

Center for Experimental Medicine and Systems Biology

Laboratory of Molecular Pathogenesis

システム疾患モデル研究センター分子病態研究分野

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Recent development of transgenic techniques has made it possible to directly analyze the functions of a particular gene in a living animal. These techniques have also made it possible to produce various animal disease models as well as tools to analyze them. Immune disorders and infectious diseases are our major concerns, and we are attempting to produce transgenic mouse models for these diseases.

1. Studies on rheumatoid arthritis models

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Rheumatoid arthritis (RA) is one of the most serious medical problems worldwide with approximately 1% of the people in the world affected. The disease is autoimmune in nature and characterized by the chronic inflammation of synovial tissues in multiple joints that leads to joint destruction. High levels of inflammatory cytokine expression in the joints are a characteristic of the disease, although the pathogenesis has not been elucidated completely. We have been studying the pathogenesis of the disease using two arthritis models that we originally developed. One is HTLV-I transgenic (Tg) mice (Iwakura et al., *Science*, 1991) and the other is IL-1 receptor antagonist-deficient (*Il1rn*^{-/-}) mice (Horai et al., *J. Exp. Med.*, 2000). Both of these models develop autoimmunity and chronic inflammatory arthropathy closely resembling RA

in humans.

To identify genes involved in the pathogenesis of arthritis, we analyzed the gene expression profiles of these animal models by using high-density oligonucleotide arrays, and identified genes which are overexpressed in the affected joints in the RA-related gene locus (Fujikado et al., *Arthritis Res. Ther.*, 2006). Furthermore, we have also searched for pathogenesis-related genes by analyzing the effect of genetic backgrounds on arthritis development, because BALB/cA strain mice were highly susceptible to develop arthritis in these models, whereas C57BL/6J strain mice were resistant. We performed linkage-analysis using BALB/c-HTLV-I Tg backcross progenies into C57BL/6J, and identified several RA-related gene loci that affected the strain specificity of arthritis susceptibility. We are now analyzing the roles of these genes in the pathogenesis of arthritis and autoimmunity by generating the gene targeted mice of these genes.

Among these genes identified by microarray analysis and genetic linkage analysis, we are now analyzing the functions of two cytokine re-

ceptors and four novel genes including “*Tora*” and “*Kusa*”, which encode cytoplasmic proteins, “*Shimi*”, which encodes transmembrane protein, and “*Mura1*”, which encodes secreted protein. We have generated gene-targeted mice for these genes. Both *Tora*^{-/-}, *Kusa*^{-/-}, *Shimi*^{-/-} and *Mura1*^{-/-} mice were fertile, were born at the expected mendelian ratios, and showed no obvious phenotypic abnormalities. However, we found that both *Mura1*^{-/-} mice and *Kusa*^{-/-} mice were highly susceptible to type 2 collagen-induced arthritis, an experimental model for RA, whereas *Tora*^{-/-} and *Shimi*^{-/-} showed no obvious abnormality to collagen-induced arthritis. We are now analyzing the function of these genes.

2. IL-17-producing $\gamma\delta$ T cells are important for the development of arthritis in a rheumatoid arthritis mouse model

Aoi Akitsu, Shinobu Saijo, and Yoichiro Iwakura

IL-17 is a proinflammatory cytokine that activates T cells and other immune cells to induce a variety of cytokines, chemokines, and cell adhesion molecules. Although it is widely accepted that IL-17 producing-CD4⁺ T (Th17) cells are involved in the pathogenesis of many autoimmune diseases, the roles of other IL-17-producing T cells, such as $\gamma\delta$ T cells, remain to be elusive. We found that IL-17 is mainly produced in $\gamma\delta$ T ($\gamma\delta$ 17) cells rather than Th17 cells in the affected joints of *Il1rn*^{-/-} mice, a model of RA in which IL-17 plays a crucial role. Anti-TCR $\gamma\delta$ or anti-CD4 suppressed the development of arthritis in *Il1rn*^{-/-} mice. However, CD4- or TCR δ -gene deficiency did not affect, because $\gamma\delta$ T cells and CD4⁺ $\gamma\delta$ -T cells produced IL-17 in these mutant mice, respectively. Interestingly, a combination of CD4⁺ T cells and $\gamma\delta$ 17 cells was required for the development of arthritis in *scid/scid* mice. These observations suggest that $\gamma\delta$ 17 cells are required for the amplification of inflammation and CD4⁺ T cells direct the tissue specificity.

