeric satellite families in Arabidopsis halleri and lyrata」，16th International Chromosome Conference，Amsterdam，8/25-8/29
5．Kondo, R., Oshima, M., Yoshifuji, Y., Inomata, N., Itoh, M., and Takano-Shimizu, T.「Linkage disequilibrium analyses of synonymous and replacement polymorphisms in Drosophila chemoreceptor genes.」，48th Annual Drosophila Research Conference，Philadelphia, Pennsylvania，3/7-11
6．Tanaka, K., Takahashi, K. R., and Takano-Shimizu, T.「The fixation probability of a newly arisen gene duplication.」，The 79th Annual Meeting of the Genetics Society of Japan，Okayama, Okayama，9/19-21
7．Takahashi, K. H., and Takano-Shimizu, T.「Developmental buffering of Hsp70 under environmental stresses.」，The 79th Annual Meeting of the Genetics Society of Japan，Okayama, Okayama，
8．Takahashi, A., Itoh, M., Kondo, R., Inomata, N., and Takano-Shimizu, T.「Natural variants of a pigmentation-controlling gene that affects mate preference in *Drosophila melanogaster*.」，The 79th Annual Meeting of the Genetics Society of Japan，Okayama,

Okayama , 9/19-21
9 . Takano-Shimizu, T. 「 Measuring variation and estimating population genetics parameters. 」, The 79th Annual Meeting of the Genetics Society of Japan , Okayama, Okayama , 9/19-21
10 . Takahashi, K. H., Tanaka, K., Itoh, M., and Takano-Shimziu, T. 「 Natural selection acting on *X* chromosome of *Drosophila melanogaster*. 」, 48th Annual Drosophila Research Conference , Philadelphia, Pennsylvania , 3/7-11
11 . Takahashi, K. H., Tanaka, K., Itoh, M., and Takano-Shimziu, T. 「 Natural selection acting on *X*-linked chemoreceptor genes. 」, The 8th Japanese Drosophila Research Conference , Awaji, Hyogo , 7/2-4

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E. DEPARTMENT OF INTEGRATED GENETICS
E-a. Division of Human Genetics

E. DEPARTMENT OF INTEGRATED GENETICS
E-a. Division of Human Genetics
Hiroyuki Sasaki

RESEARCH ACTIVITIES

(1) Establishment and maintenance of DNA methylation imprints in the germline and early mouse embryos

Hiroyuki SASAKI, Yuzuru Kato, Ryutaro HIRASAWA, Hatsune CHIBA, Kenji KUMAKI, Hiroyasu FURUUMI, Masahiro KANEDA[1], Masaki OKANO[2], En LI[3], Mizue HISANO[4], Masami NOZAKI[4], Tomohiro SUZUKI[5], Shigeharu WAKANA[5] and Toshihiko SHIROISHI[5]
([1]Gurdon Inst. Cancer Dev. Biol.; [2]CDB, RIKEN; [3]Novartis; [4]OSAKA UNIV.; [5]GSC, RIKEN)

Genomic imprinting, an epigenetic gene-marking phenomenon in the germline, causes parent-of-origin-specific monoallelic expression of a subset of mammalian genes in the offspring. DNA methylation serves as an important gene marking mechanism to distinguish the parental alleles of the imprinted genes. Evidence suggests that imprinted genes are regulated by nearby differentially methylated regions (DMRs). We previously showed by conditional gene targeting that the de novo DNA methyltransferase gene Dnmt3a, but not Dnmt3b, is essential for the establishment of the methylation imprints in both male and female germlines. We have now studied the methylation defects in the male germ cells from various Dnmt mutants and found that Dnmt3L also plays a critical role in methylating the DMRs. In the Dnmt3a, Dnmt3b and Dnmt3L mutant germ cells, various repeat sequences including both interspersed and tandem types are also affected (submitted). Another question is how the methylation imprints are maintained in cleavage stage mouse embryos, in which the rest of the genome is extensively demethylated. We are therefore studying cleavage stage embryos lacking either Dnmt1, Dnmt3a, Dnmt3b, or combinations of these to see which methyltransferase(s) maintains the imprints. Lastly, we have also set out to screen ENU-treated mutant mouse stocks for new mutants that have a defect in establishment of the imprints.

(2) Search for the sequence features common to the imprinted DMRs

Hiroyuki SASAKI, Hisato KOBAYASHI, Chikako SUDA, Takashi ABE, Yuji KOHARA and Toshimichi IKEMURA[1] ([1]SOKENDAI)

Although the imprinted DMRs, which show differential methylation depending on parental origin, play crucial roles in imprinting, features common to the DMRs have not been identified. We therefore set out to look for the sequence features common to the DMRs by computer-assisted programs. We first determined the extent of each mouse DMR by bisulphite sequencing in 12.5-day embryos. We found that most DMRs are more CpG-rich than most part of the genome but less CpG-rich than the CpG islands. Furthermore, the paternally methylated DMRs contain less CpGs than the maternally methylated DMRs

(Kobayashi et al. 2006). These findings provide a basis for the further characterization of DMRs.

(3) Identification and characterization of novel classes of small RNAs in the mouse germline

Hiroyuki SASAKI, Toshiaki WATANABE, Yuji KOHARA, Atsushi TAKEDA[1], Tomoyuki TSUKIYAMA[1], Kazuyuki MISE[1], Tetsuro OKUNO[1], Naojiro MINAMI[1], Hiroshi IMAI[1], Satomi MIYAGAWA[2], Toru NAKANO[2], Yasushi TOTOKI[3], Atsushi TOYODA[3], Yoshiyuki SASAKI[3], Yayoi OBATA[4] and Tomohiro KONO[4] ([1]Kyoto Univ.; [2]Osaka Univ.; [3]RIKEN GSC; [4]Tokyo Univ. Agr.)

Small RNAs are involved in the regulation of gene expression through translational repression, mRNA degradation, and chromatin modification. We speculated that small RNAs expressed in germ cells might play a role in transposon silencing and possibly genomic imprinting. As a first step, we have cloned and characterized the small RNAs in adult mouse testis and full-grown oocytes. We identified siRNAs corresponding to various retroelements in oocytes and gsRNAs/piRNAs mapping to various regions of the genome in clusters (Watanabe et al. 2006). These results suggest that small RNA pathways other than the miRNA pathway are also conserved in diverse animal species. We have now set out to clone and characterize small RNAs in fetal prospermatogonia and growing oocytes. We also described the methods to clone and characterize small RNAs (Watanabe et al. in press).

(4) Whole genome analysis of DNA methylation using microarrays

Hiroyuki SASAKI, Yusuke MIYANARI, Masayuki FUKASAWA[1], Mika KIMURA[1], Sumiyo MORITA[1] and Izuho HATADA[1] ([1]Gumma Univ.)

DNA methylation is involved in gene silencing in normal tissues and in tumors. We have devised two novel methods to profile promoter methylation in a genome-wide scale: the MIAMI method and the PMAD technique (Hatada et al. 2006; Fukasawa et al. 2006). The application of these methods to tumors such as lung cancer demonstrated the usefulness of the methods. However, since both methods use methylation-sensitive enzyme and therefore the number of promoters that can be analyzed are limited, we now use anti-5mC antibody and methyl-CpG binding domain proteins to pull down methylated DNA. We will apply these tools and technologies to crack the ゞepigenome〒 of humans and mice.

(5) Tsix defective in splicing is competent to establish Xist silencing

Takashi SADO, Yuko HOKI and Hiroyuki SASAKI

Dosage differences of X-linked genes between male and female mammals are compensated for by a mechanism known as X-inactivation, and the non-coding Xist gene plays a crucial role in this process. The expression of Xist is regulated in cis by its non-coding antisense gene, Tsix. In fact, recent studies demonstrated that Tsix modulates Xist expression through modification of the chromatin structure. It is still unknown, however, whether the RNA product is important for the function of Tsix or whether the antisense transcription is sufficient. To obtain insight into this issue, we eliminated the splicing products of Tsix in the mouse and explored the effects of this elimination on Tsix-mediated Xist silencing. To our surprise, the Xist locus was stably repressed on the X carrying the splicing-defective Tsix allele. Moreover, the repressive chromatin configuration was properly established at the Xist locus. These results indicate that the splicing products are dispensable for Tsix-mediated Xist silencing (Sado et al. 2006).

(6) Tsix-mediated Xist silencing requires antisense transcription across the Xist promoter

Takashi SADO, Tatsuya OHHATA, Yuko HOKI and Hiroyuki SASAKI

We recently demonstrated that Tsix silences Xist through modification of chromatin structure in the Xist promoter region. This finding prompted us to investigate the significance of antisense transcription across the Xist promoter in Tsix-mediated silencing. We have now demonstrated that the premature termination of Tsix before the Xist promoter abolishes the antisense regulation of Xist with a concomitant loss of repressive modifications, especially in the extraembryonic tissues. The results establish the fundamental role of the antisense transcription across the Xist promoter in Xist silencing. Unexpectedly, the mutated X, expressing nearly intact Xist RNA, is defective in undergoing inactivation. This new mutation provides insight into how Xist becomes activated after a cessation of Tsix transcription on the same chromosome (submitted).

(7) Role of the A-repeat in Xist during mouse development

Takashi SADO, Naomi KIMURA, Yuko HOKI, Yuko AMAKAWA and Hiroyuki SASAKIA

Previous study employing an inducible mutant Xist expression system in ES cells suggested that a repeat element in Xist RNA, called A-repeat, is essential for the silencing function of Xist. However, the mutant RNAs lacking A-repeat accumulated on the X chromosome. In this project, we have introduced a new mutant Xist allele lacking A-repeat into mice and examined the effects. Our results are consistent with the previous finding that A-repeat has a critical role in X-inactivation. Unexpectedly, however, neither RNA-FISH nor RT-PCR could detect the expression of Xist_A RNA even in the tissues where the mutated X is programmed to undergo inactivation. The findings suggest that the A-repeat is involved in either transcriptional upregulation of Xist or stabilization of Xist RNA.

(8) Role of Dnmt3L in gametogenesis

Kenichiro HATA, Maki KUSUMI, Takaaki YOKOMINE, Shinichi TOMIZAWA, En LI[1] and Hiroyuki SASAKI ([1]Novartis)

The Dnmt3L (Dnmt3-Like) gene encodes a protein of 421 amino acid residues and harbors a putative zing finger domain that shares a high degree of homology with the PHD-like domains of Dnmt3a and Dnmt3b. The C-terminal part of Dnmt3L is related to Dnmts, but it does not possess critical motifs for methyltransferase activity. While Dnmt3L-/- mice grow normally, embryos from pregnant Dnmt3L-/- mothers die around E10.5, due to defects in maternal imprints. By contrast, Dnmt3L-/- male mice showed azoospermia and the apoptotic germ cells have methylation defects in paternally imprinted DMRs and IAP retrotransposon sequences (Hata et al. 2006). We speculate that Dnmt3L functions via interactions with Dnmt3a to control de novo methylation of the DMRs and other sequences including retrotransposons. We have now set out to isolate factors that interact with the Dnmt3a/Dnmt3L complex by two-hybrid screen to know the detailed regulatory mechanisms of de novo methylation.

(9) Role of Dnmt3L in placentation

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Although Dnmt3L protein lacks DNA methyltransferase activity, it cooperates with Dnmts to establish methylation imprints. Oogenesis proceeds normally in Dnmt3L-/- female mice but their heterozygous offspring (Dnmt3Lmat-/-) die before midgestation probably due to the lack of maternal imprints. The Dnmt3Lmat-/- embryos showed defective formation of the labyrinth, reduced formation of the spongiotrophoblast layer, excess trophoblast giant cells and insufficient attachment between the chorion layer and ectoplacental cone. Cells of the extraembryonic tissues were arrested but not apoptotic. Dnmt3Lmat-/- trophoblastic stem cells showed a disturbed cell fate in vitro (Arima et al. 2006). Intriguingly, our comparative studies showed that the Dnmt3L gene is present only in the species that have imprinting. The acquisition of Dnmt3L by a common ancestor of eutherians and marsupials may be

closely related to the evolution of imprinting (Yokomine et al., 2006).

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2．佐々木裕之　山梨大学医学部講義　山梨大学医学部講義　山梨大学医学部　6/28
3．佐々木裕之　障害児歯科学　九州大学歯学部講義　九州大学歯学部　7/3
4．佐々木裕之　ゲノム刷り込みの概念と分子機構　横浜市立大学大学院医学セミナー　横浜市立大学医学部　7/5
5．佐々木裕之　Mechanisms of genomic imprinting and transposon silencing in the mammalian germline　第10回グローバルCOEリエゾンラボ研究会　熊本大学発生医学研究センター　12/5
6．佐々木裕之　エピジェネティク・コード　COE特別講義「言語から読み解くゲノムと生命システム」 東京大学柏キャンパス　10/24

POSTER PRESENTATIONS

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2．木村直美，保木裕子，佐々木裕之，佐渡敬「 Xist遺伝子Aリピートの胚発生における役割 」，日本分子生物学会第7回春季シンポジウム，淡路，4/23-4/24
3．佐々木裕之「 哺乳類生殖細胞のインプリンティングと反復配列のサイレンシング 」，第1回日本エピジェネティクス研究会年会「エピジェネティクス研究の現在と未来」，吹田，6/15-6/16
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5．木村直美，保木裕子，佐々木裕之，佐渡敬「 Xist遺伝子Aリピートの胚発生における役割 」，第1回日本エピジェネティクス研究会年会 「エピジェネティクス研究の現在と未来」，吹田，6/15-6/16
6．尼川裕子，保木裕子，佐々木裕之，佐渡敬「 マウス内部細胞塊におけるX染色体再活性化の阻害 」，　第1回日本エピジェネティクス研究会年会 「エピジェネティクス研究の現在と未来」，吹田，6/15-6/16
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31．佐渡敬「マウス胚におけるXist機能ドメインのコード領域の役割」，遺伝研研究会「クロマチン研究会―ゲノム・細胞核から個体発生まで―」，三島，10/26
32．佐々木裕之「マウスの雌雄生殖系列におけるゲノムインプリンティングとトランスポゾン抑制」，特定領域研究「性分化機構の解明」第4回領域会議，掛川，10/29-10/31
33．Yamaguchi, S., Sasaki, H.,Nakatsuji, N., and Tada, T.「Molecular roles of Nanog in mouse germ cell development」，International Symposium on Regenerative Medical Therapy，Kyoto，9/19-9/20
34．Hirasawa, R., Chiba, H., Kaneda, M., Okano, M., Jaenisch, R., Li, E., and Sasaki, H.「Role of DNA Methyltransferases(Dnmts) in Maintenance of the Methylation Imprint during Mouse Pre-implantation Development」，Wellcome Trust Conference on Mouse Molecular Genetics，Hinxton, UK，9/5-9/9
35．Sado,T.「Role of the A-repeat in the Xist gene during mouse development」，Gordon Research Conference「Epigenetics」，New Hampshire，8/5-8/10
36．Sasaki,H.「Genome imprinting mechanisms in the mouse germline and early embryos」，Gordon Research Conference「Epigenetics」，New Hampshire，8/5-8/10
37．佐々木裕之「エピジェネティクス研究の現状」，第1回胎生期エピジェネティクス制御研究所シンポジウム「胎生期発育環境によって疾患の源が刻印される可能性とその対応」，東京，8/25
38．佐々木裕之「エピジェネティクスから見た遺伝学」，第14回日本遺伝子診療学会大会「遺伝子診断による個別化医療を目指して」，愛媛，7/27-7/28
39．Sasaki,H.「Epigenomics in reproduction and development」，The Asian Network of Epigenomics「Epigenomics: Technology, Products, and Obstacles」，Suita，6/14

EDUCATION

1．Whnshaw-Boris, T., Anderson, K., Sasaki, H., Skarnes, B. Wellcome Trust Conference on Mouse Molecular Genetics Hinxton, UK 9/5-9/9

OTHERS

1．佐々木 裕之，3，Journal of Human Genetics Editorial Board（編集委員）
2．佐々木裕之，1，日本生殖再生医学会理事
3．佐々木裕之 ，1，日本人類遺伝学会評議員
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9．佐々木裕之　，1，日本エピジェネティクス研究会副代表幹事

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E. DEPARTMENT OF INTEGRATED GENETICS
E-b. Division of Agricultural Genetics
Keiichi Shibahara

RESEARCH ACTIVITIES

RESEARCH ACIVITIES

(1) Mechanism of nucleosome assembly during DNA repkication

Tetsuya Ono, Yasunari Takami[1], Fumiyuki Sanematsu, Tatsuo Nakayama[1], and Kei-ichi Shibahara

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A newly repicated DNA is assembled into nucleosome soon after the passage of replication fork. This rapid formation of nucleosome is functionally linked to DNA replication machineries and plays a critical role for the maintenance of genome integrity in pvoliferating cells. Two histone binding proteins CAF-1 (Chromatin Assembly Factor-1) and ASF1 (Anti-Silencing Function 1), are involved in some process of this nucleosome assembly reaction. In collaboration with Dr. Nakayama in University of Miyazaki, using CAF-1 and ASF-1-deficine chicken DT4- celllines, we recently showed that without CAF-1 and/or ASF-1 function, S-phase progression was delayed and a rapid nucleosome assembly during DNA replication was disturbed in vivo (Sanematsu, F., et al., J. Biol. Chem., in press, 2006). This is the first direct evidence for the involvement of CAF-1 and ASF1 in a rapid nucleosome assembly during DNA replication in vivo. In addition, we obtained some interesting evidence for that CAF-1 is involved in Chk1-dependent checkpoint pathway after the treatment with HU (Takami, Y., et al., submitted).

(2) Physiological implications of CAF-1 and CAF-1-dependent nucleosome assembly in higher eukaryotes

Tatsuya Ono, Hidetaka Kaya[1], Shin Takeda[2], Tetsuji Kakutani, Takashi Araki[1], Kei-ichi Shibahara

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The Genetic approachof Arabidopsis is a powerful tool to see physiological implication of CAF-1 and CAF-1 dependet nucleosome assembly in higher eukaryotes. We have analyzed loss-of-function mutants oa caf-1 (fasciata: fas) in Arabidopsis and have shown that the fas mutants displayed severely disturbed cellular and functional organization of both meristems (Kaya et al., Cell, 2001; Takeda, et al., Genes Dev., 2004). We recently showed

that transcriptional gene silencing (TGS) of endogenous CACTA transposons was relased infrequently in a stochastic manner in fas, without decreasing DNA methylation. Other endogenous silent genes at different chromosomal site were also transcriptionally activated non-concomitantly with each other. Furthermore, TGS of the silent transgene Beta-glucuronidase (GUS) was also de-pressed randomly in fas mutant plants, irrespectively of developmental abnormalities, and the activated state of GUS was aintained during growth to produce clusters of cells expressing GUS (Ono et al., Genes Cells, 2006). Taken together, we strongly suggest that CAF-1 ensures stable ineritance of epigenetic states through multiple rounds of cell divisions and that defects in CAF-1 functions explain in the stochastic occurrence of pleiotropic phenotypes in the fas mutants.

(3) Histone macroH2A-mediated formation of transcriptionally repressed states of chromatin

Yuya Ogawa[1], Hitoshi Nishijima, and Kei-ichi Shibahara

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The unusual hitone variant macroH2A (macroH2A) is predicted to be functionally associated with transcriptional repression as it appears to be enriched in the inactive X chromosome by immunostaining. However, molocular function of macroH2A in mdulating chromatin structure remains unknown. To reveal the roles of macroH2A, we purified macroH2A-containing nucleosome by afinity purification with anti-epitope tag antidodies, and eventuaaly, we found mono-ubiquitinated form of macroH2A and determined the ubiquitinated sites inmacroH2A (Ogawa, Y. et al., 2005). We are currently clarifying the unction of these modifications and trying to isolate the molecules enriched in and associate with macroH2A-containing nucelosomes.

(4) Analysis of S. pombe RanGAP SpRna1 protein in the heterochromatin assembly via histone H3

Hitoshi Nishijima, Ayumi Kusano[1], Tomoyiki Ohba[1], Hideo Nishitani[1],Kei-ichi Shibahara, Takeharu Nishimoto[1]

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We have isolated temperature-sensitive mutants of the RanGAP homologue, Sprna1, in S. pombe. Spran1^{ts} srains display a strong defect in mitotic chromosome segregation (Kusano, A., et al., Mol. Biol. Cell, 2004). This phenotype is suppressed by theoverexpression of C1r4, which methylated Lys9 of histone H3 (H3K9). We found that histone H3 controls the RanGAP activity of SpRnal to prevent disruption of the RanGTP/GDP gradient and that SpRna1 enhances the activity of the C1r4-dependent methylation of histone H3K9 (Nishijima, H., et al., Mol. Biol. Cell, 2006). In addition, we had siolated another suppressor, Snf2RS, which is likely to be a novel member of the SNF2 family inolved in the Ran GTPase cycle (Ohba, T., et al., in preparation).

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1．西嶋仁,柴原慶一　ヒト細胞における遺伝子発現誘導型ノックアウト細胞株樹立法の開発と目的遺伝子の機能解析と展望　宮崎大学大学院医学研究科（招待講演） 1/29
2．柴原慶一　ヒト遺伝子改変細胞株樹立システムとその創薬開発への活用　医学生物学研究所セミナー（招待講演） 医学生物学研究所　7/7
3．柴原慶一　ヒトNalm-6細胞を用いた誘導型遺伝子発現ノックアウト細胞株樹立法の開発および展望　静岡県がんセンターセミナー（招待講演） 静岡県がんセンター研究所　4/26

POSTER PRESENTATIONS

1．井原詠子,牧野美幸,西嶋仁,柴原慶一,古川和弘,掘米恒好 「 クロマチン間領域局在タンパク質ISP36の結合タンパク質の検索 」， 日本分子生物学会、日本生化学会 ， 横浜 ， 12/11-12/15
2．小野達也,柴原慶一 「 ヒト細胞における条件的ノックアウト細胞株の樹立とヒト細胞における条件的ノックアウト細胞株の樹立とこれを用いたヒト DDM1の解析 」，クロマチン研究会 ，三島（国立遺伝学研究所），10/25
3．西嶋仁,小野達也,足立典隆,小山秀機,柴原慶一 「 ヒト細胞における誘導型ノックアウト細胞株樹立法の開発とhDDM1の染色体維持機構の解 析 」，第２４回染色体ワークショップ ，唐津，1/31-2/2
4．小野達也，柴原慶一 「 ヒト細胞における条件的ノックアウト細胞株の樹立とヒト細胞における条件的ノックアウト細胞株の樹立とこれを用いたヒトDDM1の解析 」， クロマチン研究会 ，三島市，10/25

PATENT

1．JP2007/070665，テトラサイクリン誘導型遺伝子発現細胞株および条件的遺伝子ノックアウト細胞株の製造方法ならびにその用途 ， 柴原慶一、小野達也、西嶋仁 ， 大学共同利用機関法人情報・システム研究機構
2．2007-119791，標的組換え細胞とランダム組換え細胞とを判別する方法及び用途 ，柴原慶一，西嶋　仁，国田嘉元」，大学共同利用機関法人情報・システム研究機構

OTHERS

1．柴原慶一，3，BioScience TrendsのEditorial board

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E. DEPARTMENT OF INTEGRATED GENETICS
E-b. Division of Agricultural Genetics
Tetsuji Kakutani

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1． Saze H,Kakutani T （2007） Heritable epigenetic mutation of a transposon-flanked Arabidopsis gene due to lack of the chromatin-remodeling factor DDM1， **EMBO Journal.** ，26，3641 - 3652
2． Ito H,Miura A,Takashima K,Kakutani T （2007） Ecotype-specific and chromosome-specific expansion of variant centromeric satellites in Arabidopsis thaliana， **MGG**，277，23 - 30
3． Kinoshita Y,Saze H,Kinoshita T,Miura A,Soppe W,Koornneef M,Kakutani T （2007） Control of FWA gene silencing in Arabidopsis thaliana by SINE-related direct repeats.， **Plant J**，49，38 - 45

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2．藤本龍、木下由紀、高嶋和也、木下哲、三浦明日香、角谷徹仁「インプリント遺伝子FWAの構造と発現制御の進化：反復配列の役割について」， 第1回日本エピジェネティクス研究会年会，大阪，6/15-16
3．Saze, H., Kakutani, T.「Genetic dissection of DNA methylation at the BONSAI locus」, Gordon Research Conference “Epigenetics”，Holderness，8/5-10
4．Kakutani T「Epigenetic inheritance of developmental variation, transposon activity, and DNA methylation in Arabidopsis thaliana」，日本分子生物学会年会第7回春期シンポジウム，淡路市，4/23-24
5．角谷徹仁「シロイヌナズナにおけるエピジェネティックな遺伝」，日本エピジェネティクス研究会第1回年会，大阪，6/15-6/16
6． 角谷徹仁「シロイヌナズナにおけるエピジェネティックな遺伝」， オミックスワールドの全貌～ゲノミクスからメタボロミクスまで～，生駒市，9/27-28
7．Kakutani T「Epigenetic inheritance of developmental variation, transposon activity, and DNA methylation in Arabidopsis thaliana」， Developmental Biology and Biomedical Research，Agra, India，10/18-1019
8．角谷徹仁「DNAメチル化とゲノム動態」，植物生理学会シンポジウム「植物トランスクリプトーム解析の新展開」，，3/28
9． 中村みゆき、三浦明日香、木下由紀、木下哲、加藤政臣、角谷徹仁 「 継代によるCACTA1トランスポゾンの転移活性変化」，日本植物生理学会，，3/29
10． Saze H, Kakutani T 「BONSAI: LOSS-OF-FUNCTION EPIGENETIC MUTATION INDUCED IN THE DDM1 (DECREASE IN DNA METHYLATION) BACKGROUND」，Cold

Spring Harbor Meeting, Plant Genomes , Cold Spring Harbor, NY , 3/15-3/18

OTHERS

1．角谷徹仁，1，日本エピジェネティクス研究会幹事
2．木下哲，2，植物生理学会奨励賞

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E. DEPARTMENT OF INTEGRATED GENETICS
E-c. Division of Brain Function
Tatsumi Hirata

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1． Fouquet, C., Di Meglio, T., Ma, L., Kawasaki, T., Long, H., Hirata, T., Tessier-Lavigne, M., Chedotal, A., Nguyen-Ba-Charvet, K.T. （2007） Robo1 and robo2 control the development of the lateral olfactory tract.， **J. Neurosci.**，27，3037 - 3045

ORAL PRESENTATION

1．平田たつみ　神経発生学　集中講義　　名古屋大学・理学部　1/16-17

POSTER PRESENTATIONS

1．川崎能彦,平田たつみ「 Guidance of main and accessory olfactory bulb axon 」，第40回日本発生生物学会，福岡，5/28
2．鈴木郁夫,平田たつみ,五條堀孝 「 大脳皮質層構造の進化的起原 」，第9回　日本進化学会，京都，8/31
3．伊藤圭祐,川崎能彦,平田たつみ「 Repulsive effect of Sema3F on lot cells, the guidepost neurons in the lateral olfactory tract 」，第30回日本神経科学大会，横浜，9/9
4． 鈴木郁夫,平田たつみ,五條堀孝 「 大脳皮質層構造形成の進化的起原 」，第30回　日本分子生物学会，横浜，12/11
5．平田たつみ「 4回膜貫通タンパク質M6aが引き起こす軸索伸長停止反応 」，日本発生生物学会　秋季シンポジウム，岡崎，11/6

OTHERS

1．平田たつみ，1，日本神経科学学会男女共同参画推進委員長
2．平田たつみ，3，科学技術振興機構　男女共同参画アドバイザリーコミッティー

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F. GENETIC STRAINS RESEARCH CENTER
F-a. Mammalian Genetics Laboratory

Toshihiko Shiroishi

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．城石俊彦（2007）マウス亜種間コンソミック系統によるゲノム機能解析，学術月報，60，21 - 27
2．Tanaka S., Tamura M., Aoki A., Fujii T., Komiyama H., Sagai T. and Shiroishi T.（2007）A new *Gsdma3* mutation affecting anagen phase of first hair cycle，**Biochem. Biophys. Res. Commun.**，359，902 - 907
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4．Aiba, A., Inokuchi, K., Ishida, Y., Itohara, S., Kobayashi, K., Masu, M., Mishina, M., Miyakawa, T., Mori, H., Nakao, K., Obata, Y., Sakimura, K., Shiroishi, T., Wada, K. and Yagi, T.（2007）Mouse liaison for integrative brain research，**Neurosci. Res.**，58，103 - 104
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2 . 田村勝、田中成和、藤井智明、加藤依子、 城石俊彦 「 Gasdermin family遺伝子群とヒト疾患 」, 日本遺伝学会第79回大会 , 岡山 , 9/19-21
3 . 田中成和、三浦郁生、吉木淳、加藤依子、横山晴香、篠木晶子、桝屋啓志、若菜茂晴、田村勝、城石俊彦「 突然変異マウスを用いたケラチン・ヘテロダイマーの遺伝学的解析 」, 日本遺伝学会第79回大会 , 岡山 , 9/19-21
4 . 高田豊行, 三田晃彦, 前野哲輝, 森脇和郎, 米川博通, 城石俊彦 「 マウス亜種間コンソミック系統群を用いたエネルギー代謝関連形質の遺伝解析 」, 日本遺伝学会第79回大会 , 岡山 , 9/19-21
5 . 山本博美, 水品洋一, 山谷宣子, 田村勝, 城石俊彦 「 絶滅したbactrianus亜種由来野生マウス系統の凍結精子を用いた復元の試み 」, 平成18年度日本実験動物技術者協会関東支部総会 第32回懇談会 , 東京 , 2/17
6 . 岡垣郁香, 山谷宣子, 三田旻彦, 高田豊行, 田村勝, 城石俊彦 「 マウス亜種間コンソミック系統凍結胚の融解移植成績の検討 」, 平成18年度日本実験動物技術者協会関東支部総会 第32回懇談会 , 東京 , 2/17
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8 . Tanaka, S., Miura, I., Yoshiki, A., Kato, Y., Masuya, H., Wakana, S., Tamura, M., Shiroishi, T. 「 Analysis of three wavy hair mouse mutations support that the α-helix termination motif is essential for assembly of the type II and the type I IRS keratin proteins 」, 日本発生生物学会第40回大会 , 福岡 , 5/28-5/30
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11 . Shiroishi, T. 「 Functional genomics of genomics of complex trains with inter-subspecific consomic strains 」, 21th International Mammalian Genome Conference , Kyoto , 10/28-11/1
12 . Shiroishi, T. 「 Functional Genomics of Complex Traits Based on Mouse Inter-Subspecific Differences 」, 第23回国際生物学賞シンポジウム , Kyoto , 10/29
13 . 城石俊彦 「 統計・情報技術を駆使したゲノム多型と表現型多様性の連関解析システムの開発 」, 融合研究シンポジウム「地球と生命の新パラダイム創造への挑戦 , 東京 , 10/29
14 . Oka, A., Takada, Y., Koseki, H., Mita, A., Moriwaki, K., Shiroishi, T.「 Meiotic arrest in males of the B6.ChrXMSM consomic strain 」, 21th International Mammalian Genome Conference , Kyoto , 10/28-11/1
15 . Tamura, M., Tanaka, S., Fujii, T., Kato, Y., Shiroishi, T. 「 Genomic analysis of Gasdermin A (*Gsdma*) and Gasdermin C (*Gsdmc*) loci in the mammalian genome 」, 21th International Mammalian Genome Conference , Kyoto , 10/28-11/1
16 . Hosoya, M., Amano, T., Yada, Y., Sagai, T., Tamura, M., Shiroishi, T. 「 Genome alteration of a polydactyly mutation *Rim4*. 」, 第30回日本分子生物学会年会・第80回日本生化学会大会 合同大会 , 横浜 , 12/11-15
17 . 田村勝、田中成和、藤井智明、加藤依子、城石俊彦 「 マウスGasdermin (*Gsdm*) family遺伝子の進化的多様性 」, 第30回日本分子生物学会年会・第80回日本生化学会大会 合同大会 , 横浜 , 12/11-15
18 . 田中成和、田村勝、桝屋啓志、若菜茂晴、城石俊彦 「 ENU誘発による優性突然変異マウスを用いたGasdermin A3の変異解析 」, 第30回日本分子生物学会年会・第80回日本生化学会大会 合同大会 , 横浜 , 12/11-15
19 . 藤井智明、田村勝、城石俊彦「 Gasdermin D (*Gsdmd*)の発現および機能解析 」, 第30回日本分子生物学会年会・第80回日本生化学会大会 合同大会 , 横浜 , 12/11-15
20 . Takada, T., Ebata, T., Narita, T., Shin-I, T., Abe, K., Sakaki, Y., Toyoda, A., Sagai T., Mita, A., Moriwaki, K., Kohara, Y. and Shiroishi, T.「 Whole genome shotgun sequencing of M. M. Molossinus-derived MSM/Ms and detection of vast amount of SNPs against C57BL/6. 」, 21th International Mammalian Genome Conference , Kyoto , 10/28-11/1

21．Shiroishi, T.「Genome anatomy of C57BL/6 and exploration of SNPs for energy metabolism」, EUMODIC First Annual Meeting , Barcelona , 2/22-2/23
22．田村　勝「上皮形態・恒常性維持に関与する新規遺伝子ファミリー“Gasdermin”」, 第21回モロシヌス研究会 , 神戸 , 6/29-6/30
23．高田　豊行「B6.MSMコンソミック系統を用いた代謝関連表現型解析」, 国立遺伝学研究所研究会「多因子疾患の遺伝解析：糖尿病・メタボリックシンドロームを中心に」, 三島 , 3/16-3/17
24．高田　豊行「アレルギー疾患とそのモデル：アトピー性皮膚炎を中心に.」, 第54回日本実験動物学会総会 , 東京 , 5/23-5/25
25．城石　俊彦「生命システム理解のための動物実験と実験技術者の役割」, 日本実験動物技術者協会　関東支部　平成18年度総会・第32回談話会 , 東京 , 2/7
26．城石　俊彦「ゲノム解読から見えてきた実験用マウスの起源：新たな実験用マウス系統の開発と利用」, 第6回四国免疫フォーラム , 愛媛 , 7/14
27．城石　俊彦「マウスモデルから歯形成を考える」, 日本小児歯科学会第45回大会 , 東京 , 7/19-7/20
28．Oka, A.「Disruption of genetic interaction between two autosomal regions and the X chromosome causes reproductive isolation between mouse strains derived from different subspecies」, The Fifth Okazaki Biology Conference: ”Speciation and Adaptation” , Kakegawa , 3/11-3/16

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2．田村　勝（2007）マウスを使って実験をしよう ”マウス解剖学入門” **Medical Bio**　0 - 0

PATENT

1．2007-003398 , モデルマウス、その製造方法およびその用途 , 城石俊彦、田村勝、藤井智明 , 大学共同利用機関法人情報・システム研究機構

OTHERS

1．城石俊彦 , 1 , 日本遺伝学会評議員
2．城石俊彦 , 1 , 実験動物学会評議員
3．城石俊彦 , 1 , Editorial board of Mammalian Genome
4．城石俊彦 , 1 , Advisory Board of The European Mouse Disease Clinic (EUMODIC)
5．城石俊彦 , 1 , Editorial board of DNA Research
6．城石俊彦 , 1 , Editor of Genes & Genetic Systems
7．城石俊彦 , 1 , "The Scientific World" Associate editor for Genetics

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Yumiko Saga

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1 . Suzuki ,A., Tsuda, M., and Saga, Y. (2007) Functional redundancy among Nanos proteins and a distinct role of Nanos2 during male germ cell development. , **Development** , 134 , 77 - 83
2 . Kokubo ,H., Miyagawa-Tomita, S.,and Saga Y. (2007) Hesr1/Hey1 and Hesr2/Hey2 regulate atrial-ventricular boundary formation in the developing heart through the repression of Tbx2. , **Development** , 134 , 747 - 755
3 . Moriyama ,A., Kii ,I., Sunabori, T., Kurihara, S., Takayama ,I., Shimazaki, M. ,Tanabe, H., Oginuma ,M., Fukayama, M., Matsuzaki, Y., Saga, Y., and Kudo, A. (2007) GFP transgenic mice reveal active canonical Wnt signal in neonatal brain and in adult liver and spleen. , **Genesis** , 45 , 90 - 100
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5 . Morimoto ,M., Sasaki, N., Oginuma, M., Kiso, M., Igarashi, K., Aizaki, K., Kanno, J.,and Saga ,Y. (2007) The negative regulation of Mesp2 by mouse Ripply2 is required to establish the rostro-caudal patterning within a somite. , **Development** , 134 , 1561 - 1569
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POSTER PRESENTATIONS

1．岡村佳明,相賀 裕美子,「 Pofut1 ノックアウトマウスを用いたNotch シグナルの機能解析 」,第30回日本分子生物学会、第80回日本生化学会，横浜，12/11～14
2．岡村佳明,相賀 裕美子,「 Pofut1 ノックアウトマウスを用いたNotchシグナルの解析 」,第30回日本分子生物学会、第80回日本生化学会，横浜，12/11～14
3．小久保博樹,宮川-冨田幸子,相賀 裕美子「 心房と心室の境界領域形成におけるHesrの役割 」,第30回日本分子生物学会、第80回日本生化学会，横浜，12/11～14
4．Yumiko Saga「 The spatio-temporal regulation of somitogenesis 」, The Notch Meeting，Athens，9/23-9/27
5．Yumiko Saga 「 The Mesp2 transcription factor establishes segmental borders by suppressing Notch activity 」, KORNBERG symposium，Tokyo，7/23-24
6．Yumiko Saga 「 The spatio-temporal regulation of the periodic Mesp2 expression 」, Pan-American SDB Congress，Cancun，6/16
7．相賀 裕美子 「 体節形成過程で機能する転写因子Mesp2の時空的制御機構 」, 分子・細胞・組織操作を目指したシステム細胞工学，東京，8/11
8．鈴木 敦, 佐波理恵、相賀裕美子 「 生殖細胞の性分化におけるNanos2の機能解析 」, 第9回RNA meeting シンポジウム，名古屋，7/28
9． Atsushi ,Suzuki.,Yumiko,Saga 「 Nanos2 Suppresses Meiosis and Promotes the Acquisition of Male Germ Cell Identity 」, CDB Symposium 2007，神戸，3/26-28
10．佐々木伸雄, 森本充, 荻沼政之,相賀 裕美子 「 Mesp2の負の制御因子Ripply2による体節の前後極性決定機構の解析 」, 第40回 日本発生生物学会、第59回 日本細胞生物学会合同大会，福岡，5/28～30
11．柴田朋子,相賀 裕美子,赤坂甲治「 ウミシダ（棘皮動物）における分節構造形成の分子的解析 」, 第40回 日本発生生物学会、第59回 日本細胞生物学会合同大会，福岡，5/28～30
12．Masayuki Oginuma,Yumiko Saga「 A negative feedback regulation of Tbx6 by Mesp2 is critical to reset the spatial information and is required for the periodic somitogenesis 」, 第40回 日本発生生物学会、第59回 日本細胞生物学会合同大会，福岡，5/28～30
13． Yu Takahashi,Atsuya Takagi,Jun Kanno,Shuichi Hiraoka,Haruhiko Koseki,Alan Rawls,Yumiko Saga「 Transcription factors Mesp2 and Mesp2 and Paraxis have critical roles in axial musculoskeletal formation 」, 第40回 日本発生生物学会、第59回 日本細胞生物学会合同大会，福岡，5/28～30
14． Yukuto Yasuhiko,Seki Haraguchi,Satoshi Kitajima,Yu Takahashi,Jun Kanno, Yumiko Saga「 Tbx6 controls Mesp2 expression in forming somites 」, 第40回 日本発生生物学会、第59回 日本細胞生物学会合同大会，福岡，5/28～30
15．Yoshiaki Okamura,Yumiko Saga「 The role of Notch signaling in the enteric nervous system development 」, 第40回 日本発生生物学会、第59回 日本細胞生物学会合同大会，福岡，5/28～30
16．Yumiko Saga「 THE SPATIO-TEMPORAL REGULATION OF SOMITOGENESIS 」, IMGC2007(第21回国際哺乳類ゲノム会議)，京都，10/28～11/1
17． Yumiko Saga 「 Translation of the Temporal Information Provided by the Segmentation Clock 」, THE TERATOLOGY SOCIETY 47th Annual Meeting，Pittsburgh，6/23-6/28
18．Yumiko Saga「 Function of Nanos Proteins in Mouse Germ Cell Development 」, The Fifth NIBB-EMBL Meeting "Cell and Developmental Biology"，Okazaki，5/24-5/26
19． 小久保博樹,宮川-冨田幸子,相賀 裕美子 「 Molecular mechanism for atrioventricular boundary formation:Regulation by Hesr genes. 」, 第30回日本分子生物学会、第80回日本生化学会，横浜，12/11～14
20． 佐々木伸雄,木曾誠,相賀 裕美子 「 マウス体節形成時における転写因子Mesp2の分子機能の解析 」, 第30回日本分子生物学会、第80回日本生化学会，横浜，12/11～14

EDUCATION

1．Matuno K, Saga Y Notch シグナル研究会 遺伝研研究会 三島 7/5-7/6

F. GENETIC STRAINS RESEARCH CENTER
F-c. Mouse Genomics Resource Laboratory
Tsuyoshi Koide

RESEARCH ACTIVITIES

Aberrant neurological development caused by genetic incompatibility

Juzoh Umemori1, Ryouta Kondou1, Shigeki Yuasa2, Tsuyoshi Koide1

1MGRL, Natl Inst Genet, Transd Res Integ Cent, Res Org Info Syst, Mishima, Japan, 2Natl Cent Neuro Psy, Tokyo, Japan

There have been many reports on neurological disease involving tremor and ataxia. Several familial studies have identified causative genes and mutations related to the disease. However, most of the neurological diseases are so complex and multifactorial that affected by multiple genes. Furthermore, some sporadic neurological diseases that showing low heritability might be caused by aberrant epistatic interaction of multiple genes. Thus, it is important to analyze genetic basis of complex disease using an animal model. In the present study, we analyzed mice that exhibit neurological defect to elucidate an aberrant genetic interaction which is called as genetic incompatibility.
In our laboratory, many mouse strains including wild-derived strains were crossed and analyzed for behavioral traits to identify quantitative trait loci related to several kinds of behaviors. In the course of these studies, we found aberrant mice indicating defective growth, degenerative eye development, tremor (FURUE) and ataxia. The aberrant mice, FURUE emerged in a F2 (KLF2) population made between two wild-derived mouse strains, BLG2 and KJR. Because both BLG2 and KJR never indicate such neurological and developmental defects, this aberration seemed to be caused by genetic incompatibility. We analyzed the genotype of 160 FURUE mice in the KLF2 population using microsatellite markers, and found that all the FURUE mice are homozygote of KJR allele at the small region of chromosome 13. We analyzed the genotype of this locus in the whole KLF2 progeny including normal mice and FURUE, and found that a half of progeny which carry homozygous KJR allele at this locus is lethal, one-forth of that is normal, and remaining one-forth exhibits FURUE phenotype. These results indicated that this locus is one of the factors causing FURUE and lethality by genetic incompatibility. Thus, the locus on chromosome 13 was named as *Genetic incompatibility 1 (Genic1)*. Furthermore, allelic frequency of two loci on chromosome 3 and 4 did not obey the Mendelian's ratio and exhibited high ratio of BLG2 homozygous allele. Thus, these two loci, *Genic2* on chromosome 3 and *Genic3* on chromosome 4 (*Genic2* $^{L/L}$ and *Genic3* $^{L/L}$), are expected as other genetic elements which might interact with the KJR allele of Genic1 (*Genic1* $^{K/K}$).
Many kinds of tremor and ataxic mice, such as shiverer and shaker are known to have defect in myelin structure in central or peripheral nervous system (CNS and PNS). Electron microscopic analysis indicated that adult FURUE mice also showed dismyelination in the

white matter of spinal cord, corpus callosum and optic nerve. Adult FURUE mice showed that the layers of myelin are reduced comparing to that of normal KLF2. Furthermore, some myelinated axons are failed to compact cytoplasm of oligodendrocyte that form myelin sheath in the CNS. These results suggested that FURUE is defective in myelination of axon especially in interaction mechanism between myelin and axon, or in development of oligodendrocyte.

We have established a Genic1 congenic strain carrying *Genic1* $^{K/L}$ on the background of BLG2. The *Genic1* $^{K/K}$ congenic mice indicate similar phenotype as FURUE in KLF2. We have narrowed down the *Genic1* locus to 2.4 Mbp genomic region. Observation of *Genic1* $^{K/K}$ congenic mice showed that onset of growth defect and lethality initiated between embryonic 12.5 and 18.5 day. Furthermore, histological observations showed that neonatal mice (P0) of *Genic1* $^{K/K}$ congenic mice have cardiac abnormalities. One of the mice showed that ectopic and excess heart septums, thus there are partially three cardiac ventricules. Another *Genic1* $^{K/K}$ congenic mice also showed some kind of septal defects. These results imply that lethality in FURUE mice caused by such cardiac defects at late embryonic stage.

There are approximately fifty genes in *Genic1* in the database of NCBI build36.1, but no genes related to the neural development or cardiac diseases have been reported. Furthermore, there are several gaps in the region, probably because of difficulty of assembling BAC sequence due to many duplicated sequences. Thus, this region needs to be characterized by re-assembling BAC sequences in this region.

Forward genetics approach toward complex traits using consomic mouse strains established from C57BL/6J and wild-derived MSM

Aki Takahashi, Akinori Nishi, Ayako Ishii, Toshihiko Shiroishi, & Tsuyoshi Koide

Individual differences in behavior are arising from quantitative genetic variations in addition to environmental factors. We aimed to reveal those genetic mechanisms underlying individual divergence of behavior by using consomic strains (CSSs) of mouse established from C57BL/6J and MSM. By examining a panel of CSSs on many behavioral traits, such as spontaneous activity, anxiety-like behavior, pain sensitivity, and social behavior, we systematically mapped the chromosomes that have a locus or loci affecting those phenotypes.

To dissect complex traits into fine genetic element, we focused on one strain B6-17MSM, which have substituted chromosome 17 from MSM. B6-17MSM showed reduced novelty-induced activity and increased risk-assessment behavior, but no differences in their home-cage activity or motor coordination compared to C57BL/6J. They also showed increased fear memory in the fear conditioning test. Thus, it was expected that there are genetic locus/loci related to emotionality on the chromosome 17. They also exhibited highly increased social interaction behavior. In addition, we found that B6-17MSM had “hydrocephalus-like” enlarged brain ventricle size. To identify genetic loci related to those phenotypes, we established a series of congenic mouse strains of B6-17MSM. Analysis of congenic strains successfully revealed two novel genetic loci for the brain ventricle size in the proximal region of chromosome 17. In contrast, our result suggested that genetic interaction between two or more loci is required to show increased social contact as B6-17MSM. There are multiple loci for the behaviors associated with novelty-induced activity and two genetic loci for risk-assessment. We focused on one locus around telomeric region, which had as strong effect on the emotionality-related traits as B6-17MSM but independent from hydrocephalus phenotype, and are trying to narrow this locus down to identify the gene.

We are also interested in inter-male aggression. We found male of one consomic strain B6-15MSM, which have MSM chromosome 15, showed increased aggressive behavior in resident-intruder test. Behavioral analysis showed that the increased aggression of B6-

15MSM was mainly caused by the effect of intruder. Several congenic strains of B6-15MSM were established to identify the genetic locus/loci related to the aggressive behavior, and revealed that there are several genetic loci that increased or decreased the aggressive behavior on the chromosome 15.