3. The role of IL-6 in the development of Th17 cells in *Il1rn*^{-/-} mice

Satoshi Ikeda, Shinobu Saijo, and Yoichiro Iwakura

Il1rn^{-/-} mice develop autoimmune arthritis in which IL-17 plays a crucial role. Although many studies have indicated that Th17 cell differentiation is dependent on TGF- β and IL-6, we found that IL-6 deficiency does not affect the develop-

ment of arthritis in *Il1rn*^{-/-} mice at all. Interestingly, Th17 cells developed normally in *Il1rn*^{-/-} *Il6*^{-/-} mice. Then, we analyzed the mechanisms of Th17 cell differentiation in *Il1rn*^{-/-} *Il6*^{-/-} mice. We found that IL-21 production was increased in the lymph nodes (LNs) of *Il1rn*^{-/-} mice and naïve *Il6*^{-/-} CD4⁺ T cells differentiated into Th17 cells when cultured with TGF- β and IL-21. Th17 cell differentiation was much enhanced when IL-1 was added to the culture, although Th17 cell differentiation was not induced by TGF- β or IL-1 alone, or in combination. Furthermore, IL-1 augmented the expression of Th17 cell-specific transcription factors such as *Nfkbiz* and *Batf*. These results indicate that excess IL-1 signaling can overcome the requirement of IL-6 in the differentiation of Th17 cells by inducing IL-21 and Th17 cell-specific transcription factors.

4. Dendritic cell immunoreceptor (DCIR), an inhibitory type of C-type lectin receptor, is important for the homeostasis of the immune system and bone metabolism

Tomonori Kaifu, Rikio Yabe, Takumi Maruhashi, Akimasa Seno, Guangyu Ma, and Yoichiro Iwakura

A balance between positive and negative signals through cellular receptors with opposing functions is important for the homeostasis of the immune system and bone metabolism. The homeostasis of the immune system is maintained by counterbalancing signals between activation and inhibitory receptors, whereas bone homeostasis is maintained by an equilibrium between bone resorption by osteoclasts and bone formation by osteoblasts. Disturbance of the balance between these opposite signals may cause harmful effects. In fact, continuous activation of the immune system causes inflammation, resulting in tissue damage and loss of mineral components due to excess activation of osteoclasts.

DCIR is a member of the C-type lectin with an extracellular carbohydrate recognition domain (CRD) with an atypical Ca²⁺-dependent EPS motif and an intracellular cytoplasmic region with an immunoreceptor tyrosine-based inhibitory motif (ITIM). Gene disruption of this molecule in mice causes spontaneously development of autoimmune disorders such as enthesitis and sialadenitis due to over expansion of dendritic cells. In this study, we further examined effects of DCIR deficiency on disease development and the physiology. We found that DCIR-deficient mice exacerbated experimental autoimmune encephalomyelitis, a mouse model for multiple sclerosis, and T cell proliferation of these mice was enhanced upon stimulation with

myelin oligodendrocyte glycoprotein. Interestingly, DCIR-deficient mice developed ankylosing spondylitis-like joint disorder, suggesting that DCIR is involved in the regulation of bone metabolism. Given that defective DCIR is prone to autoimmune diseases and bone-related disorders, DCIR could be a potential therapeutic target that terminates excessive activation of immune responses through ITIM-mediated negative signaling. We are now trying to identify the receptors for this molecule.

5. HIDE1 deficient mice normally respond to collagen-induced arthritis and experimental autoimmune encephalomyelitis

Kenji Shimizu, Toshimasa Kusaka, and Yoichiro Iwakura

Previously, we searched for candidate genes responsible for the development of autoimmunity and arthritis using two mouse lines with spontaneous autoimmune arthritis, i.e. HTLV-I-*tax* Tg mice and *Il1rn*^{-/-} mice. Among these genes, high expression genes of immature dendritic cell 1 (HIDE1) was found as a gene that is highly activated in these arthritic mice. HIDE1 is a type 1 membrane protein with an immunoglobulin-like domain in its extracellular region and no known motif in its intracellular region. This gene was expressed in dendritic cells, macrophages and neutrophil, but not in T cells and B cells.