PUBLICATIONS

Papers

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ORAL PRESENTATION

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POSTER PRESENTATIONS

1．Umemori, J., Kondou, R., Uno, T., Yuasa, S., Koide, T.「Aberrant neurological development caused by genetic incompatibility between two wild-derived mouse strains」, 21st International Mammalian Genome Conference，Kyoto，10/28-11/1
2．Takahashi, A., Nishi, A., Ishii,A., Shiroishi, T., Koide, T.「Systematic analysis of behavioral traits using consomic mouse strains established from C57BL/6J and wild-derived MSM」, 21st International Mammalian Genome Conference，Kyoto，10/28-11/1
3．梅森十三，近藤亮太，湯浅茂樹，小出剛「遺伝的不適合による神経発達異常」，第30回日本神経科学大会，横浜，9/10-12
4．若菜茂晴，山田郁子，和田由美子，古瀬民生，高雄啓三，中西和男，高橋阿貴，小出剛，宮川剛，桝屋啓志「マウス行動実験のためのプロトコールデータベースの開発」，第30回日本神経科学大会，横浜，9/10-12
5．高橋阿貴，富原一哉，城石俊彦，小出剛「C57BL/6JとMSM系統から作出されたコンソミックマウス系統を用いた攻撃行動の遺伝学的解析」，第30回日本神経科学大会，横浜，9/10-12
6．高橋阿貴，石井亜矢子，城石俊彦，小出剛「17番染色体コンソミック系統を用いた情動性の遺伝学的解析」，第67回日本動物心理学会，東京，10/7-8
7．近藤亮太，梅森十三，宇野毅明，小出剛「髄鞘形成異状をもたらす遺伝的不適合の原因遺伝子座Genic1の解析」，第30回日本分子生物学会，横浜，
8．石井亜矢子，西明紀，高橋阿貴，城石俊彦，小出剛「コンソミック系統を用いたマウスの活動性に関わる遺伝的メカニズムの解析」，第30回日本分子生物学会，横浜，12/11-15
9．Takahashi, A., Ishii, A., Nishi, A., Shiroishi, T., Koide, T.「Forward genetics approach toward complex traits using consomic mouse strains established from C57BL/6J and wild-derived MSM」, The International Behavioural and Neural Genetics Society Annual Meeting，Doorwerth, The Netherland，5/21-25
10．Umemori, J., Nishi, A., Takahashi, A., Kawasaki, Y., Lionikas, A., Blizard, D.A., Koide, T.「QTL analysis of differences of activities in home-cage and open-field between KJR and B6 mouse strains」, 6th Annual Meeting of the Complex Trait Consortium，Braunschweig，5/26-29

BOOK

1．高橋阿貴、小出剛（2007）野生マウスの行動と遺伝子　遺伝　0 - 0
2．小出剛（2007）マウスを使って実験をしよう　メディカルバイオ　0 - 0
3．小出剛（2007）野生由来マウス系統の遺伝的多様性を利用した行動の遺伝学的解析　岡山実験動物研究会第**23**号　10 - 16

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F. GENETIC STRAINS RESEARCH CENTER
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Noriyoshi Sakai

RESEARCH ACTIVITIES

(1) Gene targeting system with RNA interference (RNAi) in zebrafish

Minori Shinya, Kayo Kobayashi, Mika Tokumoto, Kimiko Saka, Aki Masuda and Noriyoshi Sakai

Gene silencing via small interfering RNAs (siRNAs) has proved to be a useful tool in studying gene function in plants, invertebrates and mammalian systems. To date, gene silencing effects of siRNAs have confirmed in zebrafish, which is an emerging model for developmental and diseases analysis. However, the effects were temporal (only in early developmental stages) and sometimes mosaic in an embryo because of the method injecting siRNAs into the one-cell stage of embryos. We recently succeeded in the production of transgenic zebrafish from in vitro-cultured sperm. The advantage of this technique is that the mosaicism inherent in other conventional transgenic methods is avoided. Our aim in the present study is the establishment of a rapid system with cultured sperm to generate transgenic zebrafish for gene silencing by siRNA.
As targeted genes, *sonic hedgehog* (*shh*) and *green fluorescent protein* (*gfp*) were selected because of their clear silenced phenotypes. To determine the best sequence of siRNA for the specific suppression of each gene, we tested seven sequences of siRNA for shh and one for gfp by injection of the siRNA into a one-cell stage embryo. Northern blot and real-time PCR analyses for the siRNA-injected embryos revealed that two sequences for *shh* siRNA (sishh) and one for *gfp* siRNA (sigfp) suppressed each transcript. Embryos injected with one of the sishh showed off-targeting effects by injection of higher dose, but exhibited similar phenotypes with shh mutants in lower dose injection. The other sequence of sishh did not affect the phenotype. The sigfp-injected embryos were also developed normally. We are currently working on the construction of retroviruses that express, by zebrafish U6 promoter, a short hairpin RNA (shRNA) which is processed to generate siRNA. By infecting this retroviral vector to in vitro cultured-male germ cells, we are going to produce the transgenic zebrafish with foreign DNA encoding shRNA.

(2) Analysis of factors of Sertoli cells to support male germ cell development

Yuichi Ozaki, Aki Masuda and Noriyoshi Sakai

Sertoli cells are important to germ cells in everything from male sex-determination to spermatogenesis. In spermatogenesis, Sertoli cells interact directly with germ cells in the testis to induce the complex process required for the production of functional sperm. These cells mediate the production of many molecules as well as cell junctions and adhesion. The function of many of these molecules and the regulation of gene expression remain unclear. We recently established two testicular cell lines of zebrafish with distinct functions to support

the development of male germ cells. The lines, ZtA6-2 and ZtA6-12, showed almost the same characteristics as Sertoli cells, but exhibited distinctive features when male germ cells were co-cultured with each line as feeders: the function of the ZtA6-2 cells was directed to stimulate the proliferation of spermatogonia, and ZtA6-12 to stimulate the differentiation into sperm.
These cell lines facilitate investigation of Sertoli cell molecules that contribute to the proliferation and differentiation of spermatogonia. To investigate specific factors of Sertoli cells, we performed the microarray analysis between ZtA6-2 cells and ZtA6-12 cells, and developed a protocol for frozen sections of a zebrafish testis. The section kept the testicular structure enough to determine each developmental stage of germ cells and showed fine positive signals both in *in situ* hybridization and in immunohistochemistry. In a zebrafish testis, Sertoli cells constitute a cyst structure in which single A-type spermatogonium develops and differentiates synchronously. This characteristic makes it easy to determine the stages of Sertoli cells corresponding to the stages of germ cells. We are now producing stage-specific markers of antibodies for germ cells, and will screen cDNAs that were found in the microarray analysis.

(3) Culture condition for zebrafish spermatogonial stem cells

Kenji Saito and Noriyoshi Sakai

In zebrafish, a culture system using primary cultures of male germ cells on a Sertoli cell line, in which the differentiation from spermatogonia to functional sperms can occur in vitro, allows us to generate transgenic zebrafish lines rapidly through a simple in vitro fertilization using transfected sperm. However, the proliferation of spermatogonial stem cells (SSCs) was not observed under the culture conditions. Our aim of this study is to identify the morphogenic characteristics of SSCs in zebrafish testis, and a culture condition to proliferate SSCs with newly isolated Sertoli cell line as feeder cells.
When zebrafish were treated with busulfan, we observed decline in the amount of differentiated types cells, such as spermatocytes and spermatids, and increase of A type spermatogonia. After once germ cells in the testis became only A type spermatogonia and sperm, type B spermatogonia appeared. The testis recovered spermatogenesis after 1 month and the fish became fertile. When we used enzymatically dissociated cells of testes that have only A type spermatogonia and sperm, the germ cells proliferated on newly isolated Sertoli cell line, ZtA6-6. Morphology of the germ cells resembles to the A type spermatogonia of paraffin section, and did not change during the culture. Furthermore, the cells expressed a germ cell marker gene *vas*, and asynchronous proliferations of the germ cells were observed by BrdU incorporation experiments. These results indicate that some or all of A type spermatogonia have the property of stem cells. Identification of SSCs is under investigation in combination with busulfan treatment and BrdU incorporation. We are also analyzing the effect of several growth factors to stimulate proliferation of SSCs toward better culture conditions.

(4) Analysis of the ability of cultured embryonic cells derived from different developmental stages to induce the anterior-posterior axis.

Megumi Hashiguchi, Minori Shinya and Noriyoshi Sakai

Formation of the dorsal organizer is an important process in antero-posterior (A-P) and dorso-ventral (D-V) patterning of the vertebrate embryo. In zebrafish, it is known that two molecular cascades, signaling through *bozozok/dharma* (*boz*) and *squint* (*sqt*), act in parallel to induce the organizer. We analyzed the ability of zebrafish cell lines, which were derived from embryos and larvae at various developmental stages, to induce the organizer when they implanted into mid-blastula; a cell lines derived from the earlier stage induced a complete secondary axis while a cell lines from the later stage induced only posterior structures. The expression of organizer marker genes was induced ectopically around implanted cultured cells. The notochord was derived from host cells in implanted embryos, and no secondary axis was induced when cultured cells were implanted into early gastrula. These data suggest that secondary axis axes induced by cell lines result from organizer

induction.
Interestingly, ectopic expression of *boz* was not found around cultured cells. Furthermore, the cell lines induced secondary axes even in Maternal-Zygotic *one-eyed pinhead* mutants in which Sqt signaling was disturbed, without rescuing their phonotypes. These findings indicate that the dorsal organizer is induced by these embryo-derived cultured cell lines with neither the upstream activation of *boz* upstream nor the activation of the Sqt signaling pathway.

PUBLICATIONS

Papers

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2． Kimura, T.,Shimada, A.,Sakai, N.,Mitani, H.,Naruse, K.,Takeda, H.,Inoko, H.,Tamiya, G.,Shinya, M.（2007）Genetic Analysis of Craniofacial Traits in the Medaka，**Genetics**，177，2379 - 2388

POSTER PRESENTATIONS

1． 酒井則良,新屋みのり 「 精原細胞培養系を用いたトランスジェニックゼブラフィッシュ作製法と精子形成調節因子の解析 」， 2007年度国立遺伝学研究所研究集会「生殖細胞と生殖腺形成の普遍性と多様性」，三島，7/23-7/24
2．斉藤憲二,酒井則良「 ゼブラフィッシュA型精原細胞の幹細胞特性とその培養系の試み 」，「生殖細胞の発生プロセス・再プログラム化とエピジェネティクス」第6回公開シンポジウム， 東京，11/21-11/22
3． Shinya, M.,Kobayashi, K.,Masuda, A.,Saka, K.,Sakai, N. 「 RNA interference by expressing shRNAs in the zebrafish cells 」，第40回日本発生生物学会，福岡，5/28-30
4． Hashiguchi, M.,Shinya, M.,Sakai, N.「 Secondary axis formation upon induction of the dorsal organizer in zebrafish embryonic and larval cultured cell lines 」， 5th European Zebrafish Genetics and Development Meeting，Amsterdam, The Netherlands，7/12-15
5． Shinya, M.,Kimura, T.,Shimada, A.,Sakai, N.,Mitani, H.,Naruse, K.,Takeda, H.,Inoko, H.,Tamiya, G.「 Genetic Analysis of Craniofacial Traits in the Medaka 」， 5th European Zebrafish Genetics and Development Meeting，Amsterdam, The Netherlands，7/12-15
6． Shinya, M.,Kobayashi, K.,Masuda, A.,Tokumoto, M., Ozaki, Y.,Kawasaki, T.,Saka, K.,Sakai, N.「 An approach to gene silencing by shRNA in the zebrafish cells 」，第30回日本分子生物学会，横浜，12/11-15
7． Sakai, N.,Saito, K.,Hashiguchi, M.「 培養細胞系を中心とした雄生殖細胞と背側化因子の解析 」， 国立遺伝学研究所研究会「脊椎動物の器官形成とバイオイメージング」， 三島，3/15-16

EDUCATION

1．山下正兼, 酒井則良　生殖細胞と生殖腺形成の普遍性と多様性　2007年度国立遺伝学研究所研究会　三島　7/23-7/24

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F. GENETIC STRAINS RESEARCH CENTER
F-e. Plant Genetics Laboratory

Nori Kurata

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1． Schaller, G.E.,Doi, K., Hwang, I., Kieber, J.J., Khurana, J.P., Kurata, N., Mizuno, T., Pareek, A., Shiu, S.H., Wu P., Yip, W.K. （2007） Nomenclature for two-component signaling elements of rice.， **Plant Physiol.**，143，555 - 557
2． Nonomura, K, Morohoshi, A., Nakano, M., Eiguchi, M., Miyao, A., Hirochika, H. and Kurata, N.（2007）A germcell-specific gene of the ARGONAUTE family is essential for the progression fo premeiotic mitosis and meiosis during sporogenesis in rice.， **Plant Cell**，19，2583 - 2594
3．Miyabayashi, T., Nonomura, K.I., Morishima, H. and Kurata, N.（2007）Genome size of twenty wild species of Oryza determined by flow cytometric and chromosome analyses.， **Breeding Science**，57，73 - 78

ORAL PRESENTATION

1．野々村賢一　イネの生殖細胞発生および減数分裂に関わる遺伝子の解析　公開セミナー（遺伝子資源工学専攻・遺伝子資源開発研究センター）　21世紀交流プラザ第2講義室(九州大学大学院農学研究院) 10/26

POSTER PRESENTATIONS

1．野々村賢一「生殖細胞で特異的に発現するイネARGONAUTEファミリー遺伝子*MEL1*の機能」，2007イネ分子遺伝学ワークショップ，名古屋市，7/2-3
2．津田勝利「*KNOX*遺伝子の発現制御機構の研究」，2007イネ分子遺伝学ワークショップ，名古屋市，7/2-3
3．久保　貴彦「3遺伝子座間相互作用に支配されるイネのF2不稔」，2007イネ分子遺伝学ワークショップ，名古屋市，7/2-3
4．水多陽子「イネ亜種間交雑における生殖的隔離障壁遺伝子のポジショナルクローニング」，2007イネ分子遺伝学ワークショップ，名古屋市，7/2-3
5． Nonomura K., Nakano, M., Eiguchi, M., Miyao, A., Hirochika, H., Kurata, N.「Rice meiosis and its relation to small RNA-mediated gene silencing」，EMBO world workshop, 8th European Meiosis Meeting，Hayama, Kanagawa, Japan，9/13-18
6．上田健治,豊澤恵子,高橋幸子,宮尾安藝雄,廣近洋彦,野々村賢一,倉田のり,井上正保「イネ花粉突然変異体TosO216の解析」，日本植物学会第71回大会，野田市，9/6-9
7． Ken-Ichi Nonomura「A germ-cell specific ARGONAUTE gene and its function in reproductive gene regulation」， The 5th International Symposium of Rice Functional Genomics，つくば市，10/15-17

8．Nori Kurata, Tadzunu Suzuki, Toshihiro Kumamaru, Hikaru Satoh「High Performance Rice Mutant Screening by using modified TILLING and MNU-induced mutant pools」, The 5th International Symposium of Rice Functional Genomics，つくば市，10/15-17
9．津田勝利,伊藤幸博,宮尾安藝雄,廣近洋彦、倉田のり「KNOX遺伝子を葉で異所的に発現するイネ突然変異体の解析」，日本育種学会第112回講演会，鶴岡市，9/22.23
10．伊藤幸博,津田勝利,永口貢,倉田のり「KNOX遺伝子を葉で異所的に発現するイネ突然変異体の解析2」，日本育種学会第112回講演会，鶴岡市，9/22,23
11．板橋悦子,藤田雅丈,倉田のり,鳥山欽哉「BT型細胞質雄性不稔イネの花粉発達に関与する核遺伝子の発現解析」，日本育種学会第112回講演会，鶴岡市，9/22,23
12．藤田雅丈「イネ生殖全ステージを用いたアレイ解析の現状」，国立遺伝学研究所研究集会，三島，11/16
13．堀内陽子、藤澤洋徳、川喜田雅則、望月孝子、春島嘉章、坂口隆之、江口真透、倉田のり「Affymetrix Rice Genome Arrayを用いたSFP検出手法の開発」，第30回　日本分子生物学会年会，横浜，12/11-15
14．米田典央、野々村賢一、倉田のり「イネPot1ホモログの単離と解析」，日本遺伝学会第79回大会，岡山，9/19-21
15．堀内陽子,藤澤洋徳,川喜田雅則,望月孝子,春島嘉章,坂口隆之,倉田のり「Affymetrix Rice Genome Arrayを用いたSFP検出手法の開発」，日本育種学会第112回講演会，鶴岡市，9/22.23
16．水多陽子,春島嘉章,倉田のり「イネ雑種花粉で作用する生殖的隔離障壁遺伝子のポジショナルクローニング」，日本育種学会第112回講演会，鶴岡市，9/22,23
17．春島嘉章,倉田のり「栽培イネの第3染色体の雄性配偶体型生殖的隔離障壁と相互作用する第6染色体の雌性親遺伝子のポジショナルクローニング」，日本育種学会第112回講演会，鶴岡市，9/22,23
18．水多陽子,春島嘉章,倉田のり「イネ雑種花粉で相互作用する2遺伝子座に起因する生殖的隔離」，日本遺伝学会第79回大会，岡山市，9/19-21
19．久保貴彦,吉村淳,倉田のり「イネの交雑後代に見出されたF_2雌性不稔の遺伝機構」，日本遺伝学会第79回大会，岡山市，9/19-21
20．藤田雅丈,堀内陽子,上田弥生,水多陽子,倉田のり「イネの生殖過程を通じた遺伝子発現プロファイリング」，日本遺伝学会第79回大会，岡山市，9/19-21
21．津田勝利,伊藤幸博,倉田のり「イネのKNOX遺伝子OSH1の発現制御機構の解析」，日本遺伝学会第79回大会，岡山市，9/19-21
22．春島嘉章,栗木哲,水多陽子,藤澤洋徳,倉田のり「イネF_2集団における生殖的隔離障害の相互作用の検出」，日本遺伝学会第79回大会，岡山市，9/19-21
23．山中慎介,江花薫子,倉田のり,呉健忠,松本隆,D. A. Vaughan, 大川安信,奥野員敏,福岡修一,河瀬真琴「イネAゲノム近縁野生種のDiversity Research Set作成に向けた多様性解析 II. 候補系統の選定」，日本育種学会第111回講演会，水戸，3/30-31
24．野々村賢一「イネ生殖細胞形成過程を制御する遺伝子群の単離と機能解析」，第111回日本育種学会、日本育種学会奨励賞受賞講演，水戸市，3/29

EDUCATION

1．倉田のり　「植物ゲノム障壁」第1回若手ワークショップ　仙台　11/5-7
2．倉田のり、渡辺正夫　高等植物の受粉・受精形質（雌雄間相互作用形質）を統御する遺伝子の分子遺伝学的解析　国立遺伝学研究所研究集会　三島　11/16

BOOK

1．Kurata, N.（2007）Chromosome and genome evolution in rice. **Rice Biology in the Genomics Era.** 235 - 243
2．Ohtsubo, H., Tsuchimoto, S., Xu, J-H., Cheng, C., Kuroda, M.Y., Kurata, N. and Ohtsubo, E.（2007）Riice retroposon, p-SINE, and its use for classification and identification of Oryza species. **Rice Biology in the Genomics Era.** 277 - 289
3．倉田のり,春島嘉章（2007）イネゲノムと生殖的隔離　植物の進化（細胞工学別冊）97 - 101

OTHERS

1．野々村　賢一，2，野々村賢一「イネ生殖細胞形成過程を制御する遺伝子群の単離と機能解析」平成18年度日本育種学会奨励賞
2．野々村賢一，1，日本育種学会幹事
3．倉田　のり，1，日本遺伝学会評議員
4．倉田　のり，3，生物遺伝資源イネ小委員会委員長
5．Nori Kurata，3，NSF project proposal reviewer
6．倉田　のり，3，日本学術会議　育種学分科会幹事
7．倉田のり，3，日本学術会議　植物科学分科会会員
8．Nori Kurata，3，Rice Genetics Newsletter Editor

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F. GENETIC STRAINS RESEARCH CENTER
F-f. Microbial Genetics Laboratory
Hironori Niki

RESEARCH ACTIVITIES

(1) A defect in positioning of bacterial nucleoid

Kumiko Higuchi, Yoshiharu Yamaichi (Tufts Univ. USA) and Hironori Niki

We have found a centromere-like element (migS) on the Escherichia coli genome. We searched gene products that genetically interact with migS. Transposon (Tn) insertion mutations of phoU showed a growth defect under migS deletion mutation. It was reported that PhoU functions in phosphate uptake and intercellular phosphate metabolism, although several group claimed those were not its primary functions. The phoU Tn insertion mutant (phoU::Tn) lacked a few amino acid residues from the carboxyl terminal of phoU gene, and the null mutant did not show the synthetic lethal phenotype with migS mutant. phoU::Tn cells showed mislocated nucleoid from centre of the cells, while in wild type cells have the nucleoid at central region of the cell. Daughter nucleoids were not clearly separated at cell division in the mutant. In fact, frequency of DNA-less cells increased in the phoU mutant. This phenotype was exaggerated in slmA deficient cells where septum inhibition mechanism over unseparated nucleoids was absent. lnΔslmA, phoU::Tn double mutant cells, frequency of anucleate cells were increased compared to the wild type cells and guillotine typed cells were appeared. We concluded that the truncated PhoU protein perturbed correct positioning of daughter nucleoids and this could lead mitotic catastroph.

(1) Screening of mutants that are defect in chromosome segregation or cell division

Masako Sakai, Hironori Niki

We are screening null mutants that are defective in chromosome segregation or cell division. The E. coli genome has been completely sequenced, and about 4,400 open reading frames (ORFs) are estimated on the genome, determined by a statistical method of ORF prediction. A collection of systematic null mutants of the ORFs, KEIO collection, has been constructed by Dr. Mori's group and maintained in the Microbial genetics laboratory and this provides a very useful screening tool. We went through and have taken images of about 2,000 mutant cells by using DNA specific staining and found a new mutants that produce DNA-less cells or elongated cells. We will construct a database including photographic images of the morphology and it will be open for public.

(3) Fission yeast Schizosaccharomyces japonicus as a novel genetic system in chromosome biology

Kanji Furuya, Hironori Niki

Yeasts are powerful genetic tool to identify new elements or new phenotypes in a wide range of biology. However, due to its small cell size, there is a limitation in detailed cell biological analysis. Schizosaccharomyces japonicus is an alternative fission yeast. Although this haploid organism is poorly developed as a genetic tool, its nearly twice large nuclear size and more fibrously condensed mitotic chromosomes compare to the other yeasts can be more suitable model system to understand mechanism of chromosome organization in vivo, such as mitotic chromosome segregation or interphase chromosome compartment. Our final aim is to discover new gene functions which regulate chromosome cycle through the isolation of mutants with novel cytological phenotypes. We have so far isolated 1100 high temperature and 40 cold temperature sensitive mutants. We have just started examining each mutant. Taking advantage of our well-equipped microscopes and our long experience in cytological study in smaller organism (E.coli), we are hoping to have a collection of mutants with abnormal chromosome shape or nuclear structure. In pararell, thanks to full-genome sequence information provided by the Broad Institute, we have been able to clone all six SMC (Structural Maintenance of Chromosome) genes which functions in chromosome condensation, chromatid cohesion and DNA replication. The cloned gene will be used to obtain antibodies to visualize those key elements in chromosome dynamics and will be useful to understand molecular basis of the chromosome behavior in this yeast. We have been setting up tools and methods as well. We have generated heterothallic haploid to ease crossing different alleles. We have been trying to modify key genes to create genetic markers. We have already cloned ura4 and ade6 to create equivalent point mutation to use same genetic tool such as plasmids or minichromosome of closely related fission yeast, S. pombe.

PUBLICATIONS

Papers

1．仁木 宏典（2007）バクテリアのセントロメア様領域，実験医学，25，114 - 118
2．仁木 宏典（2007）大腸菌:完備された網羅的遺伝資源，細胞工学，26，941 - 943
3． Kai M., Furuya, K., Paderi F., Carr AM. Wang TS. （2007） Rad3-dependent phosphorylation of the checkpoint clamp regulates repair-pathway choice， **Nature Cell Biology**，9，691 - 697
4． Gerding, M.A., Ogata, Y., Pecora, N.D., Nik,i H., and de Boer, PA.（2007） The trans-envelope Tol-Pal complex is part of the cell division machinery and required for proper outer-membrane invagination during cell constriction in E. coli.， **Mol Microbiol.**， 63，1008 - 1025
5． Cu,i T., Moro-oka, N., Ohsumi K., Kodama, K., Ohshima, T., Ogasawara, N., Mori, H., Wanner, B., Niki, H., and Horiuchi, T. （2007） Escherichia coli with a linear genome， **EMBO Rep**，8，181 - 187

ORAL PRESENTATION

1．古谷寛治,仁木宏典　DNAチェックポイント因子の視覚化　中部東海DNA研究会　四季の家／乗鞍
2．古谷寛治,仁木宏典　DNAチェックポイント因子によるゲノム安定性への貢献　中部東海DNA 研究会　四季の湯･強羅静雲荘　8/11
3．中島玲子　塩基ミスマッチを標的としたMu ファージの転移組換え　2007中部東海DNA研究会　四季の宿あづみ館　7/26

POSTER PRESENTATIONS

1． 古谷寛治,仁木宏典 「 Mulistep activation of genomic stability pathway 」， Pombe Meeting，Copenhagen，6/11
2． 古谷寛治,仁木宏典 「 分裂酵母japonicus で観られる核小体の分離 」，RNA若手の会，神戸，9/10
3．古谷寛治,仁木宏典「 Multistep activation of genomic stability pathway 」，分子生物学会

, 横浜 , 12/14
4 . 田口温子,仁木宏典「 核様体形態変化から染色体分配機能を探る～培養条件による核様体形態解析～ 」, 第4回 21世紀大腸菌研究会 , 静岡県藤枝市 , 7/18-7/19
5 . 田口温子,仁木宏典「 核様体形態変化から染色体分配機能を探る～培養条件による核様体形態解析～ 」, 中部・東海DNA研究会 , 長野県松本市 , 7/25-7/27
6 . 久田香織,仁木宏典「 呼吸鎖複合体Ⅰとそのサブユニットがバクテリアのセントロメア様領域の機能に果たす役割 」, 中部・東海DNA研究会 , 長野県松本市 , 7/25
7 . Niki, H.「 Plasmid DNA segregation in bacteria: cytoskeletal proteins guide plasmids on to daughter cells 」, 30th anniversary of Institute of Biological Chemistry (IBC), Academia Sinica: Proteins 宴鈴 from Chemistry to Biology , Taipei , 10/24
8 . Furuya, K. and Niki, H. 「 GENETIC ANALYSIS IN Schizosaccharomyces japonicus, WHICH IS A NEW MODEL YEAST FOR RESEARCH OF CHROMOSOMA AND NUCLEUS 」, Fourth International Fission Yeast Meeting , Copenhagen , 6/11
9 . Furuya, K. and Niki, H., 「 CHROMOSOME AND NUCLEUS DYNAMICS OF THE FISSON YEAST, S. japonicus DURING MITOSIS AND MEOSIS 」, Fourth International Fission Yeast Meeting , Copenhagen , 6/11
10 . Niki, H.「 Segregation of nucleolus during mitosis 」, Gordon Research Conference "Chromosome Dynamics" , Biddeford, ME , 8/12
11 . Hatano, T.,Yamaichi, Y.and Niki, H. 「 DYNAMICS OF HELIX FORMING MOTER PROTEIN FOR PLASMID PARTITIONING, SopA 」, Functional Organization of the Nucleus , 淡路 , 1/9
12 . 田口温子,仁木宏典 「 大腸菌の核様体形態変化から染色体分配機能を探る 」, 第1回日本ゲノム微生物学会 , 千葉県木更津市 , 3/1
13 . 古谷寛治,仁木 宏典「 分裂酵母DNAチェックポイントタンパク質Rad9の複製キナーゼHsk1によるリン酸化は複製フォーク損傷応答を制御する 」, 染色体ワークショップ , 唐津 , 1/30
14 . 仁木 宏典 「 バクテリアに見いだされた細胞骨格タンパク質 」, 平成18年度生理研研究会「位相差断層電子顕微鏡の医学・生物学的応用」, 岡崎 , 1/25

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F. GENETIC STRAINS RESEARCH CENTER
F-g. Invertebrate Genetics Laboratory

Ryu Ueda

RESEARCH ACTIVITIES

PUBLICATIONS

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4 . Takahashi A, Takahashi K, Ueda R, Takano-Shimizu T. (2007) Natural variation of ebony gene controlling thoracic pigmentation in Drosophila melanogaster. , **Genetics** , 29 , 0 - 0

5 . Sasaki, N., Yoshida, H., Fuwa, T. J., Kinoshita-Toyoda, A., Toyoda, H., Hirabayashi, Y., Ishida, H., Ueda, R. and Nishihara, S. (2006) Drosophila beta1,4-N-acetylgalactosaminyltransferase-A synthesizes the LacdiNAc structures on several glycoproteins and glycosphingolipids. , **Biochem. Biophys. Res. Commun.** , 354 , 522 - 527

6 . Tajiri, R., Tsuji, T., Ueda, R., Saigo, K. and Kojima, T. (2006) Fate determination of Drosophila leg distal regions by trachealess and tango through repression and stimulation, respectively, of Bar homeobox gene expression in the future pretarsus and tarsus. , **Dev Biol.** , 303 , 461 - 473

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8 . Chertemps, T., Duportets, L., Labeur, C., Ueda, R., Takahashi, K., Saigo, K., and Wicker-Thomas, C. (2006) A female-biased expressed elongase involved in long-chain hydrocarbon biosynthesis and courtship behavior in Drosophila melanogaster. , **Proc. Natl. Acad. Sci. USA** , 104 , 4273 - 4278

9 . Okamura, T., Shimizu, H., Nagao, T., Ueda, R., and Ishii, S. (2007) ATF-2 regulates fat metabolism in Drosophila. , **Mol. Cell. Biol.** , , 0 - 0

10 . 上田 龍 (2006) 誘導型RNAiによるショウジョウバエゲノムの機能解析 , 生物の科学

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POSTER PRESENTATIONS

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2．Ueda, R., Sado, Y., Fujitani, K., and Takahashi, K.「NIG FLY, AN RNAi MUTANT FLY BANK FOR COMPREHENSIVE GENE FUNCTION ANALYSES IN DROSOPHILA.」, European Drosophila Research Conference 2007 , Viena , 9/12-14
3．西原祥子、上山盛夫、山本（日野）美紀、吉田英樹、不破尚志、後藤聡、豊田英尚、上田龍「ショウジョウバエを用いた糖鎖関連遺伝子の網羅的機能解析」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
4．神山伸、合田絵美、佐々木紀彦、上山盛夫、吉田英樹、成松久、地神芳文、上田龍、西原祥子「ヒトおよびショウジョウバエにおけるPAPS輸送体と硫酸化」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
5．神山伸、合田絵美、佐々木紀彦、上山盛夫、吉田英樹、成松久、地神芳文、上田龍、西原祥子「ヒトおよびショウジョウバエにおけるPAPS輸送体と硫酸化」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
6．須鎗理、奥村美江子、井田寛之、吉田英樹、上田龍、坂口謙吾、山口政光「ショウジョウバエDNAポリメラーゼε触媒サブユニットはendoreplicationに必要である」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
7．吉田祐果、大堀真希、大久保洋之、田村郁雄、多羽田哲也、山口（武井）ゆき、渡辺晃、北田祐介、上田龍、松野健治「ショウジョウバエNotchの細胞内小胞輸送を制御する遺伝子の探索」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
8．阿部将人, 富永由香, 田中翼, 中村輝, 高橋邦明, 上田龍, 後藤聡「ホスファチジルイノシトール3 リン酸（PI(3)P）による細胞接着・細胞極性の制御」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
9．矢野環、三田静香、大森弘子、大島吉輝、上田龍、吉森保、倉田祥一郎「ショウジョウバエPGRP-LEによる細胞内寄生細菌の認識とオートファジー誘導」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
10．山本（日野）美紀、矢野弘之、蟹江善美、粟野若枝、平井ゆう、桑原玲子、木下（青木）聖子、上田龍、西原祥子、蟹江治、後藤聡「ショウジョウバエを用いた糖鎖修飾制御因子のゲノムワイドスクリーニング」, 第30回日本分子生物学会年会 , 横浜 , 12/11-15
11．高橋邦明「RNAi変異体バンク ー ゲノム機能解析のためのリソースとして」, 特定ゲノム4領域・領域横断昆虫ゲノム研究会 , 東京 , 2/27,28
12．Yasugi, T., Uematsu, D., Murakami, S., Takahashi, K., Saigo, K., Ueda, R., Yoshida, S., Sato, M., and Tabata, T.「Role for the JAK/STAT signaling pathway in the optic lobe development.」, 48th Annual Drosophila Research conference , Philadelphia , 3/7-11
13．Ueda, R., Takahashi, K., Sado, Y., and Fujitani, K.「RNAi fly bank - a resource for the functional genomics.」, The 48th Annual Drosophila Research conference , Philadelphia , 3/7-11

EDUCATION

1．黒田行昭、上田龍　RNA干渉（RNAi）による遺伝子サイレンシング　第79回日本遺伝学会大会　岡山市　9/19-21

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G. CENTER FOR GENETIC RESOURCE INFORMATION
G-a. Genetic Informatics Laboratory

Yukiko Yamazaki

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1． Honda, H., Kataoka, F., Nagaoka, S., Kawai, Y., Itoh, H., Kimura, K., Takemoto, N., Yamazaki, Y., Tateno, Y. and Saito, T. （2007） Beta-galactosidase, phospho-beta-galactosidase and phospho-beta-glucosidase activities in lactobacilli strains isolated from human faeces.， **Lett Appl Microbiol**， 45， 461 - 466
2． Shin Watanabe, Tsuyoshi Mizoguchi, Koh Aoki, Yasutaka Kubo, Hitoshi Mori, Shunsuke Imanishi, Yukiko Yamazaki, Daisuke Shibata, Hiroshi Ezura （2006） Ethylmethanesulfonate (EMS) mutagenesis of Solanum lycopersicum cv. Micro-Tom for large-scale mutant screens， **Plant Biotechnology**， 24， 33 - 38

POSTER PRESENTATIONS

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2． Watanabe, T., Watanabe, K., ,Tsuchiya, R., Sharoh, Y., and ,Yamazaki,Y.「Plant Genetic Resource Databases」, Plant and Animal Genome XV， San Diego， Jan.13-17
3． 坂庭信吾,土屋里枝,山川武広,野々村賢一,倉田のり,山崎由紀子「Next Generation of Rice Database - Oryzabase -」, BMB2007， 横浜， Dec.11-15
4． 山崎由紀子,土屋里枝,矢野澄子,山川武広,渡辺功二,齋藤睦美,吉岡美春,坂庭真悟, シャローイップ,渡辺融,木村学,佐賀正和,坂本盛宇「NBRP「情報」:リソースとリサーチの好循環を支える情報センター」, BMB2007， 横浜， Dec.

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3．山崎由紀子（2007）バイオリソース（生物遺伝資源）情報センター 細胞工学 1446 - 1449
4． Baltazar A. Antonio, C.Robin Buell, Yukiko Yamazaki, Immanuel Yap, Christophe Perin, and Richard Bruskiewich（2007） Informatics Resources for Rice Functional Genomics. **Rice Functional Genomics** 355 - 394

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G. CENTER FOR GENETIC RESOURCE INFORMATION
G-b. Genome biology Laboratory

G. CENTER FOR GENETIC RESOURCE INFORMATION
G-b. Genome biology Laboratory

Yuji Kohara

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1 . Kasahara, M., Naruse, K., Sasaki, S., Nakatani, Y., Qu, W., Ahsan, B., Yamada, T., Nagayasu, Y., Doi, K., Kasai, Y., Jindo, T., Kobayashi, D., Shimada, A., Toyoda, A., Kuroki, Y., Fujiyama, A., Sasaki, T., Shimizu, A., Asakawa, S., Shimizu, N., Hashimoto, S-I., Yang, J., Lee, Y., Matsushima, K., Sugano, S., Sakaizumi, M., Narita, T., Ohishi, K., Haga, S., Ohta, F., Nomoto, H., Nogata, K., Morishita, T., Endo, T., Shin-I, T., Takeda, H., Morishita, S. and Kohara, Y. (2007) The medaka draft genome and new insights into vertebrate genome evolution , **Nature** , 446 , 714 - 719

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H. STRUCTURAL BIOLOGY CENTER
H-a. Biological Macromolecules Laboratory

Makio Tokunaga

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．Yamasaki S, Sakata-Sogawa K, Hasegawa A, Suzuki T, Kabu K, Sato E, Kurosaki T, Yamashita S, Tokunaga M, Nishida K, Hirano T. （2007） Zinc is a novel second messenger.，**J. Cell Biol.**，177，637 - 645

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1．Tokunaga, M.　1分子研究を核にした新しい分子システム科学の開拓　東京工業大学資源科学研究所セミナー　横浜　12/17
2．徳永万喜洋　免疫分子動態の可視化と1分子イメージング　第35回愛媛リウマチ研究会　松山市医師会　4/7
3．徳永万喜洋　細胞1分子イメージング　－分子からシステムへ－　北海道大学リサーチ＆ビジネスパーク構想推進協議会・北海道大学先端生命科学研究院次世代ポストゲノム研究センター共催「次世代ポストゲノムセミナー」 北海道大学 創成科学研究棟　2/23

POSTER PRESENTATIONS

1．Tokunaga, M.「 免疫分子動態の可視化と1分子イメージング・定量解析 」，産学官連携を指向した最前線セミナー「分子細胞イメージングと疾患・創薬研究 研究を加速するバイオイメージング技術とその応用」，東京，7/11
2．Tokunaga, M.「「分子間力顕微鏡による1分子計測とMDシミュレーション」」，第1回バイオナノ研究会，東吾妻，9/17-18
3．Tokunaga, M.,Shinkura, K.,Sakata-Sogawa K「 細胞内分子ダイナミクス・相互作用の1分子イメージングと3次元・マルチカラー・定量 」，第30回日本分子生物学会年会・第80回日本生化学会大会　合同大会(BMB2007) シンポジウム「光イメージングの最先端　-生体から分子まで-」，横浜，12/11-15
4．SHIINA, N.,Tokunaga M.「 神経RNA granuleタンパク質RNG105による局所的翻訳制御とシナプス形成　」，　第30回日本分子生物学会年会・第80回日本生化学会大会　合同大会(BMB2007)，横浜，12/11-15
5．Isono, K.,Hiroshima, M.,Sakata-Sogawa K,Tokunaga, M.,Koseki, A.「 Evidence for hyper-dynamics of Polycomb repressive complexes by quantitative imaging and high-speed imaging 」，第59回日本細胞生物学会大会・第40回日本発生生物学会年会・合同大会，福岡，5/28-30
6．Isono, K.,Hiroshima, M.,Sakata-Sogawa K,Tokunaga, M.,Koseki, A.「 哺乳類ポリコーム群の標的遺伝子座上ダイナミクスによるエピジェネティック制御 」，産学官連携を指向した最前線セミナー「分子細胞イメージングと疾患・創薬研究　研究を加速するバイオイメージング技術と

その応用」, 東京 , 7/11
7 . Sakata-Sogawa K,Tokunaga, M. 「 1分子イメージングによる転写因子の核内動態解析」, 日本生物物理学会第45回年会 , 横浜 , 12/21-23
8 . Fukagawa A.,Hiroshima, M.,Kuwajima, K.,Tokunaga, M. 「 一分子計測およびMDシミュレーションによるタンパク質アンフォールディングの確率的経路と複数の中間状態の検出 」, 日本生物物理学会第45回年会 , 横浜 , 12/21-23
9 . Shinkura, K.,Sakata-Sogawa K,Kimura H.,Tokunaga, M. 「 転写因子の免疫刺激による共局在の変化:マルチカラー分子イメージング 」, 日本生物物理学会第45回年会 , 横浜 , 12/21-23
10 . SHIINA, N.,Tokunaga, M. 「 神経RNA granuleタンパク質RNG105ノックアウトによる興奮性・抑制性シナプスバランスの異常 」, 日本生物物理学会第45回年会 , 横浜 , 12/21-23
11 . Sakata-Sogawa K.,Shinkura K.,Kimura H.,Tokunaga M. 「 Multi-color molecular imaging of transcription factors in T cell activation. 」, Focus on Microscopy 2007 , Valencia , 4/10-13
12 . 椎名伸之,徳永万喜洋 「 神経RNA granuleタンパク質RNG105ノックアウトによる興奮性・抑制性シナプスバランスの異常 」, 第7回日本分子生物学会春季シンポジウム , 淡路 , 4/23-24
13 . 椎名伸之,徳永万喜洋 「 A deficiency of the RNA granule protein RNG105 impairs the excitatory/inhibitory synaptic balance 」, 第59回日本細胞生物学会大会・第40回日本発生生物学会年会・合同大会 , 福岡 , 5/28-30
14 . 徳永万喜洋 「 免疫分子動態の可視化と1分子イメージング・定量解析 」, 産学官連携を指向した最前線セミナー , 東京 , 7/11
15 . 深川暁宏、廣島通夫、桑島邦博、徳永万喜洋 「 Title:SNase の機械的伸張におけるアンフォールディング経路 」, 日本顕微鏡学会 SPM研究部会 第9回研究会 , 湯沢町 , 3/18
16 . 徳永万喜洋 「 新しい細胞内1分子イメージング顕微鏡創出による生体分子定量解析技術の開発 」, ダイナミックバイオH18年度・第2回研究開発委員会 , 東京 , 1/26

BOOK

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H. STRUCTURAL BIOLOGY CENTER
H-b. Molecular Biomechanism Laboratory
Nobuo Shimamoto

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．嶋本伸雄（2007）ナノバイオロードマップと生物ナノマシンの秘密，ケミカルエンジニアリング，52，8 - 15

ORAL PRESENTATION

1．嶋本伸雄　機能分子としてのタンパク質　神奈川科学技術アカデミー　東京大学医科研　5/17

POSTER PRESENTATIONS

1．Shimamoto,N., Susa,M., Miyamoto,T., Imashimizu,M., Fujita,R.「Ten Q's and A's on moribund complex」, FASEB Summer Research Conference , Saxton River,Vermont,USA，6/22～28
2．雨宮陽介、嶋本伸雄「Hard and bioactive multilayer of silane introduced on a diamond surface」, New Diamond and Nano Carbons (NDNC2007)，大阪市，5/28～31
3．Imashimizu,M., Shimamoto,N.「Cyanobacterial RNA polymerase has distinct sensitivity to Mn++」, FASEB Summer Research Conference，Saxton River,Vermont,USA，6/22～28
4．Miyamoto,T., Shimamoto,N.「Coupling between transcription initiation and DNA damage」, FASEB Summer Research Conference，Saxton River,Vermont,USA，6/22～28
5．中山秀喜、嶋本伸雄、伊藤耕一「翻訳終結経路における分岐経路の発見」, 第9回RNAミーティング，名古屋市，7/28～31
6．今清水正彦、嶋本伸雄「転写開始におけるRNA polymerase の活性型と不活性型のスイッチ機構」, 日本生物物理学会第45回年会，横浜市，12/21～23
7．中山秀喜、嶋本伸雄、伊藤耕一「翻訳終結経路における分岐経路の発見」, 日本生物物理学会第45回年会，横浜市，12/21～23
8．雨宮陽介、嶋本伸雄、中山秀喜、山田貴壽、上塚洋、鹿田真一「Multilayer of aminosilane on diamond surface with high mechanical strengh and bioactivity」, 日本生物物理学会第45回年会，横浜市，12/21～23
9．宮本貴史、嶋本伸雄、須佐太樹「UV-sensor motifs of promoters」, 日本生物物理学会第45回年会，横浜市，12/21～23
10．今清水正彦、嶋本伸雄「シアノバクテリアRNA polymeraseにおけるMg2+, Mn2+誘導性のabortive転写」, ゲノム微生物学会若手会，八王子市，10/22～23
11．中山秀喜、嶋本伸雄、伊藤耕一「翻訳終結経路における分岐経路の発見」, 第30回日

本分子生物学会，横浜市，12/11～15
12．今清水正彦、嶋本伸雄「シアノバクテリアRNA polymeraseにおける転写開始のスイッチ機構」，第30回日本分子生物学会，横浜市，12/11～15
13．宮本貴史、嶋本伸雄、須佐太樹「UV-sensor motifs of promoters」，第30回日本分子生物学会，横浜市，12/11～15
14．藤田龍介、嶋本伸雄、伴戸久徳「RNAポリメラーゼのプロモーター認識機構解明への挑戦」，第30回日本分子生物学会，横浜市，12/11～15
15．　今清水正彦、嶋本伸雄　「　ラン藻のRNA　polymeraseにおけるメタルイオン誘導性のabortive転写」，ラン藻の分子生物会2007，木更津市，12/3～4

BOOK

1．嶋本 伸雄（2007）ナノバイオロジー　バイオサイエンス　317 - 325
2．嶋本伸雄（2007）生物物理学、ナノバイオ大辞典　生物物理学、ナノバイオ大辞典　0 - 0

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H. STRUCTURAL BIOLOGY CENTER
H-c. Multicellular Organization Laboratory
Isao Katsura

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．Bauer Huang, SL., Saheki, Y., VanHoven, MK., Torayama, I., Ishihara, T., Katsura, I., van der Linden, A., Sengupta, P., Bargmann, CI（2007）Left-right olfactory asymmetry results from antagonistic functions of voltage-activated caclium channels and the Raw repeat protein OLRN-1 in *C. elegans*.，**Neural Development**，2，24 - 0
2． Eki, T., Ishihara, T., Katsura, I., Hanaoka, F.（2007） A genome-wide survey and systematic RNAi-based characterization of helicase-like genes in *Caenorhabditis elegans*.，**DNA Research**，14，183 - 199
3．Kobayashi, T., Gengyo-Ando, K., Ishihara, T., Katsura, I., and Mitani, S.（2007）IFT-84 and IFT-71 are required for intraflagellar transport in *C. elegans*.，**Genes to Cells**，12，593 - 602
4． Torayama, I.,Ishihara, T.,Katsura, I.（2006） Caenorhabditis elegans integrates the signals of butanone and food to enhance chemotaxis to butanone.，**J. Neurosci.**，27，741 - 750

POSTER PRESENTATIONS

1．Kimura, K., Katsura, I.「Enhancement of odor avoidance by preexposure is regulated by dopamine in *C. elegans*.」，Gordon Research Conferences: Neural Circuits & Plasticity，Newport, RI, USA，7/2
2．木村幸太郎「線虫C. elegansの「脳」による情報処理とは？ ～忌避行動可塑性の統合的解析から～」，Neuro2007: 日本神経科学会・日本神経化学会・日本神経回路学会合同大会／シンポジウム「新世代神経行動学のストラテジー」，横浜，9/11
3．Ichijo, H., Torayama, I., Kimura, K., Katsura, I.「Genetic mapping of a novel butanone enhancement mutant」，16th International *C. elegans* Meeting，Los Angeles，6/27-7/1
4． Kimura, K., Katsura, I.「Enhancement of avoidance behavior to 2-nonanone by preexposure, and its regulation by *cat-2*」，16th International *C. elegans* Meeting，Los Angeles，6/27-7/1
5． Katsura, I.「How do worms change their behavior by smelling environments?」，International Symposium "Gene Expression Control and Genome Evolution"，岡山，9/19-21
6．木村幸太郎, 桂勲「事前刺激で増強される線虫*C. elegans*の匂い忌避行動はドーパミンによって制御される」，第30回日本分子生物学会第80回日本生化学会合同大会，横浜，12/11-15

OTHERS

1．桂　勲，1，Genes to Cells, Associate Editor
2．石渡信一, 桂勲, 桐野豊, 美宅成樹，3，「生物物理ハンドブック」朝倉書店の編集

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H. STRUCTURAL BIOLOGY CENTER
H-d. Biomolecular Structure Laboratory

Yasuo Shirakihara

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1． Gao, YG., Yao, M.,Itou, H.,Zhou, Y., Tanaka, I.（2007） The structures of transcription factor CGL2947 from Corynebacterium glutamicum in tow crystal forms: A novel homodimer assembling and the implication for effector-binding mode，**Protein Sci.**，16，1878 - 1886

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1． Shirakihara, Y.,Shiratori A., Murakami S., Suzuki T., Yoshida M.「Crystallization and crystal analysis of ATPsynthase」，生物物理45回年会，横浜，12/21-12/23
2． 今清水正彦、伊藤啓、田中寛、村上勝彦、嶋本伸雄「シアノバクテリアRNA polymeraseにおける転写開始のスイッチ機構」，BMB2007，横浜，12/11-15
3． 今清水正彦、伊藤啓、田中寛、村上勝彦、嶋本伸雄「転写開始におけるRNA polymeraseの活性型と不活性型のスイッチ機構」，生物物理学会年会2007，横浜，12/21-23
4． Itou, H., Suzuki, M., Wachi, M., Watanabe, N., Tanaka, I.,「バクテリアの多剤耐性調節転写因子CGL2612タンパク質による、薬剤・DNA認識機構の構造学的研究」，日本蛋白質科学会2007年年会，宮城県仙台市，5/24
5． Gao, YG., Yao, M., Suzuki, M., Itou, H., Wachi, M., Watanabe, N., Tanaka, I.,「Corynebacterium glutamicum由来蛋白質CGL2915の構造と機能解析：乳酸と炭水化物利用に関わる新規転写リプレッサー」，日本蛋白質科学会2007年会，宮城県仙台市，5/24

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H. STRUCTURAL BIOLOGY CENTER
H-e. Gene Network Laboratory
Emiko Suzuki

RESEARCH ACTIVITIES

POSTER PRESENTATIONS

1．Sone,M.,Uchida,A.,Komatsu,A.,Suzuki,E.,Okazawa,H.,Hoshino,M.,and Nabeshima,Y.「Loss of a novel regulator for protein trafficking results in neurodegeneration」, The 8th Japanese Drosophila Research Conference，淡路，7/2-7/4
2． Kurusu,M.,Maruyama,Y.,Okabe,M.,Suzuki,E.,and Furukubo-Tokunaga,K.「Tailless maintains neural stem cell renewal by activating cell-cycle genes and repressing Prospero in the *Drosophila* brain」，第30回日本神経科学大会，横浜，9/10-9/12
3．Sone,M.,Uchida,A.,Komatsu,A.,Suzuki,E. Okazawa,H.,Hoshino,M.,and Nabeshima,y.「Loss of a novel regulator for protein trafficking results in degeneration in *Drosophila*」，第30回日本神経科学大会，横浜，9/10-9/12
4． Kurusu,M.,Maruyama,Y.,Okabe,M.,Suzuki,E.,and Furukubo-Tokunaga,K.「Tailless Maintains Neural Stem Cell Renewal by Activating Cell-cycleGenes and Repressing Prospero in the *Drosophila* Brain」，The 8th Japanese Drosophila Research Conference，淡路，7/2～7/4
5．鈴木えみ子「ハエの神経回路形成メカニズム～行動や思考の源を探る～」，遺伝学公開講演会，東京，11/10
6． Sone,M.,Uchida,A.,Komatsu,A.,Suzuki,E.,Hoshino,M.,Nabeshima,Y.「Yata regulates intracellular trafficking and is required for survival of animals」, 48th Annual Drosophila research conference，Pennsylvania，3/7-3/11

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I. CENTER FOR INFORMATION BIOLOGY AND DNA DATA BANK OF JAPAN
I-a. Laboratory for DNA Data Analysis

Takashi Gojobori

RESEARCH ACTIVITIES

Search for the evolutionary origin of protozoan lens-eye
(Hayakawa S, Hwang JS, Takaku Y, Nagai S, Horiguchi T, Suga H, Ikeo K, Gehring W and Gojobori T)
The dinoflagellates (division Pyrrhophyta, class Dinophyceae) are a group of unicellular phytoplankton in marine and fresh waters, which are composed of more than 2,000 species. One of families in dinoflagellates, Warnowiaceae, consists of three heterotrophic genera, Warnowia, Erythropsidinium and Nematodinium, which are identified by distinct structure so-called “ocelloid”. “Ocelloid” is one type of various eye-spot organelle seen in dinoflagellate, but characterized with the lens-like structure which exists only in this family.
With the aim of examining if this protozoan lens-eye is actually the evolutionary origin of human camera-eyes, we attempted to identify the genes that may be involved with the formation and function of the ocelloid. In practice, we collected samples of the species for the three genera of Warnowiaceae, which were carefully identified by morphological traits. Isolating DNAs from those samples, we first confirmed species identification by constructing molecular phylogenetic tree of SSU rDNAs and mitochondrial genes. Then, we constructed cDNA libraries and sequenced cDNA clones. When we made the annotation on those clone sequences, we found that there were homologues for photoreceptor-related genes such as rhodopsin and plastid-targeting proteins. More interestingly, we also found a number of gene homologues that can be apparently related to morphogenesis of the ocelloid and retinal body. From these reasons, we think it reasonable to conclude that at least some genes in protozoan ocelloid shared the common ancestry with mammalian camera-eyes. The coming issue will be to know by which mechanisms this can be brought, straightforward evolution or horizontal gene transfer. This will be discussed in this report.