Because HIDE1 is a member of the immunoglobulin super family and highly expressed in DCs under inflammatory conditions, we investigated the physiological functions of this molecule in the development of arthritis by generating HIDE1 deficient mice. These mice were fertile, were born at a normal mendelian ratio, and showed no obvious phenotypic abnormalities. We also found no apparent abnormalities in the cell populations of the spleen, lymph nodes, thymus, and bone marrow. We examined the susceptibility of HIDE1 deficient mice to collagen-induced arthritis. Contrary to our expectation, incidence and severity scores were normal. To further investigate the involvement of HIDE1 in other diseases, we induced experimental autoimmune encephalomyelitis and contact hypersensitivity. However, no difference was found in the incidence and severity of inflammation between wild type mice and HIDE1 deficient mice. Thus, we conclude that HIDE1 is dispensable for the development of inflammatory diseases.

6. Roles of IL-17A and IL-17F in host defense against bacteria, inflammatory colitis, and intestinal polyp formation

Ce Tang, Motohiko Kadoki, Tomonori Kamiya, Yamato Sasaki, Shigeru Kakuta, and Yoichiro Iwakura

IL-17A is a cytokine produced by Th17 cells and plays important roles in the development of allergic and autoimmune diseases. IL-17A also plays important roles in the host defense mechanism against bacteria and fungi. We showed that IL-17F, the highest homologous member to IL-17A in the IL-17 family, plays only marginal roles in the development of allergic or autoimmune diseases, but is equally important with IL-17A in the host defense against mucosal epithelial bacterial infection, such as *Staphylococcus* and *Citrobacter*. Now, we are investigating the effects of IL-17F and IL-17A on naïve CD4⁺ T cells and on Th1/Th17-type immune responses during *Mycobacteria* infection. We are also analyzing the role of IL-17F in the induction of CD45RB^{high} CD4 T cell-induced colitis and the development of polyps in Apc^{Min} mice.

7. Attempts to generate HIV-1 susceptible mice for AIDS research

Takuya Tada, Motohiko Kadoki, and Yoichiro Iwakura

Attempts to produce mouse models for AIDS have been hampered by species-specific host range barriers in mice. To overcome these barriers, we have generated Tg mice carrying the HIV-1 genome and showed that bacterium-derived LPS induces the activation of HIV-1 through the induction of TNF and IL-1 in splenocytes, while LPS directly activates HIV-1 gene expression in macrophages. In parallel with these studies, we also attempted to generate HIV-1 susceptible mice in which corresponding human genes responsible for the host range barriers were introduced into the mouse genome. Accordingly, we have generated Tg mice carrying the human CD4, CXCR4, CCR5, Cyclin T1, and CRM1 genes, all of which are suggested to be involved in the host range barrier. Although the initial viral infection steps, such as viral adsorption and uncoating, and viral transcription came to proceed efficiently in these Tg mice, these mice were still refractory to the infection of HIV-1, suggesting the involvement of additional host factors in the host range barrier. Regarding this, we previously showed that the efficiency of nuclear import of HIV-1 preintegration complex (PIC) was lower in

mouse cells and that this was due to inefficient nuclear entry of HIV-1 integrase (IN). Because we previously found that lens epithelium-derived growth factor transcription coactivator p75 (LEDGF/p75), a host factor that binds IN, is involved in the nuclear transport of IN, we examined if Tg mice carrying the human (h) LEDGF/p75 can overcome the host range barrier in mice. Nuclear translocation of GFP-IN was monitored using embryonic fibroblasts (MEF) of the Tg mice. We found that GFP-IN efficiently localized in the nucleus of hLEDGF/p75 Tg MEF compared with non-Tg mice. These results suggest that LEDGF/p75 is a critical host factor for HIV-1 nuclear import. The Tg mice carrying the human CD4, CXCR4, CCR5, Cyclin T1, CRM1, and LEDGF genes should give a better susceptibility to HIV-1 infection.

8. The role of glucocorticoids in pregnancy, parturition, lactation, and nurturing in melanocortin receptor 2-deficient mice

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Maternal glucocorticoids are critical for fetal development, although overexpression can be

deleterious. Previously, we established a mouse line deficient in melanocortin receptor 2 (MC2R). MC2R^{-/-} mice have undetectable levels of corticosterone despite high levels of ACTH and defects resembling those in patients with familial glucocorticoid deficiency. In this study, we analyzed the role of glucocorticoids in pregnancy, parturition, lactation, and nurturing in MC2R^{-/-} mice. MC2R^{-/-} mice were fertile and produced normal litters when crossed with MC2R^{+/+} mice. However, MC2R^{-/-} females crossed with MC2R^{-/-} males had no live births, and about 20% of the embryos at day 18.5 of pregnancy were of normal body size but were dead. MC2R^{-/-} pregnant females crossed with MC2R^{+/+} males had detectable serum corticosterone levels, suggesting transplacental passage of corticosterone from fetus to mother. MC2R^{+/+} pups delivered from MC2R^{-/-} dams crossed with MC2R^{+/+} males thrived poorly with MC2R^{-/-} dams, but grew to adulthood when transferred to a foster mother after birth, suggesting that MC2R^{-/-} females are poor mothers or cannot nurse. Mammary glands were smaller in MC2R^{-/-} females, with normal formation of alveoli and reduced expression of milk proteins. Myoepithelial cells, which force milk out of the alveoli, were fully developed and differentiated in MC2R^{-/-} mammary glands. Pup retrieval behavior was intact in MC2R^{-/-} mice. Exogenous corticosterone rescued mammary gland development in MC2R^{-/-} females, and the pups of treated females grew to adulthood. Our results reveal the importance of glucocorticoids for fetal survival late in pregnancy, mammary gland development, and milk protein gene expression.

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Original papers

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Gene targeting technology has revealed many aspects of gene functions in vivo. Knock out mice offer the opportunities of not only analyzing the complex gene functions in vivo, but also presenting various human disease models, where new therapeutic approaches can be explored. To allow more detailed dissection of gene function, we introduce a point mutation or disrupt genes in certain lineages (or stages) using Cre-loxP system, a method of conditional gene targeting. In the process of analyzing knock out mice, we have isolated spontaneous mutant mice which develop chylous ascites and edematous limbs. In order to understand the mechanism of lymphatic development and functions in more detail, we are also generating various knock-out/knock-in mouse lines including a conditional knock out mouse. In addition, we focus on analysis of neural development, aiming to understand the molecular mechanism of the maintenance of stemness and neural differentiation and to advance towards cell therapy of the damaged or degenerating nervous system. For this purpose, we are generating several conditional knock out mouse lines.

1. Mastermind-like 1 (MamL1)/Mastermind-like 3 (MamL3) are essential for Notch signaling in vivo.

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Mastermind (Mam) is one of the elements of Notch signaling, a system that plays a pivotal role in metazoan development. Mam proteins form transcriptionally activating complexes with the intracellular domains of Notch, which are generated in response to the ligand-receptor interaction, and CSL DNA-binding proteins. In mammals, three structurally divergent Mam isoforms (MamL1, MamL2 and MamL3) have been identified. There have also been indications that Mam interacts functionally with various other

transcription factors, including the p53 tumor suppressor, β -catenin and NF- κ B. We have demonstrated previously that disruption of MamL1 causes partial deficiency of Notch signaling in vivo. However, MamL1-deficient mice did not recapitulate total loss of Notch signaling, suggesting that other members could compensate for the loss or that Notch signaling could proceed in the absence of Mam in certain contexts. Here, we report the generation of lines of mice null for MamL3. Although MamL3-null mice showed no apparent abnormalities, mice null for both MamL1 and MamL3 died during the early organogenic period with classic pan-Notch defects. Furthermore, expression of the lunatic fringe gene, which is strictly controlled by Notch signaling in the posterior presomitic mesoderm, was undetectable in this tissue of the double-null embryos. Neither of the single-null embryos exhibited any of these phenotypes. These various roles of the three Mam proteins could be due to their differential physical characteristics and/or their spatiotemporal distributions. These results indicate that engagement of Mam is essential for Notch signaling, and that the three Mam isoforms have distinct roles in vivo.

2. Polypyrimidine tract-binding protein regulates the cell cycle through IRES-dependent translation of CDK11p58 in mouse embryonic stem cells.