A NOVEL PROTEIN FOR THE SENSORY APPARATUS OF HYDRA NEMATOCYTE
(Hwang JS, Takaku Y, Chapman J, Ikeo K, David CN and Gojobori T)
All Hydra nematocytes possess the cnidocil apparatus. The cnidocil apparatus is a sensory receptor protruded from the apical surface of Hydra nematocyte, a stinging cell used for prey capture. Ultrastructural studies of the cnidocil apparatus have clearly shown that the cnidocil apparatus is a microtubule-containing cilium (‘9+0’ pattern) surrounded by 7 ~ 12 actin filaments called stereocilia at the distal region, and a shorter inner row of microvillar rods. This structure is comparable with the sensory cilia of vertebrate hair cell. Except microtubule and actin-filled stereocilia, no genetic details of other parts of cnidocil apparatus have been known so far. A cnidarian-specific protein, which we named as nematocilin, is identified from Hydra. Nematocilin contains coiled-coil heptad repeats and is a new member of intermediate filament family. Immunofluorescence showed that expression of nematocilin in the cytoplasm was initiated at the late differentiation of nematocyte and later the protein was deposited in the modified cilium of cnidocil apparatus. Immunogold

electron microscopy also confirmed that nematocilin constitutes the electron-dense filament at the core of cilium and is surrounded by doublets and single microtubules. The existence of nematocilin-filled filament in the cilium provides the stiffness to the structure during the discharge of nematocyte. However, not all cnidarians possess the nematocilin in the cnidocil apparatus, the class Anthozoa and some hydrozoans lack nematocilin-filled filaments and only microtubules are present in the modified cilium. Searching the genome of Nematostella vectensis (Anthozoa) failed to find the orthologous gene of nematocilin. Therefore, nematocilin could have emerged in Cnidaria after the divergence of Anthozoa and evolved with specialized properties for supporting the discharge of nematocyte.

Search for the evolutionary origin of neural tube: Gene expression analysis of ciliary band in sea urchin embryo (Kinjo S, Ikeo K and Gojobori T)
In the nervous system, vertebrates have neural tube whereas invertebrates do not. Because the neural tube produces spinal cord and brain in vertebrates during the development, we examined if invertebrates have an ancestral organ of neural tube, in order to understand the evolutionary origin of neural tube. Sequencing about 5,000 ESTs in the cDNA library of the ciliary band tissues of sea urchin larva in which some of structural descriptions are common to neural tube of vertebrates, we examined whether the gene expression profile of the ciliary band is similar to that of neural tube. As a result of homology search, we found that most of the ESTs were from mitochondrial or cytoskeletal genes, and that there were few ESTs related to nervous system. This result seems indicate that ciliary band is not a central nervous system but a sort of peripheral nerves where the ciliary and the nerve cells coexist. Therefore ciliary band would not be the ancestral organ of neural tube from the viewpoint of gene expression profile at least.

Compensatory change of interacting amino acids in the coevolution of transcriptional coactivator MBF1 and TATA-box-binding protein.
(Liu Q-X, Nakashima-Kamimura N, Ikeo K, Hirose S and Gojobori T)
To elucidate the transcriptional regulation in eukaryotic genome network, it is important to understand coevolution of transcription factors, transcriptional coactivators, and TATA-box-binding protein (TBP). In this study, coevolution of transcriptional coactivator multiprotein-bridging factor 1 and its interacting target TBP was first evaluated experimentally by examining if compensatory amino acid changes took place at interacting sites of both proteins. The experiments were conducted by identifying interaction sites and comparing the amino acids at these sites among different organisms. Here, we provide evidence for compensatory changes of transcription coactivator and its interacting target, presenting the 1st report that transcription coactivator may have undergone coevolution with TBP. This study was published in Molecular Biology and Evolution. (2007) Vol. 24: 1458-1463.

Functional analysis of Drosophila TDF during the eye development
(Liu Q-X, Ikeo K, Hiromi Y, Hirose S and Gojobori T)
In Drosophila, the tracheas defective (tdf) gene encodes a bZIP protein that required for the development of trachea, heart, head and neural system. TDF is highly expressed in the cells of the morphogenetic furrow (MF) region. Loss of TDF function causes defects in the eye development. Overexpression of TDF in the eye disc induced abnormal eyes. The targets of tdf responsible for these responses have not been identified. To identify tdf downstream genes in a comprehensive manner, we used genome-wide oligonucleotide arrays and analyzed differential gene expression in wild-type embryos versus tdf mutant embryos. Upon knockout of tdf function, expression of 340 genes decreased and 338 genes increased. Many of these genes can be assigned to specific aspects of the tracheal and neural system development. We also discovered tdf target genes that are likely to play specific roles in eye morphogenesis. This study was won the best paper award in the 79th annual meeting of the genetics society of Japan.

Midline governs axon pathfinding by coordinating expression of two major guidance systems
(Liu Q-X, Hiramoto M, Ueda H, Gojobori T, Hiromi Y and Hirose S)

Formation of the neural network requires concerted action of multiple axon guidance systems. How neurons orchestrate the expression of multiple guidance genes is poorly understood. Here we show that Drosophila T-box protein Midline controls expression of multiple axon guidance molecules: Frazzled, ROBO, and Slit. In midline mutant expression of all these molecules are reduced, resulting in severe axon guidance defects, whereas misexpression of Midline induces their expression. Midline is present on the promoter regions of these genes, indicating that Midline controls transcription directly. We propose that Midline coordinates the expression of two guidance systems with opposing outputs for axon pathfinding.

The Evolutionary Origin of the Layered Structure of the Mammalian Neocortex
(Suzuki I, Hirata T and Gojobori T)
The mammalian brain is known to have some unique features, one of which is the 6-layered structure of the neocortex and the columnar unit of the neural circuit through such layers. The evolutionary origin of the neocortical lamination have not been enough studied so far, although the functional and developmental aspects of the research has been actively done. With the aim of elucidating the evolutionary origin, we studied a chick brain from the viewpoint of comparative developmental biology. Then, we found the following three points. 1) We discovered that the chick dorsal telencephalon possesses the similar neuronal variety in the mammalian neocortex, according to the expression patterns of gene markers. 2) We also found that the chick shares with mammals the temporal order of the differentiation of neurons. 3) Our fate-mapping experiment demonstrated that the generation site of a particular type of neuron is distinct from that of another type of neuron in the chick dorsal telencephalon, however the stem cell in all the area of the mammalian neocortex can generate all types of cortical neurons. Thus, we concluded that the distinct neurogenetic pattern makes the difference of neuronal organization between the mammalian layered neocortex and the chick non-layered telencephalon.

Inferring natural selection operating on conservative and radical substitution at single amino acid sites (Suzuki Y)
Natural selection operating on amino acid substitution at single amino acid sites can be detected by comparing the rates of synonymous (rS) and nonsynonymous (rN) nucleotide substitution at single codon sites. Amino acid substitutions can be classified as conservative or radical according to whether they retain the properties of the substituted amino acid. Here methods for comparing the rates of conservative (rC) and radical (rR) nonsynonymous substitution with rS at single codon sites were developed to detect natural selection operating on these substitutions at single amino acid sites. A method for comparing rC and rR at single codon sites was also developed to detect biases toward these substitutions at single amino acid sites. Charge was used as the property of the amino acids. In a computer simulation, false-positive rates of these methods were always < 5%, unless termination sites were included in the computation of the numbers of sites and estimates of transition/transversion rate ratio were highly biased. The frequency of detection of natural selection operating on conservative substitution was almost independent of the presence of natural selection operating on radical substitution, and vice versa. Natural selection operating specifically on conservative and radical substitution was detected more efficiently by comparing rS with rC and rS with rR than by comparing rS with rN. These methods also appeared to be robust against the occurrence of recombination during evolution. In an analysis of class I human leukocyte antigen, negative selection operating on conservative substitution, but not positive selection operating on radical substitution, was observed at some of the codon sites with rR > rC, suggesting that rR > rC may not necessarily be an indicator of positive selection operating on radical substitution.

Multiple transmissions of tick-borne encephalitis virus between Japan and Russia (Suzuki Y)
Tick-borne encephalitis (TBE) is a zoonotic disease causing meningitis, encephalitis, and meningoencephalitis. Tick-borne encephalitis virus (TBEV) is the etiological agent of TBE. From an analysis of five distinct sequences of Japanese TBEV, it has been proposed that

Japanese TBEV was transmitted from Russia to Japan on just a single occasion 260-430 years ago. Here, to better understand the origin and evolution of Japanese TBEV, thirteen distinct nucleotide sequences encoding the entire region of the envelope protein for Japanese TBEV were analyzed. It is shown, from the phylogenetic analysis, that Japanese TBEV belongs to the Far Eastern subtype, which is known to be highly pathogenic. Japanese TBEV was divided into three groups, and TBEV was inferred to have been transmitted between Japan and Russia at least three times, possibly through migratory birds, with five possible scenarios. TBEV was inferred to have been endemic to Japan for several hundred years. These results indicate that vaccines against TBEV should be licensed in Japan.

Search for the evolution of gap junction
(Takaku Y, Hwang JS, Hayakawa S, Wolf A, Svensson L, David CN, Ikeo K and Gojobori T)
Cnidarians represents the first animal phylum, in evolution, that possesses a simple nervous system as well as active behaviors. In Hydra, a member of phylum Cnidaria, the typical gap junction has been revealed by EM, and more than a dozen of innexin genes had been found. With the aim of elucidating functional importance of gap junction in nervous system during evolution, we conducted the following experiments: (1) Using heptanol as a gap junction inhibitor, we compared movements of intact Hydra (a standard wild-type strain 105 of Hydra magnipapillata) with those of epithelial Hydra that were completely devoid of nerve cells. Then, we found that in the presence of heptanol, though quick contractile movements of body column were completely prevented in both normal Hydra and epithelial Hydra, only a part of the feeding behavior by their tentacles remained in normal Hydra. It was thought that only chemical synapses in nervous system contribute to these movements, suggesting that gap junction is important for the feeding behavior by tentacles. (2) We also performed in situ hybridization to localize expression to specific innexin of nervous system in Hydra. The different expression patterns of the different innexins indicate that they could have different functions or regulators - regulators that interact with the varying c-terminals. From the results of those experiments, we concluded that without gap junctions, sophisticated and coordinated modulations in nervous system would not have been evolutionarily attainable.

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2 . Hirahata, M., Abe, T., Tanaka, N., Kuwana, Y., Shigemoto, Y., Miyazaki, S., Suzuki, Y. and Sugawara, H. (2007) Genome Information Broker for Viruses (GIB-V): database for comparative analysis of virus genomes , **Nucleic Acids Research** , 35 , 339 - 342
3 . Suzuki, Y. (2007) Inferring natural selection operating on conservative and radical substitution at single amino acid sites , **Genes & Genetic Systems** , 82 , 341 - 360
4 . Suzuki, Y. (2007) Multiple transmissions of tick-borne encephalitis virus between Japan and Russia , **Genes & Genetic Systems** , 82 , 187 - 195
5 . Matsuya, A., Sakate, R., Kawahara, Y., Koyanagi, KO., Sato, Y., Fujii, Y., Yamasaki, C., Habara, T., Nakaoka, H., Todokoro, F., Yamaguchi, K., Endo, T., OOta, S., Makalowski, W., Ikeo, K., Suzuki, Y., Hanada, K., Hashimoto, K., Hirai, M., Iwama, H., Saitou, N., Hiraki, AT., Jin, H., Kaneko, Y., Kanno, M., Murakami, K., Noda, AO., Saichi, N., Sanbonmatsu, R., Suzuki, M., Takeda, J., Tanaka, M., Gojobori, T., Imanishi, T. and Itoh, T. (2008) Evola: Ortholog database of all human genes in H-InvDB with manual curation of phylogenetic trees , **Nucleic Acids Res.** , 36 , 787 - 792
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7 . Tanaka, T., Itoh, T., Sasaki, T., Gojobori, T., Hsing, Y., Han, B., McCombie, W., Apweiler, R., Tyagi, A., Haberer, G., Bruskiewich, R., Bureau, T., Tatusova, T., An, G.,

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9 . Yuge, K., Ikeo, K. and Gojobori, T. （2007） Evolutionary origin of sex-related genes in the mouse brain , **GENE** , 406 , 108 - 112

10 . 牧野 能士、五條堀 孝 （2007） タンパク質間相互作用がタンパク質分子の進化に与える影響 , 生体の科学 タンパク質間相互作用 , 58 , 348 - 351

11 . 日紫喜 光良、五條堀 孝 （2007） 世界における疾患データベースの現状 , 最新医学 , 62 , 44 - 55

12 . Jung Shan, H., Ohyanagi, H., Hayakawa, S., Osato, N., Nishimiya-Fujisawa, C., Ikeo, K., David, C., Fujisawa, T. and Gojobori, T. （2007） The evolutionary emergence of cell type specific genes inferred from the gene expression analysis of hydra , **Proc. Natl. Acad. Sci. USA** , 104 , 14735 - 14740

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15 . Osato, N., Suzuki, Y., Ikeo, K. and Gojobori T. （2007） Transcriptional interferences in cis natural antisense transcripts of human and mouse , **Genetics** , 176 , 1299 - 1306

16 . Liu, QX., Nakashima-Kamimura, N., Ikeo, K., Hirose, S. and Gojobori T. （2007） Compensatory Change of Interacting Amino Acids in the Coevolution of Transcriptional Coactivator MBF1 and TATA-Box Binding Protein TBP , **Mol. Biol. Evol.** , 24 , 1458 - 1463

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ORAL PRESENTATION

1 . 鈴木 善幸 データベース検索実習2 FASTA、BLASTの使い方 第17回DDBJing講習会 国立遺伝学研究所 5月

2 . 鈴木 善幸 ClustalWの講義と実習 第17回DDBJing講習会 国立遺伝学研究所 5月

3 . 鈴木 善幸 BLASTを中心とする相同性検索の方法と実習 第18回DDBJing講習会 香川大学 11月

4 . 五條堀孝 脳・神経系に特異的に発現する遺伝子の進化的描像 遺伝子実験施設セミナー 東京大学 1/29

5 . 五條堀孝 脳・神経系に特異的に発現する遺伝子の進化的描像 2006年生物科学専攻修士一回生自主セミナー 京都大学理学部 3/9

6 . Gojobori, T. Genomic Evolution 2007 Sino-Japan-Korea Bioinformatics Training

POSTER PRESENTATIONS

1．Suzuki, Y.「New methods for detecting positive selection at single amino acid sites」, The 883rd National Institute of Genetics Colloquium , Mishima , 4月
2．鈴木 善幸「インフルエンザウイルスの分岐年代」, 第21回インフルエンザ研究者交流の会シンポジウム , 横浜 , 5月
3．鈴木 善幸「Multiple transmissions of tick-borne encephalitis virus between Japan and Russia」, 第9回日本進化学会大会 , 京都 , 8月-9月
4．鈴木 善幸「Natural selection on the influenza virus and hepatitis virus genomes」, 第9回日本進化学会大会 , 京都 , 8月-9月
5．鈴木 善幸「日本とロシアの間におけるダニ媒介性脳炎ウイルスの複数回伝播」, 第79回日本遺伝学会大会 , 岡山 , 9月
6．鈴木 善幸「同義置換速度と非同義置換速度の比較による自然選択圧検出法の展開」, 国立遺伝学研究所研究会 , 三島 , 12月
7． Gojobori, T. 「Transcriptional Landscape of Human Genome and its Evolutionary Implication to Isochore Structures」, Symposium on Evolutionary Genomics , San Jose, Costa Rica , 1/8
8．五條堀孝「健康情報産業のこれから」, 福岡県バイオ産業拠点推進会・H18年度顧問会議 , 福岡 , 2/15
9．五條堀孝「ゲノムネットワーク・プラットフォームにおける知識基盤形成と転写制御ネットワーク解明への展望」,『医学・生物学へ展開するゲノムネットワーク』、第3回GNPシンポジウム , 東京 , 2/16
10．五條堀孝「ゲノムネットワーク・プラットフォームにおける知識基盤形成と転写制御ネットワーク解明への展望」,『医学・生物学へ展開するゲノムネットワーク』、第3回GNPシンポジウム , 東京 , 2/16
11．五條堀孝「分子情報基盤データベース「DDBJについて」」, 機構シンポジウム「情報とシステム2007～利用者のためのライフサイエンスデータベース－その現状と将来-」, 東京 , 3/1
12．五條堀孝「脳・神経系に特異的に発現する遺伝子の進化解析」, 平成18年度病態発現機構客員研究部門研究発表会 , 東京 , 3/20
13．五條堀孝「GTOP: Never STOP」, 西川教授退職研究会「タンパク質の構造からゲノム情報解析まで」, 静岡県三島市 , 3/22
14．Ikeo,K.「ゲノムの配列比較から見た生物進化」, 上智大学 , 東京 , 2/27

EDUCATION

1．五條堀孝 Disease Edition Meeting 東京都江東区 1/31-2/2
2． 堀田凱樹、五條堀孝 機構シンポジウム「情報とシステム2007～利用者のためのライフサイエンスデータベース-その現状と将来-」 東京 3/1

BOOK

1．Makino, T. and Gojobori, T.（2007）Evolution of Protein-Protein Interaction Network **Gene and Protein Evolution. Genome Dynamics Vol,3** 13 - 29

OTHERS

1．五條堀 孝，1，Editor of FEBS Letters
2．五條堀 孝，1，Editor of GENE
3．五條堀 孝，1，Associate Editor of Molecular Biology and Evolution
4．五條堀 孝，1，Associate Editor of PLoS Genetics
5．五條堀 孝，1，Editorial Board of OMICS A Journal of Integrative Biology
6．五條堀 孝，1，Editorial Board of Gene Therapy and Molecular Biology
7．五條堀 孝，1，Editorial Board of BMC Genomics
8．五條堀 孝，1，DNA鑑定学理事長
9．五條堀 孝，1，日本進化学会評議委員
10．五條堀 孝，1，日本遺伝学会評議員

11．五條堀　孝，1，日本組織適合性学会理事
12．五條堀　孝，1，遺伝学普及会常務理事
13．五條堀　孝，2，Pontifical Academy of Sciences会員(法王庁科学アカデミー会員（バチカン市国）)

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I. CENTER FOR INFORMATION BIOLOGY AND DNA DATA BANK OF JAPAN
I-c. Laboratory for Gene Function Research
Yoshio Tateno

RESEARCH ACTIVITIES

PUBLICATIONS
Papers

1 . Sugawara, H., Ogasawara, O., Okubo, K., Gojobori, T. and Tateno, Y. (2008) DDBJ with new system and face , **Nucleic Acids Res** , 36 , 22 - 24
2 . Itho, T., Tanaka, T, Barrero, R. A. et al. (2007) Curated genome annotation of Oryza sativa ssp. japonica and comparative genome analysis with Arabidopsis thaliana , **Genome Reserarch** , 17 , 175 - 183
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4 . Fukami-Kobayashi, K., Minezaki, Y., Tateno, Y. and Nishikawa, K. (2007) A tree of life based on protein domain organizations , **Mol Biol Evol** , 24 , 1181 - 1189
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6 . Sugawaea, H., Abe, T., Gojobori, T. and Tateno, Y. (2006) DDBJ working on evaluation and classification of bacterial genes in INSDC , **Nucleic Acids Res** , 35 , 13 - 15
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ORAL PRESENTATION

1 . Tateno, Y. Bioinformatics I-BIO Program, Pohang University of Science and Technology, Pohang, Korea 1/11 - 1/16
2 . Tateno, Y. Molecular population genetics The 6th China-Japan-Korea Bioinformatics Training Course Shanghai Jiao Tong University, Shanghai, China 3/27-3/30

POSTER PRESENTATIONS

1 . Y. Tateno 「 A tree of life constructed by domain organizations of proteins 」, Biodiversity Workshop , Tibet, China , 6/6 - 6/15
2 . Y. Tateno 「 A tree of life constructed by genome-wide information 」, BioEco2007 International Conference , Tianjin, China , 6/26 - 6/28
3 . Tateno, Y. 「 Genomic analysis of MHC genes in primates 」, ICQBIC2007 , Tokyo

Science University, Noda, Chiba-pref., Japan , 3/14-3/17

EDUCATION

1 . SCBIT/DDBJ/KRIBB The 6th JKC Bioinformatics Training Course Shanghai, China 3/27 - 3/30

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I. CENTER FOR INFORMATION BIOLOGY AND DNA DATA BANK OF JAPAN
I-d. Laboratory for Research and Development of Biological Databases

Hideaki Sugawara

RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1．Hirahata M, Abe T, Tanaka N, Kuwana Y, Shigemoto Y, Miyazaki S, Suzuki Y, Sugawara H.（2007）“Genome Information Broker for Viruses (GIB-V): database for comparative analysis of virus genomes”，**Nucleic Acids Res.(Database)**，35，339 - 342

2．Sugawara H, Abe T, Gojobori T, Tateno Y.（2007）“DDBJ working on evaluation and classification of bacterial genes in INSDC”，**Nucleic Acids Res. (Database)**，35，13 - 15

ORAL PRESENTATION

1．菅原秀明　標準化がもたらす異種データベースの相互運用性　蛋白研セミナー:「生命・医科学データベースとその高度化」 大阪大学蛋白質研究所　3/12

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I. CENTER FOR INFORMATION BIOLOGY AND DNA DATA BANK OF JAPAN
I-e. Laboratory for Gene-Expression Analysis

Kousaku Okubo

RESEARCH ACTIVITIES

A Theoretical Model of GeneExpressionEvolution

Ogasawara O, Okubo K

With the advent of genome wide gene expression profiling techniques, an increasing number of studies have been published reporting comparisons of gene expression profiles within or among species in order to identify general pattern of the heritable variations in gene expression profiles, and to estimate the relative impact of the evolutionary forces acting on gene expression evolution.

However the reported patterns were not necessarily consistent with each other. In some report there was an at least modest correlation between the expression divergence within and among species, whereas in another reported there was only poor correlation between them.

Estimated proportion of genes being subject to the stabilizing selection ranged from 7% to 99%. Although there were a number of reason for this discrepancy, we found that the one obvious reason was the lack of a commonly accepted statistical procedures for comparative analysis of gene expression profiles. Especially, there was no well-established theoretical model which could be used as a null hypothesis of statistical test.

By using a theoretical model of gene expression evolution we proposed previously for explaining the genesis of a general pattern of the mRNA abundance distribution called the Zipf's law of transcriptome, we examined the causes of the observed discrepancies. Consequently, we found that in some studies the proportion of genes being subject to the stabilizing selection might be heavily overestimated, and we concluded that for majority of genes evolutionary changes in mRNA abundance would be selectively neutral.

In quest of a new post-genomic view in the evolution and expression of proteins encoded in the yeast Saccharomyces cerevisiae

Luis Fernando Encinas Ponce

Why do proteins evolve at different rates?
How to explain the links between expression level and rate of evolution?

Judging by the diversity of high-throughput data available, it is not longer tenable to suppose that protein evolution is affected only by selection acting at one level. There is a need for a new “post-genomic view” in which protein evolution should be approached from a holistic perspective.
In that direction and in trying to make the most of the emerging field of evolutionary systems

biology, we are aimed to develop integrative analyses of different functional and structural factors that showed to have a particular influence not only on the evolutionary rate but also on the level a gene expresses. Our initial results demonstrated that rather than taking mRNA levels as overall constraints of sequence evolution, other expression-related variables such as translational efficiency should be considered.

Making extensive use of statistical methods we could quantify the importance of many gene/protein characteristics and found that, in general, structural variables are more important than those we have classified as functional. While these results contradict the findings of previous reports that stressed the influence of variables such as dispensability and essentiality, they allow us to extend our discussion to some hypotheses proposed to explain the underlying associations between expression level and rate of evolution.

Finally, a theoretical framework that represents all possible biological interactions among variables was devised and constitutes the basis of a modeling process that not only helps us to reveal the complexity of associations existing between variables, but also shows how, at least in theory, we can predict the behavior of some of them using information from others.

PUBLICATIONS

Papers

1．Hoshino H, Uchida T, Otsuki T, Kawamoto S, Okubo K, Takeichi M, Chisaka O（2007） Cornichon-like Protein Facilitates Secretion of HB-EGF and Regulates Proper Development of Cranial Nerves.，**Molecular Biology of the Cell**，，1143 - 1152

ORAL PRESENTATION

1．大久保公策　生命研究者として情報基盤を考える　第900回遺伝研内部交流セミナー　国立遺伝学研究所　10/19
2．大久保公策　生命情報基盤から読み解く「科学の仕組み」～オタクとカガクはおんなじか～　国立遺伝学研究所　公開講演会2007　東京　11/10

POSTER PRESENTATIONS

1．大久保公策「ライフサイエンスのデータベースの現状と課題」，情報・システム研究機構シンポジウム，東京，3/1
2．大久保公策「生命科学情報の情報基盤を考える:「知」のめぐりは充分か？」，「生命をはかる」研究会　第20回研究会，東京，3/12
3．大久保公策「生命科学分野でのDB統合の意味と意義」，ライフサーベイヤ技術開発計画会議，伊東市，5/28
4．大久保公策「生命科学分野でのDB統合の意味と意義」，日本バイオインフォマティクス学会　第1回JSBi合同研究会，東京，5/29
5．大久保公策「補完的課題「生命科学データベース統合に関する調査研究」報告」，生命科学の基礎・基盤連携群シンポジウム，東京，11/29
6．大久保公策「生命研究者として情報基盤を考える」，関西眼疾患研究会特別講演，京都，12/19
7．大久保公策「ライフサイエンスのデータベースの現状と課題」，情報・システム研究機構シンポジウム，東京，3/1
8．大久保公策「生命科学情報の情報基盤を考える:「知」のめぐりは充分か？」，「生命をはかる」研究会　第20回研究会，東京，3/12

BOOK

1．大久保公策（2007）「生命科学データベースの現状と課題」 雑誌『科学』 364 - 369
2．大久保公策（2007）「生命科学データベース統合化の背景」【シリーズ「ライフサイエンス分野の統合データベース」第1回】「蛋白質核酸酵素」 1027 - 1031
3．大久保公策（2007）生命科学データベースの現状と課題ーパラダイム転換の最後のバリアー　科学 **Vol.77 No.4**　364 - 369

DB SOFT

1．Ogasawara O, Arikawa K, Watanabe K, Iizuka T, Okubo K，文部科学省データベース統合プロジェクト　ヒト統合ボディーマップ
http://okubolab.genes.nig.ac.jp/bodymap_i/

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J. CENTER FOR FRONTIER RESEARCH
J-b. Neural Morphogenesis Laboratory
Emoto Kazuo

RESEARCH ACTIVITIES

Genetic and Epigenetic control of neural network

Kazuo Emoto

Little is know about how neurons establish and maintain their unique dendritic fields in development. Drosophila dendrite arborization (da) sensory neurons can be classified into 4 subtypes (I-IV) based on their dendritic morphology, and the dendritic field of class IV da neurons is shaped in part through a like-repels-like tiling behavior of dendrite terminals. We have previously identified the protein kinase Tricornered (Trc) as an essential regulator of dendritic tiling and branching in class IV da neurons (Emoto et al., Cell 119 245, 2004). In this year, we have obtained compelling evidence that the tumor suppressor gene hippo (hpo), which encodes a Ste-20 like kinase, functions together with trc to ensure dendritic tiling. In larvae transheterozygous for null mutations of trc and hpo, tiling is defective in class IV neurons, demonstrating that trc and hpo interact in vivo. Hpo physically associates with Trc in neurons and can phosphorylate Trc in vitro, consistent with a model in which Hpo regulates Trc activity. In addition to this novel interaction with Trc, we have found that Hpo-mediated regulation of dendrite morphogenesis also requires the function of the Warts/Lats (Wts) kinase, which is known to function with Hpo to promote cell cycle arrest and apoptosis and to share a homologous kinase domain and conserved phosphorylation sites with Trc. However, unlike trc, wts mutations cause a progressive reduction in the number and length of class IV dendritic branches, similar to the phenotype observed in hpo mutant clones. Taken together, we propose that Hpo kinase regulates multiple aspects of dendrite development in maturing class IV da neurons through distinct downstream signaling pathways: the Trc kinase pathway for dendrite branching and tiling and the Wts kinase pathway for dendrite maintenance.

PUBLICATIONS

Papers

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2 . Parrish, J. Z. Emoto, K., Kim, M. D., and Jan, Y. N. (2007) Mechanisms that regulate establishment, maintenance, and remodeling of dendritic fields. , **Annu. Rev. Neurosci.** , 30 , 399 - 423
3 . Parrish, J.Z., Emoto, K., Jan, L.Y., Jan, Y.N. (2007) Polycomb genes interact with the tumor suppressor hippo and warts in the maintenance of Drosophila sensory neuron dendrites. , **Genes and Development** , 21 , 956 - 972

POSTER PRESENTATIONS

１．　榎本和生　「 ニューロン受容領域を決定・維持するキナーゼシグナル・ネットワーク 」, BMB2007 , 横浜 , 12/14

BOOK

１．榎本和生 （2007） ニューロンはいかにして固有の受容領域を獲得し、それを維持・管理するのか？　蛋白質核酸酵素　842 - 852
２．榎本和生、小池（熊谷）牧子 （2007） ニューロン受容領域のタイル化を制御するリン酸化シグナルネットワーク　細胞工学　806 - 810

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J. CENTER FOR FRONTIER RESEARCH
J-c. Cell Architecture Laboratory
Kimura Akatsuki

RESEARCH ACTIVITIES

POSTER PRESENTATIONS

1．Kimura, A.「線虫初期胚における核と染色体の配置メカニクス」，クロマチン研究会，三島，10/26
2．Hara, Y.「線虫C. elegans初期胚における細胞の大きさ依存的な紡錘体伸長メカニズムの定量的解析」，第30回日本分子生物学会年会・第80回日本生化学会大会　合同大会，横浜，12/11
3．Kimura, K.「線虫C.elegansの初期胚における微小管に依存したオルガネラの配置」，第30回日本分子生物学会年会・第80回日本生化学会大会合同大会(BMB2007)，横浜，12/12
4．Niwayama, R.「Measurement and modeling of cytoplasmic flow in the one cell stage C. elegans embryo」，日本生物物理学会45 回年会，横浜，12/23
5．Koyama, H.「Experimental and theoretical analyses of cell shape transformation during cell division in Caenorhabditis elegans early embryonic cells」，日本生物物理学会第45会年会，横浜，12/23
6．Kimura, A.「デジタル細胞を利用した仮説発見―細胞空間のデザイン原理への機能的アプローチ―」，情報・システム研究機構　融合研究シンポジウム「地球と生命の新パラダイム創造への挑戦」，東京，10/18
7．Kimura, A.「線虫C. elegans初期胚をモデルとした核の細胞内配置を決定する力の解析」，第30回日本分子生物学会年会・第80回日本生化学会大会合同大会(BMB2007)，横浜，12/14
8．Kimura, A.「Mitosis-coupled positioning of centrosomes in C. elegans embryo」，第40回日本発生生物学会第59回日本細胞生物学会合同大会，福岡，5/28

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Papers

1 . Gerding, M. A., Ogata, Y., Pecora, N. D., Niki, H., de Boer, P. A. (2007) The trans-envelope Tol-Pal complex is part of the cell division machinery and required for proper outer-membrane invagination during cell constriction in E. coli. , **Mol. Microbiol.** , 63 , 1008 - 1025

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Papers

1．Ken-Ichi Nonomura, Akane Morohoshi, Mutsuko Nakano, Mitsugu Eiguchi, Akio Miyao, Hirohiko Hirochika and Nori Kurata （2007） A Germ Cell-Specific Gene of the ARGONAUTE Family Is Essential for the Progression of Premeiotic Mitosis and Meiosis during Sporogenesis in Rice，**Plant Cell**，19，2583 - 2594
2．Schaller, G.E., Doi, K., Hwang, I., Kieber, J.J., Khurana, J.P., Kurata, N., Mizuno, T., Pareek, A., Shiu, S.H., Wu, P., Yip, W.K. （2007） Nomenclature for two-component signaling elements of rice.，**Plant Physiol.**，，555 - 557
3．Suzuki, T., Eiguchi, M., Kumamaru, T., Satoh, H., Matsusaka, H., Moriguchi, K. and Kurata N.（0）MNU-induced mutant pools and high performance TILLING enable finding of any gene mutation in rice.，**Mol. Genet. Genomics**，279，213 - 223
4．Miyabayashi, T., Nonomura, K.I., Morishima, H. and Kurata, N.（2007）Genome size of twenty wild species of Oryza determined by flow cytometric and chromosome analyses.，**Breeding Science**，57，73 - 78

ORAL PRESENTATION

1．野々村賢一　イネの生殖細胞発生および減数分裂に関わる遺伝子の解析　公開セミナー（遺伝子資源工学専攻・遺伝子資源開発研究センター）　21世紀交流プラザ第2講義室(九州大学大学院農学研究院) 10/26

POSTER PRESENTATIONS

1．Nonomura, K.I., Nakano, M., Eiguchi, M., Miyao, A., Hirochika, H., Kurata, N.「Rice meiosis and its relation to small RNA-mediated gene silencing」, EMBO world workshop, 8th European Meiosis Meeting，Hayama, Kanagawa, Japan，9/13-18
2．Ken-Ichi Nonomura「A germ-cell specific ARGONAUTE gene and its function in reproductive gene regulation」, The 5th International Symposium of Rice Functional Genomics，つくば市，10/15-17
3．津田勝利,伊藤幸博,宮尾安藝雄,廣近洋彦,倉田のり「KNOX遺伝子を葉で異所的に発現するイネ突然変異体の解析1」, 日本育種学会第112回講演会，鶴岡市，9/22,23
4．米田典央、野々村賢一、倉田のり「イネPot1ホモログの単離と解析」, 日本遺伝学会　第79回大会，岡山，9/19-21
5．上田健治,豊澤恵子,高橋幸子,宮尾安藝雄,廣近洋彦,野々村賢一,倉田のり,井上正保「イネ花粉突然変異体TosO216の解析」, 日本植物学会第71回大会，東京，9/6-9
6．Nori Kurata, Tadzunu Suzuki, Toshihiro Kumamaru, Hikaru Satoh「High Performance

Rice Mutant Screening by using modified TILLING and MNU-induced mutant pools」, The 5th International Symposium of Rice Functional Genomics , つくば市 , 10/15-17
7． 堀内陽子,藤澤洋徳, 川喜田雅則,望月孝子, 春島嘉章,坂口隆之,倉田のり 「 Affymetrix Rice Genome Arrayを用いたSFP検出手法の開発 」, 日本育種学会第112回講演会 , 鶴岡市 , 9/22,23
8．伊藤幸博,津田勝利,永口貢,倉田のり「 KNOX遺伝子を葉で異所的に発現するイネ突然変異体の解析2 」, 日本育種学会第112回講演会 , 鶴岡市 , 9/22,23
9．水多陽子,春島嘉章,倉田のり「 イネ雑種花粉で作用する生殖的隔離障壁遺伝子のポジショナルクローニング 」, 日本育種学会第112回講演会 , 鶴岡市 , 9/22,23
10． 春島嘉章,倉田のり 「 栽培イネの第3染色体の雄性配偶体型生殖的隔離障壁と相互作用する第6染色体の雌性親遺伝子のポジショナルクローニング 」, 日本育種学会第112回講演会 , 鶴岡市 , 9/22,23
11． 板橋悦子,藤田雅丈,倉田のり,鳥山欽哉 「 BT型細胞質雄性不稔イネの花粉発達に関与する核遺伝子の発現解析 」, 日本育種学会第112回講演会 , 鶴岡市 , 9/22,23
12． 水多陽子,春島嘉章,倉田のり 「 イネ雑種花粉で相互作用する2遺伝子座に起因する生殖的隔離 」, 日本遺伝学会第79回大会 , 岡山市 , 9/19-21
13． 久保貴彦,吉村淳,倉田のり 「 イネの交雑後代に見出されたF_2雌性不稔の遺伝機構 」, 日本遺伝学会第79回大会 , 岡山市 , 9/19-21
14． 藤田雅丈,堀内陽子,上田弥生,水多陽子,倉田のり 「 イネの生殖過程を通じた遺伝子発現プロファイリング 」, 日本遺伝学会第79回大会 , 岡山市 , 9/19-21
15． 津田勝利,伊藤幸博,倉田のり 「 イネのKNOX遺伝子 OSH1の発現制御機構の解析 」, 日本遺伝学会第79回大会 , 岡山市 , 9/19-21
16． 春島嘉章,栗木哲,水多陽子,藤澤洋徳,倉田のり 「 イネF_2集団における生殖的隔離障壁の相互作用の検出 」, 日本遺伝学会第79回大会 , 岡山市 , 9/19-21
17． 米田典央,野々村賢一,倉田のり 「 イネPot1ホモログの単離と解析 」, 日本遺伝学会第79回大会 , 岡山市 , 9/19-21
18．野々村賢一 「 イネ生殖細胞形成過程を制御する遺伝子群の単離と機能解析 」, 第111回日本育種学会講演会、育種学会奨励賞受賞講演 , 水戸市 , 3/29
19．山中慎介, 江花薫子, 倉田のり, 呉健忠, 松本隆, D. A. Vaughan, 大川安信, 奥野員敏, 福岡修一, 河瀬真琴 「 イネAゲノム近縁野生種のDiversity Research Set作成に向けた多様性解析Ⅱ. 候補系統の選定 」, 日本育種学会第111回講演会 , 水戸市 , 3/30-31

EDUCATION

1．倉田のり、渡辺正夫、野々村賢一、久保貴彦　高等植物の受粉・受精形質（雌雄間相互作用形質）を統御する遺伝子の分子遺伝学的解析　国立遺伝学研究所研究集会　三島　11/16

BOOK

1． 野々村賢一 （ 2007 ） イネ生殖細胞形成過程を制御する遺伝子群の単離と機能解析 Vol.9 育種学研究 147 - 152
2．Kurata, N.（2007）Chromosome and genome evolution in rice. **Rice Biology in the Genomics Era.** 235 - 243
3．Ohtsubo, H., Tsuchimoto, S., Xu, J-H., Cheng, C., Kuroda, M.Y., Kurata, N. and Ohtsubo, E.（2007） Rice retroposon, p-SINE, and its use for classification and Identification of Oryza species. **Rice Biology in the Genomics Era.** 277 - 289
4．倉田のり, 春島嘉章 （2007）イネゲノムと生殖的隔離　植物の進化（細胞工学別冊） 97 - 101

OTHERS

1．野々村賢一 , 2 , 野々村賢一「イネ生殖細胞形成過程を制御する遺伝子群の単離と機能解析」平成18年度日本育種学会奨励賞
2．倉田のり , 1 , 日本遺伝学会評議員
3．倉田のり , 3 , 日本学術会議　育種学分科会幹事
4．倉田のり , 3 , 日本学術会議　植物科学分科会会員
5．倉田のり , 3 , 生物遺伝資源イネ小委員会委員長

6．Nori Kurata，3，Rice Genetics Newsletter Editor
7．Nori Kurata，3，NSF project proposal reviewer
8．野々村賢一，1，日本育種学会幹事

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N. TECHNICAL SECTION
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RESEARCH ACTIVITIES

PUBLICATIONS

Papers

1. Miyabayashi, T., Nonomura, K.I., Morishima, H. and Kurata, N. (2007) Genome Size of Twenty Wild Species of Oryza Determined by Flow Cytometric and Chromosome Analyses, **Breeding Science**, 57, 73-78

POSTER PRESENTATIONS

1. 谷口美佐子「ショウジョウバエの神経回路形成に関わる新規遺伝子の探索方法について」, 第18回生物学技術研究会, 愛知県岡崎市, 2/15-16
2. 古海 弘康 「マウス精子を用いたDNAメチル化の解析」, 第18回生物学技術研究会, 愛知県岡崎市, 2/15-16

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Long, H.	E-c Division of Brain Function
Lucotte G.	D-a Division of Population Genetics
M. Ikeguchi	A-b Division of Mutagenesis

Ma, L.	E-c Division of Brain Function
Makalowski, W.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Maki KUSUMI	E-a Division of Human Genetics
Maki, H.	B-a Division of Cytogenetics
Makino, T.	I-a Laboratory for DNA Data Analysis
Manabe, T.	C-a Division of Developmental Genetics
Marra, M.A.	G-b Genome biology Laboratory
Martin, B.	F-c Mouse Genomics Resource Laboratory
Maruyama,Y.	H-e Gene Network Laboratory
Masahiro KANEDA	E-a Division of Human Genetics
Masaki Hiramoto	C-a Division of Developmental Genetics
Masaki OKANO	E-a Division of Human Genetics
Masako Sakai	F-f Microbial Genetics Laboratory
Masami NOZAKI	E-a Division of Human Genetics
Masaoki Tsudzuki	E-a Division of Human Genetics
Masayuki FUKASAWA	E-a Division of Human Genetics
Masayuki Oginuma	F-b Mammalian Development Laboratory
Mason, L.	C-c Division of Molecular and Developmental Biology
Masu, M.	F-a Mammalian Genetics Laboratory
Masuda, A.	F-d Model Fish Genomics Resource
Masuya H.	F-a Mammalian Genetics Laboratory
Masuya, H.	F-a Mammalian Genetics Laboratory
Mathur, P.	C-c Division of Molecular and Developmental Biology
Matsui Y	F-b Mammalian Development Laboratory
Matsumoto, A.	F-g Invertebrate Genetics Laboratory
Matsuno K.	F-g Invertebrate Genetics Laboratory
Matsuno M	C-a Division of Developmental Genetics
Matsusaka, H.	L EXPERIMENTAL FARM
Matsushima, K.	G-b Genome biology Laboratory
Matsuya, A.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Matsuzaki, Y.	F-b Mammalian Development Laboratory
Maximiliano, S.	C-c Division of Molecular and Developmental Biology
McBride JJ	F-b Mammalian Development Laboratory
McCombie, W.	I-a Laboratory for DNA Data Analysis
McGhee, J.D.	G-b Genome biology Laboratory
McKay, S.J.	G-b Genome biology Laboratory
Megumi Hashiguchi	F-d Model Fish Genomics Resource
Meguro-Horike,M.	E-a Division of Human Genetics
Menon MK	F-b Mammalian Development Laboratory
Messing, J.	I-a Laboratory for DNA Data Analysis
Meyers, B.	I-a Laboratory for DNA Data Analysis
Mika KIMURA	E-a Division of Human Genetics
Miki, T.	G-a Genetic Informatics Laboratory

Minami,N.	E-a Division of Human Genetics
Minamino, T.	C-c Division of Molecular and Developmental Biology
Minezaki, Y.	I-c Laboratory for Gene Function Research
Minori Shinya	F-d Model Fish Genomics Resource
Mishina, M.	F-a Mammalian Genetics Laboratory
Mita, A.	F-a Mammalian Genetics Laboratory
Mitani H	F-b Mammalian Development Laboratory
Mitani, H.	F-d Model Fish Genomics Resource
Mitani, S.	G-b Genome biology Laboratory
Mitchell, K.J.	C-a Division of Developmental Genetics
Mitsugu Eiguchi	L EXPERIMENTAL FARM
Mitsuhara, K.	I-a Laboratory for DNA Data Analysis
Miura A	E-b Division of Agricultural Genetics
Miura I.	F-a Mammalian Genetics Laboratory
Miura, I.	F-a Mammalian Genetics Laboratory
Miura, K.	I-a Laboratory for DNA Data Analysis
Miwa, Y.	G-b Genome biology Laboratory
Miyabayashi, T.	N Technical Section F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Miyagawa-Tomita, S.	F-b Mammalian Development Laboratory
Miyakawa, T.	F-a Mammalian Genetics Laboratory
Miyake A	F-b Mammalian Development Laboratory
Miyamoto,T.	H-b Molecular Biomechanism Laboratory
Miyao, A.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Miyazaki S	I-d Laboratory for Research and Development of Biological Databases
Miyazaki, S.	I-a Laboratory for DNA Data Analysis
Miyoshi A.	D-a Division of Population Genetics
Mizokami, M.	I-a Laboratory for DNA Data Analysis
Mizue HISANO	E-a Division of Human Genetics
Mizuno, H.	C-a Division of Developmental Genetics
Mizuno, T.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Mizusawa, K.	C-c Division of Molecular and Developmental Biology
Mizushima H.	F-a Mammalian Genetics Laboratory
Mizushina, Y.	F-a Mammalian Genetics Laboratory
Mochizuki, N.	C-c Division of Molecular and Developmental Biology
Moerman, D.G.	G-b Genome biology Laboratory
Montgomery, K.L.	C-c Division of Molecular and Developmental Biology
Moore,E.G.	E-a Division of Human Genetics
Mori, H.	F-a Mammalian Genetics Laboratory F-f Microbial Genetics Laboratory
Moriguchi, K.	L EXPERIMENTAL FARM
Morimoto ,M.	F-b Mammalian Development Laboratory
Morishima, H.	N Technical Section

	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Morishita, S.	G-b Genome biology Laboratory
Morishita, T.	G-b Genome biology Laboratory
Morita, M.	C-a Division of Developmental Genetics
Morita, R.	C-a Division of Developmental Genetics
Morita, Y.	F-a Mammalian Genetics Laboratory
Moriwaki K.	F-a Mammalian Genetics Laboratory
Moriwaki, K.	F-a Mammalian Genetics Laboratory
Moriyama ,A.	F-b Mammalian Development Laboratory
Moro-oka, N.	F-f Microbial Genetics Laboratory
Morohoshi, A.	F-e Plant Genetics Laboratory
Murakami R	F-b Mammalian Development Laboratory
Murakami S.	H-d Biomolecular Structure Laboratory
Murakami, K.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Murakami, S.	F-g Invertebrate Genetics Laboratory
Muramatsu,S.	B-b Division of Microbial Genetics
Murphy, J.	C-c Division of Molecular and Developmental Biology
Mutou, A.	C-c Division of Molecular and Developmental Biology
Mutsuko Nakano	L EXPERIMENTAL FARM
N. Thomson	I-c Laboratory for Gene Function Research
N.D.	G-b Genome biology Laboratory
Nabeshima,Y.	H-e Gene Network Laboratory
Nagao, T.	F-g Invertebrate Genetics Laboratory
Nagaoka, S.	G-a Genetic Informatics Laboratory I-c Laboratory for Gene Function Research
Nagayasu, Y.	G-b Genome biology Laboratory
Nagayoshi, S.	C-c Division of Molecular and Developmental Biology
Naito, A.	C-c Division of Molecular and Developmental Biology
Nakabayashi,K.	E-a Division of Human Genetics
Nakada, T.	C-c Division of Molecular and Developmental Biology
Nakagata, N.	G-a Genetic Informatics Laboratory
Nakagawa, S.	C-c Division of Molecular and Developmental Biology I-a Laboratory for DNA Data Analysis
Nakamaru, K.	C-c Division of Molecular and Developmental Biology
Nakamura, N.	F-g Invertebrate Genetics Laboratory
Nakano, M.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Nakao, K.	F-a Mammalian Genetics Laboratory
Nakaoka, H.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Nakatani, Y.	G-b Genome biology Laboratory
Nakatsuji, N.	E-a Division of Human Genetics
Nakayama, S.	G-b Genome biology Laboratory
Nakayama, T.	C-b Division of Gene Expression E-b Division of Agricultural Genetics
Naojiro MINAMI	E-a Division of Human Genetics

Naomi KIMURA	E-a Division of Human Genetics
Naomi Kimura	E-a Division of Human Genetics
Narita T	F-b Mammalian Development Laboratory
Narita, T.	G-b Genome biology Laboratory F-a Mammalian Genetics Laboratory
Naruse K	F-b Mammalian Development Laboratory
Naruse, K.	G-b Genome biology Laboratory F-d Model Fish Genomics Resource
Natsume, T.	A-b Division of Mutagenesis
Navratilova, P.	C-c Division of Molecular and Developmental Biology
Niimura, Y.	I-a Laboratory for DNA Data Analysis
Nik,i H.	F-f Microbial Genetics Laboratory
Niki, H.	F-f Microbial Genetics Laboratory G-a Genetic Informatics Laboratory K RADIOISOTOPE CENTER
Nimmo, R.	G-b Genome biology Laboratory
Nishi, A.	F-c Mouse Genomics Resource Laboratory
Nishida K	H-a Biological Macromolecules Laboratory
Nishida, H.	G-b Genome biology Laboratory
Nishide, T.	G-b Genome biology Laboratory
Nishihara, S.	F-g Invertebrate Genetics Laboratory
Nishikawa, K.	I-c Laboratory for Gene Function Research
Nishio, T.	G-b Genome biology Laboratory
Nishioka, K.	C-b Division of Gene Expression
Niwayama, R.	J-c Cell Architecture Laboratory
Noda, A.O.	D-a Division of Population Genetics
Noda, AO.	I-a Laboratory for DNA Data Analysis
Nogata, K.	G-b Genome biology Laboratory
Nomoto, H.	G-b Genome biology Laboratory
Nomura, T.	F-a Mammalian Genetics Laboratory
Nonomura K.	F-e Plant Genetics Laboratory
Nonomura, K	F-e Plant Genetics Laboratory
Nonomura, K.I.	N Technical Section F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Nori Kurata	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Norio WAKE	E-a Division of Human Genetics
Noriyoshi Sakai	F-d Model Fish Genomics Resource
Noro, Y	D-a Division of Population Genetics
Nozaki,M.	E-a Division of Human Genetics
OOta, S.	I-a Laboratory for DNA Data Analysis
Obata, Y.	F-a Mammalian Genetics Laboratory
Ogasawara O	I-e Laboratory for Gene-Expression Analysis
Ogasawara, N.	F-f Microbial Genetics Laboratory
Ogasawara, O.	I-a Laboratory for DNA Data Analysis I-c Laboratory for Gene Function Research
Ogata, Y.	F-f Microbial Genetics Laboratory

	K RADIOISOTOPE CENTER
Ogawa K.	F-a Mammalian Genetics Laboratory
Oginuma ,M.	F-b Mammalian Development Laboratory
Oginuma, M.	F-b Mammalian Development Laboratory
Ohishi, K.	G-b Genome biology Laboratory
Ohki M.	F-a Mammalian Genetics Laboratory
Ohshima, T.	F-f Microbial Genetics Laboratory
Ohsumi K.	F-f Microbial Genetics Laboratory
Ohta, F.	G-b Genome biology Laboratory
Ohtsubo, E.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Ohtsubo, H.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Ohtsuka, T.	C-c Division of Molecular and Developmental Biology
Ohtsuki K	B-a Division of Cytogenetics
Ohyanagi, H.	I-a Laboratory for DNA Data Analysis
Oka, A.	F-a Mammalian Genetics Laboratory
Oka, K.	I-a Laboratory for DNA Data Analysis
Okabe M	C-a Division of Developmental Genetics
Okabe,M.	H-e Gene Network Laboratory
Okada, M.	A-a Division of Molecular Genetics
Okada, S.	G-b Genome biology Laboratory
Okamura, T.	F-g Invertebrate Genetics Laboratory
Okano, M.	E-a Division of Human Genetics
Okano,M.	E-a Division of Human Genetics
Okazawa,H.	H-e Gene Network Laboratory
Okubo K	I-e Laboratory for Gene-Expression Analysis
Okubo, K.	I-a Laboratory for DNA Data Analysis I-c Laboratory for Gene Function Research
Ono, F.	C-c Division of Molecular and Developmental Biology
Ono, R.	G-b Genome biology Laboratory
Ono, T.	A-a Division of Molecular Genetics E-b Division of Agricultural Genetics
Oogushi, K.	G-a Genetic Informatics Laboratory
Ooki S	F-b Mammalian Development Laboratory
Oota, S.	D-a Division of Population Genetics
Osame, M.	I-a Laboratory for DNA Data Analysis
Osato, N.	I-a Laboratory for DNA Data Analysis
Oshima, M.	D-a Division of Population Genetics
Otsu,K.	E-a Division of Human Genetics
Otsuki T	I-e Laboratory for Gene-Expression Analysis
Ozaki, Y.	F-d Model Fish Genomics Resource
P. A.	K RADIOISOTOPE CENTER
P. Sterk	I-c Laboratory for Gene Function Research
Paderi F.	F-f Microbial Genetics Laboratory
Pareek, A.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM

Park K. S.	D-a Division of Population Genetics
Parker-Katiraee,L.	E-a Division of Human Genetics
Parrish, J.Z.	J-b Neural Morphogenesis Laboratory
Pask, A.J.	G-b Genome biology Laboratory
Pecora, N. D.	K RADIOISOTOPE CENTER
Pecora, N.D.	F-f Microbial Genetics Laboratory
Perry, H.G.	E-a Division of Human Genetics
Petruck, S.	C-b Division of Gene Expression
Picot, M.	F-g Invertebrate Genetics Laboratory
Pool, A.	B-a Division of Cytogenetics
Postlethwait, J.H.	C-c Division of Molecular and Developmental Biology
Prall OW	F-b Mammalian Development Laboratory
Pu,M.-T.	E-a Division of Human Genetics
Qu, W.	G-b Genome biology Laboratory
R. Kottmann	I-c Laboratory for Gene Function Research
R.A.	G-b Genome biology Laboratory
Racine, V.	A-a Division of Molecular Genetics
Rawls A	F-b Mammalian Development Laboratory
Reiss, J.	C-c Division of Molecular and Developmental Biology
Renfree, M.B.	G-b Genome biology Laboratory
Richard Bruskiewich	G-a Genetic Informatics Laboratory
Riley, K.	C-b Division of Gene Expression
Robert A. Holt	G-b Genome biology Laboratory
Robertson BR	F-b Mammalian Development Laboratory
Robertson EJ	F-b Mammalian Development Laboratory
Robertson, A.G.	G-b Genome biology Laboratory
Rodriguez-Mari, A.	C-c Division of Molecular and Developmental Biology
Ryouta Kondou1	F-c Mouse Genomics Resource Laboratory
Ryutaro HIRASAWA	E-a Division of Human Genetics
S.T.	C-c Division of Molecular and Developmental Biology
SHIINA, N.	H-a Biological Macromolecules Laboratory
Saad, N.	G-b Genome biology Laboratory
Sado, Y.	F-g Invertebrate Genetics Laboratory
Sado,T.	E-a Division of Human Genetics
Saeki N.	F-a Mammalian Genetics Laboratory
Saga Y	F-b Mammalian Development Laboratory
Saga Y.	F-b Mammalian Development Laboratory
Saga, M.	G-a Genetic Informatics Laboratory
Saga, Y.	F-b Mammalian Development Laboratory
Sagai T.	F-a Mammalian Genetics Laboratory
Sagai, T.	D-a Division of Population Genetics F-a Mammalian Genetics Laboratory
Saheki, Y.	H-c Multicellular Organization Laboratory
Saichi, N.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Saigo K	F-g Invertebrate Genetics Laboratory
Saigo, K.	F-g Invertebrate Genetics Laboratory

Saito, K.	F-d Model Fish Genomics Resource
Saito, T.	G-a Genetic Informatics Laboratory I-c Laboratory for Gene Function Research
Saito, T.L.	G-b Genome biology Laboratory
Saitou M.	F-b Mammalian Development Laboratory
Saitou N.	D-a Division of Population Genetics
Saitou, N.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Saka, K.	F-d Model Fish Genomics Resource
Sakai, N.	F-d Model Fish Genomics Resource
Sakaida, M.	G-b Genome biology Laboratory
Sakaizumi, M.	G-b Genome biology Laboratory
Sakaki, Y.	F-a Mammalian Genetics Laboratory
Sakamoto H.	F-a Mammalian Genetics Laboratory
Sakamoto, H.	C-c Division of Molecular and Developmental Biology
Sakamoto, S.	G-a Genetic Informatics Laboratory
Sakaniwa, S.	G-a Genetic Informatics Laboratory
Sakata, R.	G-b Genome biology Laboratory
Sakata-Sogawa K	H-a Biological Macromolecules Laboratory
Sakata-Sogawa K.	H-a Biological Macromolecules Laboratory
Sakate, R.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Sakimura, K.	F-a Mammalian Genetics Laboratory
Sanbo, M.	C-a Division of Developmental Genetics
Sanbonmatsu, R.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Sano M	F-b Mammalian Development Laboratory
Sasaki H.	F-a Mammalian Genetics Laboratory
Sasaki N	F-g Invertebrate Genetics Laboratory
Sasaki, H.	E-a Division of Human Genetics F-a Mammalian Genetics Laboratory
Sasaki, N.	F-b Mammalian Development Laboratory F-g Invertebrate Genetics Laboratory
Sasaki, S.	G-b Genome biology Laboratory
Sasaki, T.	G-b Genome biology Laboratory I-a Laboratory for DNA Data Analysis
Sasaki,H.	E-a Division of Human Genetics
Sasamura T	F-g Invertebrate Genetics Laboratory
Sato E	H-a Biological Macromolecules Laboratory
Sato, M.	F-g Invertebrate Genetics Laboratory
Sato, Y.	C-c Division of Molecular and Developmental Biology D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Sato,A.	E-a Division of Human Genetics
Satoh, A.	F-a Mammalian Genetics Laboratory
Satoh, H.	L EXPERIMENTAL FARM
Satoh, N.	G-b Genome biology Laboratory
Satoh,A.	E-a Division of Human Genetics

Satomi MIYAGAWA	E-a Division of Human Genetics
Satoru TANAKA	E-a Division of Human Genetics
Satoshi Kitajima	F-b Mammalian Development Laboratory
Satou, Y.	G-b Genome biology Laboratory
Saze H	E-b Division of Agricultural Genetics
Saze, H.	E-b Division of Agricultural Genetics
Schaft D	F-b Mammalian Development Laboratory
Schaller, G.E.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Schweisguth, F.	C-b Division of Gene Expression
Scott, E.K.	C-c Division of Molecular and Developmental Biology
Sedkov, Y.	C-b Division of Gene Expression
Seguchi, O.	C-c Division of Molecular and Developmental Biology
Seki Haraguchi	F-b Mammalian Development Laboratory
Seki Y	F-b Mammalian Development Laboratory
Sekimizu K	F-b Mammalian Development Laboratory
Sengupta, P.	H-c Multicellular Organization Laboratory
Setiamarga DH	F-b Mammalian Development Laboratory
Sharoh, Y.	G-a Genetic Informatics Laboratory
Shaw, G.	G-b Genome biology Laboratory
Shiao MS.	F-a Mammalian Genetics Laboratory
Shibahara, K-i	E-b Division of Agricultural Genetics
Shibahara, K.	A-a Division of Molecular Genetics
Shibano, T.	C-c Division of Molecular and Developmental Biology
Shiekhattar, R.	A-a Division of Molecular Genetics
Shigeharu WAKANA	E-a Division of Human Genetics
Shigeki Yuasa2	F-c Mouse Genomics Resource Laboratory
Shigemoto Y	I-d Laboratory for Research and Development of Biological Databases
Shigemoto, Y.	I-a Laboratory for DNA Data Analysis
Shigesada K	G-b Genome biology Laboratory
Shigeta M	F-b Mammalian Development Laboratory
Shima A	F-b Mammalian Development Laboratory
Shimada A	F-b Mammalian Development Laboratory
Shimada, A.	G-b Genome biology Laboratory F-d Model Fish Genomics Resource
Shimamoto,N.	H-b Molecular Biomechanism Laboratory
Shimazaki, M.	F-b Mammalian Development Laboratory
Shimizu H	C-a Division of Developmental Genetics
Shimizu, A.	G-b Genome biology Laboratory
Shimizu, H.	C-a Division of Developmental Genetics F-g Invertebrate Genetics Laboratory
Shimizu, M.	C-a Division of Developmental Genetics
Shimizu, N.	G-b Genome biology Laboratory
Shimizu-Ueda, Y.	G-b Genome biology Laboratory
Shimojima, T.	C-b Division of Gene Expression
Shin Watanabe	G-a Genetic Informatics Laboratory

Shin-I, T.	G-b Genome biology Laboratory F-a Mammalian Genetics Laboratory
Shin-i, T.	G-b Genome biology Laboratory
Shinichi TOMIZAWA	E-a Division of Human Genetics
Shinkai Y	F-b Mammalian Development Laboratory
Shinkura K.	H-a Biological Macromolecules Laboratory
Shinkura, K.	H-a Biological Macromolecules Laboratory
Shinogi A.	F-a Mammalian Genetics Laboratory
Shinogi, A.	F-a Mammalian Genetics Laboratory
Shintani, Y.	C-c Division of Molecular and Developmental Biology
Shinya, M.	F-d Model Fish Genomics Resource
Shirahige K	B-a Division of Cytogenetics
Shirahige, K.	B-a Division of Cytogenetics
Shirakihara, Y.	H-d Biomolecular Structure Laboratory
Shiratori A.	H-d Biomolecular Structure Laboratory
Shiratori H	F-b Mammalian Development Laboratory
Shiroishi T.	F-a Mammalian Genetics Laboratory
Shiroishi, T.	F-a Mammalian Genetics Laboratory F-c Mouse Genomics Resource Laboratory G-a Genetic Informatics Laboratory
Shiroishi,T.	E-a Division of Human Genetics
Shiu, S.H.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Shunsuke Imanishi	G-a Genetic Informatics Laboratory
Sias, C.	C-c Division of Molecular and Developmental Biology
Sibarita, J.	A-a Division of Molecular Genetics
Sleumer, M.C.	G-b Genome biology Laboratory
Soba, P.	J-b Neural Morphogenesis Laboratory
Solloway MJ	F-b Mammalian Development Laboratory
Sone,M.	H-e Gene Network Laboratory
Song, H.	C-c Division of Molecular and Developmental Biology
Soppe W	E-b Division of Agricultural Genetics
Starks, A.M.	C-c Division of Molecular and Developmental Biology
Stennard FA	F-b Mammalian Development Laboratory
Stone,C.A.	E-a Division of Human Genetics
Suetake, I.	C-c Division of Molecular and Developmental Biology
Sugano, S.	G-b Genome biology Laboratory
Sugawaea, H.	I-c Laboratory for Gene Function Research
Sugawara H	I-d Laboratory for Research and Development of Biological Databases
Sugawara H.	I-d Laboratory for Research and Development of Biological Databases
Sugawara, H.	I-a Laboratory for DNA Data Analysis I-c Laboratory for Gene Function Research
Sumiyama, K.	D-a Division of Population Genetics F-a Mammalian Genetics Laboratory
Sumiyo MORITA	E-a Division of Human Genetics

Sunabori, T.	F-b Mammalian Development Laboratory
Susa,M.	H-b Molecular Biomechanism Laboratory
Suto, F.	C-a Division of Developmental Genetics
Suto, Y.	I-a Laboratory for DNA Data Analysis
Suzuki ,A.	F-b Mammalian Development Laboratory
Suzuki T	H-a Biological Macromolecules Laboratory
Suzuki T.	H-d Biomolecular Structure Laboratory
Suzuki Y	I-d Laboratory for Research and Development of Biological Databases
Suzuki, A. C.	D-a Division of Population Genetics
Suzuki, M.	D-a Division of Population Genetics F-a Mammalian Genetics Laboratory H-d Biomolecular Structure Laboratory I-a Laboratory for DNA Data Analysis
Suzuki, S.	G-b Genome biology Laboratory
Suzuki, T.	L EXPERIMENTAL FARM
Suzuki, Y.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Suzuki,E.	H-e Gene Network Laboratory
Suzuki,E. Okazawa	H-e Gene Network Laboratory
Suzuki,M.	E-a Division of Human Genetics
Swalla, B.J.	G-b Genome biology Laboratory
Syono, K	D-a Division of Population Genetics
T. Gray	I-c Laboratory for Gene Function Research
T. Morishita	A-b Division of Mutagenesis
T. Tatusova	I-c Laboratory for Gene Function Research
Tachibana M	F-b Mammalian Development Laboratory
Tadayoshi Watanabe	C-c Division of Molecular and Developmental Biology
Tadzunu Suzuki	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Taira, M.	C-c Division of Molecular and Developmental Biology
Tajima, S.	C-c Division of Molecular and Developmental Biology
Tajiri, R.	F-g Invertebrate Genetics Laboratory
Tak,Y.-S.	B-b Division of Microbial Genetics
Takaaki YOKOMINE	E-a Division of Human Genetics
Takada, T.	F-a Mammalian Genetics Laboratory
Takada, Y.	F-a Mammalian Genetics Laboratory
Takagi A	F-b Mammalian Development Laboratory
Takahashi ,Y.	F-b Mammalian Development Laboratory
Takahashi A	F-g Invertebrate Genetics Laboratory
Takahashi H	B-a Division of Cytogenetics
Takahashi K	F-g Invertebrate Genetics Laboratory
Takahashi K.	D-a Division of Population Genetics
Takahashi Y	F-b Mammalian Development Laboratory
Takahashi, A.	D-a Division of Population Genetics F-c Mouse Genomics Resource Laboratory
Takahashi, H.	D-a Division of Population Genetics

	I-a Laboratory for DNA Data Analysis
Takahashi, K.	F-g Invertebrate Genetics Laboratory
Takahashi, K. H.	D-a Division of Population Genetics
Takahashi, K. R.	D-a Division of Population Genetics
Takahashi, S.	F-a Mammalian Genetics Laboratory
Takahashi, T.	C-c Division of Molecular and Developmental Biology
Takahashi, Y.	G-a Genetic Informatics Laboratory
Takahiro ARIMA	E-a Division of Human Genetics
Takaku, Y.	C-a Division of Developmental Genetics
Takami, Y.	A-a Division of Molecular Genetics E-b Division of Agricultural Genetics
Takano-Shimizu T.	F-g Invertebrate Genetics Laboratory
Takano-Shimizu, T	D-a Division of Population Genetics
Takano-Shimizu, T.	D-a Division of Population Genetics
Takashi ABE	E-a Division of Human Genetics
Takashi SADO	E-a Division of Human Genetics
Takashi Sado	E-a Division of Human Genetics
Takashima K	E-b Division of Agricultural Genetics
Takashima S	F-b Mammalian Development Laboratory
Takashima, S.	C-c Division of Molecular and Developmental Biology
Takayama ,I.	F-b Mammalian Development Laboratory
Takeda H.	F-b Mammalian Development Laboratory
Takeda, H.	G-b Genome biology Laboratory F-d Model Fish Genomics Resource
Takeda, J.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Takeda, M.	C-c Division of Molecular and Developmental Biology
Takeichi M	I-e Laboratory for Gene-Expression Analysis
Takemoto, N.	G-a Genetic Informatics Laboratory
Takenaka, M.	G-b Genome biology Laboratory
Takeo Katsuki	C-a Division of Developmental Genetics
Taketomo, N.	I-c Laboratory for Gene Function Research
Tamiya, G.	F-d Model Fish Genomics Resource
Tamura M.	F-a Mammalian Genetics Laboratory
Tamura, M.	D-a Division of Population Genetics F-a Mammalian Genetics Laboratory
Tanabe, H.	F-b Mammalian Development Laboratory
Tanabe, K.	C-c Division of Molecular and Developmental Biology
Tanaka N	I-d Laboratory for Research and Development of Biological Databases
Tanaka S.	F-a Mammalian Genetics Laboratory
Tanaka, H.	I-a Laboratory for DNA Data Analysis
Tanaka, I.	H-d Biomolecular Structure Laboratory
Tanaka, J.	G-b Genome biology Laboratory
Tanaka, K.	D-a Division of Population Genetics
Tanaka, M.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis

Tanaka, N.	I-a Laboratory for DNA Data Analysis
Tanaka, S.	D-a Division of Population Genetics F-a Mammalian Genetics Laboratory
Tanaka, T	I-c Laboratory for Gene Function Research
Tanaka, T.	I-a Laboratory for DNA Data Analysis
Tanaka, Y.	I-a Laboratory for DNA Data Analysis
Tanaka,S.	B-b Division of Microbial Genetics
Tanaka,T.	B-b Division of Microbial Genetics
Tanimura, T.	F-g Invertebrate Genetics Laboratory
Tanoue, T.	I-a Laboratory for DNA Data Analysis
Tateno Y.	I-d Laboratory for Research and Development of Biological Databases
Tateno, Y.	G-a Genetic Informatics Laboratory I-a Laboratory for DNA Data Analysis I-c Laboratory for Gene Function Research
Tatsuta T.	F-a Mammalian Genetics Laboratory
Tatsuya OHHATA	E-a Division of Human Genetics
Tatusova, T.	I-a Laboratory for DNA Data Analysis
Teruaki Takahashi	C-c Division of Molecular and Developmental Biology
Tessier-Lavigne, M.	E-c Division of Brain Function
Tetsuro OKUNO	E-a Division of Human Genetics
Tian W.	D-a Division of Population Genetics
Tian, H.	G-b Genome biology Laboratory
Titus, T.A.	C-c Division of Molecular and Developmental Biology
Todokoro, F.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Tokumoto, M.	F-d Model Fish Genomics Resource
Tokunaga M	H-a Biological Macromolecules Laboratory
Tokunaga M.	H-a Biological Macromolecules Laboratory
Tokunaga, M.	H-a Biological Macromolecules Laboratory
Tomatsu,C.	E-a Division of Human Genetics
Tomohiro KONO	E-a Division of Human Genetics
Tomohiro SUZUKI	E-a Division of Human Genetics
Tomoike, H.	C-c Division of Molecular and Developmental Biology
Tomoyuki TSUKIYAMA	E-a Division of Human Genetics
Torayama, I.	H-c Multicellular Organization Laboratory
Toru NAKANO	E-a Division of Human Genetics
Toshiaki WATANABE	E-a Division of Human Genetics
Toshihiko SHIROISHI	E-a Division of Human Genetics
Toshihiko Shiroishi	F-c Mouse Genomics Resource Laboratory
Toshihiro Kumamaru	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Toshimichi IKEMURA	E-a Division of Human Genetics
Totoki,Y.	E-a Division of Human Genetics

Toyoda, A.	G-b Genome biology Laboratory D-a Division of Population Genetics F-a Mammalian Genetics Laboratory
Toyoda, H.	F-g Invertebrate Genetics Laboratory
Tsuboi, M.	C-a Division of Developmental Genetics
Tsuchimoto, S.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Tsuchiya, R.	G-a Genetic Informatics Laboratory
Tsuda S	F-b Mammalian Development Laboratory
Tsuda, M.	F-b Mammalian Development Laboratory
Tsuji, T.	F-g Invertebrate Genetics Laboratory
Tsujita, T.	C-c Division of Molecular and Developmental Biology
Tsutsui, Y.	A-b Division of Mutagenesis
Tsuyoshi Koide1	F-c Mouse Genomics Resource Laboratory
Tsuyoshi Mizoguchi	G-a Genetic Informatics Laboratory
Tyagi, A.	I-a Laboratory for DNA Data Analysis
Uchida T	I-e Laboratory for Gene-Expression Analysis
Uchida,A.	H-e Gene Network Laboratory
Ueda R	F-g Invertebrate Genetics Laboratory
Ueda, R.	D-a Division of Population Genetics F-g Invertebrate Genetics Laboratory
Uematsu, D.	F-g Invertebrate Genetics Laboratory
Ueno, N.	F-g Invertebrate Genetics Laboratory
Ukai-Tadenuma, M.	F-g Invertebrate Genetics Laboratory
Umemori, J.	F-c Mouse Genomics Resource Laboratory
Umemori,T.	B-b Division of Microbial Genetics
Umetsu K.	D-a Division of Population Genetics
Uno, K.D.	F-g Invertebrate Genetics Laboratory
Uno, T.	F-c Mouse Genomics Resource Laboratory
Urasaki, A.	C-c Division of Molecular and Developmental Biology
Usui T.	F-a Mammalian Genetics Laboratory
Utsunomiya,T.	E-a Division of Human Genetics
van der Linden	H-c Multicellular Organization Laboratory
VanHoven, MK.	H-c Multicellular Organization Laboratory
W.S.	E-a Division of Human Genetics
Wachi, M.	H-d Biomolecular Structure Laboratory
Wada, K.	F-a Mammalian Genetics Laboratory
Wakana S.	F-a Mammalian Genetics Laboratory
Wakana, S.	F-a Mammalian Genetics Laboratory
Wakeno, M.	C-c Division of Molecular and Developmental Biology
Wang, C.	G-b Genome biology Laboratory
Wanner, B.	F-f Microbial Genetics Laboratory
Watanabe K	I-e Laboratory for Gene-Expression Analysis
Watanabe Y	F-b Mammalian Development Laboratory
Watanabe, H.	B-a Division of Cytogenetics
Watanabe, K.	B-a Division of Cytogenetics G-a Genetic Informatics Laboratory

Watanabe, N.	H-d Biomolecular Structure Laboratory
Watanabe, T.	C-c Division of Molecular and Developmental Biology G-a Genetic Informatics Laboratory
Watanabe,T.	E-a Division of Human Genetics
Wilson, C.	C-c Division of Molecular and Developmental Biology
Wing, R.	I-a Laboratory for DNA Data Analysis
Wise N	F-b Mammalian Development Laboratory
Wolstein O	F-b Mammalian Development Laboratory
Wong, K.	G-b Genome biology Laboratory
Woollard, A.	G-b Genome biology Laboratory
Wu P.	F-e Plant Genetics Laboratory
Wu, P.	L EXPERIMENTAL FARM
Xiao, T.	C-c Division of Molecular and Developmental Biology
Xu, B.	C-c Division of Molecular and Developmental Biology
Xu, J-H.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Xu,G.-L.	E-a Division of Human Genetics
Y. Akamatsu	A-b Division of Mutagenesis
Y. Kurokawa	A-b Division of Mutagenesis
Y. N.	J-b Neural Morphogenesis Laboratory
Y. Tateno	I-c Laboratory for Gene Function Research
Y. Tsutsui	A-b Division of Mutagenesis
Y.N.	J-b Neural Morphogenesis Laboratory
Yabuta Y	F-b Mammalian Development Laboratory
Yada, Y.	F-a Mammalian Genetics Laboratory
Yaegashi,N.	E-a Division of Human Genetics
Yagi, T.	C-a Division of Developmental Genetics F-a Mammalian Genetics Laboratory
Yakushiji, N.	F-a Mammalian Genetics Laboratory
Yakushiji,N.	E-a Division of Human Genetics
Yamada, R. G.	F-g Invertebrate Genetics Laboratory
Yamada, T.	G-b Genome biology Laboratory
Yamada,T.	E-a Division of Human Genetics
Yamaguchi, K.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Yamaguchi, S.	E-a Division of Human Genetics
Yamaichi, Y.	F-f Microbial Genetics Laboratory
Yamaji M	F-b Mammalian Development Laboratory
Yamakawa, T.	G-a Genetic Informatics Laboratory
Yamaki, A.	G-b Genome biology Laboratory
Yamamoto, H.	F-a Mammalian Genetics Laboratory
Yamamoto, M.	G-b Genome biology Laboratory C-c Division of Molecular and Developmental Biology
Yamamura, K.	G-a Genetic Informatics Laboratory
Yamanaka, S.	F-g Invertebrate Genetics Laboratory
Yamano, T.	G-b Genome biology Laboratory
Yamao, F.	A-b Division of Mutagenesis

Yamaoka, S.	G-b Genome biology Laboratory
Yamasaki S	H-a Biological Macromolecules Laboratory
Yamasaki, C.	D-a Division of Population Genetics I-a Laboratory for DNA Data Analysis
Yamashita S	H-a Biological Macromolecules Laboratory
Yamato, K.T.	G-b Genome biology Laboratory
Yamazaki K.	D-a Division of Population Genetics
Yamazaki,	G-a Genetic Informatics Laboratory
Yamazaki, S.	C-c Division of Molecular and Developmental Biology
Yamazaki, Y.	G-a Genetic Informatics Laboratory I-c Laboratory for Gene Function Research
Yamazaki,Y.	G-a Genetic Informatics Laboratory
Yan, Y.-L.	C-c Division of Molecular and Developmental Biology
Yanagihara K.	F-a Mammalian Genetics Laboratory
Yang, J.	G-b Genome biology Laboratory
Yang, S.J.	J-b Neural Morphogenesis Laboratory
Yao, M.	H-d Biomolecular Structure Laboratory
Yasugi, T.	F-g Invertebrate Genetics Laboratory
Yasuhiko ,Y.	F-b Mammalian Development Laboratory
Yasushi Hiromi	C-a Division of Developmental Genetics
Yasushi HIROMI	C-a Division of Developmental Genetics
Yasushi Hiromi	C-a Division of Developmental Genetics
Yasushi TOTOKI	E-a Division of Human Genetics
Yasutaka Kubo	G-a Genetic Informatics Laboratory
Yayoi OBATA	E-a Division of Human Genetics
Yen, T.	A-a Division of Molecular Genetics
Yip, W.K.	F-e Plant Genetics Laboratory L EXPERIMENTAL FARM
Yodoya, K.	G-b Genome biology Laboratory
Yokoi H	F-b Mammalian Development Laboratory
Yokoyama H.	F-a Mammalian Genetics Laboratory
Yokoyama, H.	F-a Mammalian Genetics Laboratory
Yonekawa, H.	F-a Mammalian Genetics Laboratory G-a Genetic Informatics Laboratory
Yoshiaki Okamura	F-b Mammalian Development Laboratory
Yoshida M.	H-d Biomolecular Structure Laboratory
Yoshida T.	F-a Mammalian Genetics Laboratory
Yoshida, H.	F-g Invertebrate Genetics Laboratory
Yoshida, S.	F-g Invertebrate Genetics Laboratory
Yoshifuji, Y.	D-a Division of Population Genetics
Yoshiharu Yamaichi	F-f Microbial Genetics Laboratory
Yoshihiro YUASA	C-a Division of Developmental Genetics
Yoshikane,N.	F-g Invertebrate Genetics Laboratory
Yoshiki A.	F-a Mammalian Genetics Laboratory
Yoshiki, A.	F-a Mammalian Genetics Laboratory
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Younger, S.	J-b Neural Morphogenesis Laboratory
Yu HT.	F-a Mammalian Genetics Laboratory
Yu Takahashi	F-b Mammalian Development Laboratory
Yu, H.H.	J-b Neural Morphogenesis Laboratory
Yu, J-K.	G-b Genome biology Laboratory
Yuasa I.	D-a Division of Population Genetics
Yuasa, S.	F-c Mouse Genomics Resource Laboratory
Yuasa, Y.	C-a Division of Developmental Genetics
Yuge, K.	I-a Laboratory for DNA Data Analysis
Yuichi Ozaki	F-d Model Fish Genomics Resource
Yuji KOHARA	E-a Division of Human Genetics
Yuji Kohara	G-b Genome biology Laboratory
Yuki Sato	C-c Division of Molecular and Developmental Biology
Yukiko Yamazaki	G-a Genetic Informatics Laboratory
Yuko AMAKAWA	E-a Division of Human Genetics
Yuko HOKI	E-a Division of Human Genetics
Yuko Hoki	E-a Division of Human Genetics
Yukuto Yasuhiko	F-b Mammalian Development Laboratory
Yumiko Saga	F-b Mammalian Development Laboratory
Yumiko,Saga	F-b Mammalian Development Laboratory
Yusuke MIYANARI	E-a Division of Human Genetics
Yuzuru Kato	E-a Division of Human Genetics
Zaffran S	F-b Mammalian Development Laboratory
Zeng,R.	E-a Division of Human Genetics
Zhang, X.	C-a Division of Developmental Genetics
Zhou, Y.	H-d Biomolecular Structure Laboratory
Zhu, S.	J-b Neural Morphogenesis Laboratory
Ziv, L.	C-c Division of Molecular and Developmental Biology
Zuccolo, M.	A-a Division of Molecular Genetics

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Biological Symposium

Apr, 11 2007	転写の忠実度の維持機構の分子遺伝学的解析（Hiroshi Koyama）
Apr, 18 2007	Molecular Genetics of Vertebrate Dorsal-Ventral Limb Patterning（Randy L. Johnson）
Apr, 18 2007	Mysteries in growth control（Georg Halder）
Apr, 19 2007	Watson-CrickによるDNAの半保存的複製からヌクレオソームの半保存的複製モデルへーヌクレオソームからの遺伝子制御機構論の構築を目指してー（Masami Horikoshi）
May, 2 2007	Genetic control of embryo/endosperm size in cereal crops（Hajime Sakai）
May, 9 2007	Random Genetic Drift: A Critique in Historical Perspective（William Provine）
May, 10 2007	Engulfed by speculation: the debated origins of the eukaryote cell（Anthony M. Poole）
May, 10 2007	新しい高速相同検索アルゴリズムを用いたゲノム解析ツールの開発（Takeaki Uno）
May, 15 2007	Long Term Evolution of the Cazy Glycosyltransferase 6 (ABO) Gene Family form Fishes to Mammals: A Birth-and-Death Evolution Model（Antoine Blancher）
May, 17 2007	Robust Time Estimation Reconciles Views of the Antiquity of Placental Mammals（Yasuhiro Kitazoe）
May, 21 2007	piRNA biogenesis and modification in Drosophila（Mikiko C. Siomi）
May, 22 2007	Control of development and polarization of the Drosophila oocyte by oskar（Anne Ephrussi）
May, 22 2007	ヘテロクロマチンにおける遺伝子発現抑制機構の解析（Tomoyasu Sugiyama）

May, 25 2007	Mitotic chromosome condensation and segregation（Frank Uhlmann）
Jun, 5 2007	Molecular genetics and evolution of dim-light and color vision in vertebrates（Shozo Yokoyama）
Jun, 7 2007	Role of mitochondrial remodeling in Drosophila programmed cell death（V. Sriram）
Jul, 12 2007	分泌性Wnt阻害因子Sfrpの機能とシグナル調節（Akihiko Shimono）
Jul, 13 2007	Mining Gene Expression in the Allen Brain Atlas（Chinh Dang）
Jul, 19 2007	新奇形質を創出する分子基盤：前口動物の付属肢を例に（Nao Niwa）
Jul, 23 2007	真核生物の翻訳開始メカニズムと制御、そして起源（Kei Asano）
Jul, 26 2007	細胞の挙動を解析してマウス着床前胚を考える（Toshihiko Fujimori）
Jul, 27 2007	The role of PIASy-mediated SUMO-2/3 modification on structural organization of chromosome segregation in Xenopus egg extracts（Yoshiaki Azuma）
Jul, 31 2007	TRPチャネルとマグネシウム恒常性調節（TRP channels and Magnesium homeostasis）（Kouichi Iwasaki）
Aug, 3 2007	“Fishing” for the in vivo mode of action of Foggy/Spt5（Su Guo）
Aug, 10 2007	植物の地上部器官を生み出す分裂組織の形成・維持に関わる分子機構（Kenichirou Hibara）
Aug, 10 2007	イネにおける生殖隔離の遺伝的機構（Takahiko Kubo）
Aug, 17 2007	Genetic control of embryo/endosperm size in rice and beyond（Nobuhiro Nagasawa）
Aug, 23 2007	Rhodopsin transport in Drosophila photoreceptors: a sensitive and accessible system to investigate in vivo membrane traffic（Akiko Satoh）
Aug, 27 2007	New Directions in Genomics from Microbes to Man（George Weinstock）
Sep, 4	Genetic analysis of dendrite maintenance and plasticity in the Drosophila peripheral

2007 nervous system（Jay Parrish）

Sep, 19 2007 Structure, dynamics and evolution of the centromere（Steven Henikoff）

Sep, 25 2007 Development and immunity in the nematode C. elegans（Jonathan Hodgkin）

Oct, 2 2007 Speciation in a super-species of bat in the Japanese Archipelago（Kyle Armstrong）

Oct, 4 2007 染色体構築の分子基盤:コンデンシンから見た新しい染色体像（Tatsuya Hirano）

Oct, 5 2007 The Formation of Functional Circuitry in the Vestibular and Auditory Pathways（Joel Glover）

Oct, 15 2007 反発性ガイダンス分子　Draxin（Hideaki Tanaka）

Oct, 15 2007 Physical constraints and limits to precision in early embryonic development（Thomas Gregor）

Oct, 15 2007 The optimal step number of the intracellular signal transduction pathway（Jun Nakabayashi）

Oct, 23 2007 比較ゲノム解析手法を用いた重複遺伝子の解析と新規遺伝子探索法の開発（Kousuke Hanada）

Nov, 5 2007 Role of Histone Methylation in Mammalian Genomic Imprinting（Philippe Arnaud & Robert Feil）

Nov, 21 2007 カリオタイプ変動の制御システム（Kohta Takahashi）

Nov, 26 2007 Localized RNAs, localized translation, and developmental asymmetry（Liz Gavis）

Nov, 30 2007 Use of Microarrays for Selection of Genomic Targets for High-Throughput Sequencing（Thomas J. Albert）

Nov, 30 2007 The neo-selectionist theory of genome evolution（Giorgio Bernardi）

Dec, 4 2007 Arabidopsis ARF GDP-GTP exchange factors in membrane traffic and development（Gerd Juergens）

Dec, 12 2007 Patterning the vertebrate embryonic axis（Olivier Pourquié）

Dec, 17 Kinetochore Specification and Function（Arshad Desai）

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Dec, 17 2007 Molecular Mechanism of DNA Demethylation（Christof Niehrs）

Dec, 17 2007 Aberrant chromosomal rearrangement induced by replication fork block at a palindrome（Ken'ichi Mizuno）

Dec, 19 2007 新奇プロテインキナーゼによるFatカドヘリン細胞外領域のリン酸化（Hiroyuki O. Ishikawa）

Dec, 26 2007 Identifying genes involved in the initiation of apomixis in Hieracium（Takashi Okada）

Jan, 7 2008 Comparative phylogeography of widespread Eurasian animals（Alexey Kryukov）

Jan, 7 2008 タンパク質ネットワークの研究とターゲットタンパク質探索への応用（Takao Iwayanagi）

Jan, 7 2008 ヒト・ゲノム研究の新展開：ヒトゲノム計画から多様性と個別のゲノム研究へ（Asao Fujiyama）

Jan, 9 2008 鳥類の発声学習にみられる進化と多様性獲得の分子基盤（Eiji Matsunaga）

Jan, 9 2008 Biosynthetic constraints and subtle adaptation in eukaryotic genomes（Hiroshi Akashi）

Jan, 9 2008 遺伝子から探る生物の形態進化と系統関係（Naoyuki Iwabe）

Jan, 15 2008 細胞周期DNAチェックポイント機構のDNA複製時のゲノム安定維持における役割（Kanji Furuya）

Jan, 15 2008 科学社会学・科学政治学からみた国立遺伝学研究所（Hazime Mizoguchi）

Jan, 17 2008 Control of Arabidopsis organ size by intercellular signalling-a molecular ruler?（Michael Lenhard）

Jan, 22 2008 微生物計測のイノベーション－非破壊的立場の微生物活性計測システムの紹介（Katsutada Takahashi）

Jan, 23 2008 Mechanisms for the amplification of retrotransposons in Bacteria and Eucarya（Kenji Ichiyanagi

Jan, 23 2008 核膜と核膜孔複合体ダイナミクス（Tokuko Haraguchi）

Jan, 23 2008 Sleep with the fishes, a concrete story（Philippe Mourrain）

Jan, 28 2008	Gタンパク質を調節するいろいろな新しい分子の解析（Hiroshi Itoh）
Jan, 30 2008	Concerted evolution and recombination in the rDNA repeats（Austen Ganley）
Feb, 2 2008	Maternal miRNAs are essential for mouse zygotic development（Masahiro Kaneda）
Feb, 15 2008	Culture and Genetic Modification of Mouse Germline Stem (GS) cells（Takashi Shinohara）
Feb, 15 2008	Biological Significance of Histone Methylation and Their Regulation Mechanisms（Yoichi Shinkai）
Feb, 19 2008	嗅神経細胞の個性に応じて軸索投射位置が決まるしくみ（Takeshi Imai）
Feb, 19 2008	哺乳類と鳥類における終脳背側領域の発生様式の比較解析（Tadashi Nomura）
Feb, 20 2008	Germ Plasm Assembly and Germ Cell Development in Drosophila（Akira Nakamura）
Feb, 20 2008	Regulation of Plant Growth in Response to The Light Environmental Stimuli（Tatsuya Sakai）
Feb, 20 2008	Mechanisms of Formation and Refinement of Mammalian Neuronal Circuits（Takuji Iwasato）
Feb, 21 2008	脊椎動物の脳における「樹状突起内セグメント」の分子的実体とその形成機構（Sachiko Nishimura-Akiyoshi）
Feb, 27 2008	Probing intracellular cholesterol trafficking: lessons from Drosophila models of Niemann Pick type C disease（Xun Huang）
Feb, 27 2008	Modeling of Fragile X mental retardation in fruitflies（Yong Q.Zhang）
Feb, 27 2008	次世代シークエンスシステムを活用したゲノム解析（Atsushi Toyoda）
Mar, 2 2008	植物の多様性と進化（Hiroshi Yuasa）
Mar, 3 2008	Order in morphological dynamics during spontaneous cell migration -Seeing the unseen by autocorrelation methods-（Yusuke T. MAEDA）
Mar, 3 2008	Genetics and Epigenetics of DNA methylation in Arabidopsis thaliana（Hidetoshi Saze）

Mar, 5 2008	Mice, microbes and models of infection（Rudi Balling）
Mar, 6 2008	Meiotic Silencing, Infertility and Mammalian X Chromosome Evolution（James MA Turner）
Mar, 8 2008	多剤排出トランスポーターの結晶構造から明らかになった多剤認識および排出機構（Satoshi Murakami）
Mar, 9 2008	Biological Significance of Protein Network Architecture: Truth or Illusion?（Jianzhi George Zhang）
Mar, 13 2008	1分子FRET法を用いた分子モーターキネシンの二足歩行運動の観察（Michio Tomishige）
Mar, 13 2008	Evolutionary Anatomies of Disease Mutations（Sudhir Kumar）
Mar, 15 2008	神経細胞の個性決定化プログラムが制御する軸索ガイダンス（Ryuichi Shirasaki）
Mar, 19 2008	Inferring demography and selection from SNP data（Wolfgang Stephan）
Mar, 20 2008	Genetic variation in the serotonin transporter and risk for emotional disorders; converging evidence from mouse and man（Andrew Holmes）
Mar, 21 2008	THE MONOGAMOUS MALE BRAIN（Zuoxin Wang）
Mar, 22 2008	Animal models of alcohol-related behavior: genetics and environment（David A. Blizard）
Mar, 25 2008	Genome-wide analyses of DNA methylation and transcription in Arabidopsis thaliana（Junshi Yazaki）
Mar, 26 2008	伸長運動の制御：何が細胞の配置を決めるのか？（Hiromasa Ninomiya）
Mar, 27 2008	The Dscam Ig-receptor code: A paradigm for molecular and genetic dissection of neuronal wiring specificity（Dietmar Schmucker）
Mar, 29 2008	Cell cycle regulation of the oocyte-to-embryo transition in C. elegans（Geraldine Seydoux）

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Foreign Visitors

Feb, 2 2007	Masahiro Kaneda		The Wellcome Trust/Cancer Research UK Gurdon Institute University of Cambridge
Feb, 27 2007	Xun Huang		Institute of Genetics and Developmental Biology, Chinese Academy of Science
Feb, 27 2007	Yong Zhang	Q.	Institute of Genetics and Developmental Biology, Chinese Academy of Science
Mar, 9 2007	Jianzhi George Zhang		University of Michigan
Mar, 19 2007	Wolfang Stephan		Biocenter, University of Munich
Mar, 20 2007	Andrew Holmes		Secion on Behavioral Science and Genetics Laboratory for Integrative Neuroscience National Institute on Alcohol Abuse and Alcoholism National Institutes of Health
Mar, 22 2007	David Blizard	A.	Center for Developmental and Health Genetics, Pennsylvania State University
Mar, 27 2007	Aloys Schepers		GSF-National Research Center for Environment and Heath Department of Gene Vectors, Munich, Germany
Mar, 29 2007	Geraldine Seydoux		Dept. of Molecular Biology and Genetics
Apr, 18 2007	Georg Halder		MD Anderson Cancer Center
Apr, 18 2007	Randy Johnson	L.	Department of Biochemistry and Molecular Biology University of Texas, MD Anderson Cancer Center
May, 2 2007	Hajime Sakai		Genetic Discovery, DuPont Crop Genetics
May, 9 2007	William Provine		Department of Ecology and Evolutionary Biology, Cornell University

May, 10 2007	Anthony M. Poole	Department of Molecular Biology & Functional Genomics Stockholm University
May, 15 2007	Antoine Blancher	Universite Paul Sabatier, Hopital Rangueil Toulouse FRANCE
May, 25 2007	Frank Uhlmann	Cancer Research UK London Research Institute
Jun, 7 2007	V. Sriram	National Centre for Biological Sciences, Bangalore, India
Jul, 13 2007	Chinh Dang	Allen Institute for Brain Science
Jul, 27 2007	Yoshiaki Azuma	Department of Molecular Biosciences, University of Kansas
Aug, 3 2007	Su Guo	University of California San Francisco
Aug, 17 2007	Nobuhiro Nagasawa	Genetic Discovery, DuPont Crop Genetics Wilmington, DE 19880, USA
Aug, 27 2007	George Weinstock	Human Genome Sequencing Center Baylor College of Medicine
Sep, 4 2007	Jay Parrish	UC San Francisco
Sep, 19 2007	Steven Henikoff	Fred Hutchinson Cancer Research Center
Sep, 25 2007	Jonathan Hodgkin	Department of Biochemistry, University of Oxford
Oct, 2 2007	Kyle Armstrong	Molhar Pty Ltd, Murdoch University, Western Australia
Oct, 5 2007	Joel Glover	University of Oslo
Nov, 5 2007	Philippe Arnaud & Robert Feil	Institute of Molecular Genetics CNRS & University of Montpellier, Montpellier, France
Nov, 11 2007	Thomas J. Albert	Director, Advanced Resarch Roche NimbleGen

Nov, 26 2007	Liz Gavis	Princeton University
Nov, 30 2007	Giorgio Bernardi	Director, Advanced Resarch Roche NimbleGen
Dec, 4 2007	Gerd Juergens	University of Tuebingen, Developmental Genetics
Dec, 12 2007	Olivier POURQUIÉ	Howard Hughes Medical Institute and Stowers Institute for Medical Research
Dec, 17 2007	Arshad Desai	Ludwig Institute for Cancer Research/Cellular & Molecular Medicine, UCSD
Dec, 17 2007	Christof Niehrs	Division of Molecular Embryology, Division of Epigenetics German Cancer Research Center Heidelberg, Germany
Dec, 17 2007	Ken'ichi MIZUNO	Genome Damage and Stability Centre, University of Sussex, Brighton, UK.
Jan, 7 2008	Alexey Kryukov	Institute of Biology and Soil Science, Far East Branch of the Russian Academy of Sciences
Jan, 9 2008	Hiroshi Akashi	Department of Biology 208 Mueller Laboratory Pennsylvania State University
Jan, 17 2008	Michael Lenhard	John Innes Centre, Norwich, UK
Jan, 23 2008	Philippe Mourrain	Stanford University Center For Narcolepsy
Mar, 5 2008	Rudi Balling	Scientific Director, Helmholtz Center for Infection Research, Braunschweig, Germany
Mar, 6 2008	James MA Turner	Division Stem Cell Biology and Developmental Genetics, MRC National Institute for Medical Research
Mar, 12 2008	Zuoxin Wang	Department of Psychology and Program in Neuroscience, Florida State University
Mar, 13 2008	Sudhir Kumar	Center for Evolutionary Functional Genomics The Biodesign Institute Arizona State University
Mar, 27	Dietmar Schmucker	Harvard Medical School, Department of Neurobiology and Dana-Farber Cancer Institute, Department of Cancer Biology

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