Satona Ohno, Masaki Shibayama, Mitsuharu Sato, Akinori Tokunaga and Nobuaki Yoshida

Polypyrimidine tract-binding protein (PTB/PTBP1/hnRNP I) is a member of the heterogeneous nuclear ribonucleoprotein family that binds specifically to pyrimidine-rich sequences of RNAs. Although PTB is a multifunctional protein involved in RNA processing and internal ribosome entry site (IRES)-dependent translation, the role of PTB in early mouse development is unclear. Ptb knockout mice exhibit embryonic lethality shortly after implantation and Ptb $^{-/-}$ embryonic stem (ES) cells have a severe proliferation defect that includes a prolonged G2/M phase. The present study shows that PTB promotes M phase progression by the direct repression of CDK11(p58) IRES activity in ES cells. The protein expression and IRES activity of CDK11(p58) in Ptb $^{-/-}$ ES cells is higher than that of wild-type ES cells, indicating that PTB is involved in the repression of CDK11(p58) expression through IRES-dependent translation in ES cells. Interestingly, CDK11(p58) IRES activity is activated by upstream of N-Ras (UNR) in 293T and NIH3T3 cells, whereas UNR is not present in the Cdk11 mRNA-protein complex in

ES cells. In addition, PTB interacts directly with the IRES region of CDK11(p58) in ES cells. These results suggest that PTB regulates the precise expression of CDK11(p58) through direct interaction with CDK11(p58) IRES and promotes M phase progression in ES cells.

3. Obesity resistance and increased hepatic expression of catabolism-related mRNAs in Cnot3 $^{+/-}$ mice.

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Obesity is a life-threatening factor and is often associated with dysregulation of gene expression. Here, we show that the CNOT3 subunit of the CCR4-NOT deadenylase complex is critical to metabolic regulation. Cnot3 $^{+/-}$ mice are lean with hepatic and adipose tissues containing reduced levels of lipids, and show increased metabolic rates and enhanced glucose tolerance. Cnot3 $^{+/-}$ mice remain lean and sensitive to insulin even on a high-fat diet. Furthermore, introduction of Cnot3 haploinsufficiency in ob/ob mice ameliorated the obese phenotype. Hepatic expression of most mRNAs is not altered in Cnot3 $^{+/-}$ vis-à-vis wild-type mice. However, the levels of specific mRNAs, such as those coding for energy metabolism-related PDK4 and IGF1, are increased in Cnot3 $^{+/-}$ hepatocytes, having poly(A) tails that are longer than those seen in control cells. We provide evidence that CNOT3 is involved in recruitment of the CCR4-NOT deadenylase to the 3' end of specific mRNAs. Finally, as CNOT3 levels in the liver and white adipose tissues decrease upon fasting, we propose that CNOT3 responds to feeding conditions to regulate deadenylation-specific mRNAs and energy metabolism.

4. Unc93B1 restricts systemic lethal inflammation by orchestrating TLR7- and TLR9-trafficking.

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Toll-like receptor-7 (TLR7) and 9, innate im-
mune sensors for microbial RNA or DNA, have
been implicated in autoimmunity. Upon activa-
tion, TLR7 and 9 are transported from the endo-
plasmic reticulum (ER) to endolysosomes for
nucleic acid sensing by an ER-resident protein,
Unc93B1. Little is known, however, about a role
for sensor transportation in controlling autoim-
munity. TLR9 competes with TLR7 for Unc93B1-
dependent trafficking and predominates over
TLR7. TLR9 skewing is actively maintained by
Unc93B1 and reversed to TLR7 if Unc93B1 loses
preferential binding via a D34A mutation. We
here demonstrate that mice harboring a D34A
mutation showed TLR7-dependent, systemic le-
thal inflammation. CD4⁺ T cells showed marked
differentiation toward T helper 1 (Th1) or Th17
cell subsets. B cell depletion abolished T cell dif-
ferentiation and systemic inflammation. Thus,
Unc93B1 controls homeostatic TLR7 activation
by balancing TLR9 to TLR7 trafficking.

5. Fbx10/Kdm2b deficiency accelerates neu- ral progenitor cell death and leads to ex- encephaly.

**Tsuyoshi Fukuda, Akinori Tokunaga, Reiko
Sakamoto and Nobuaki Yoshida**

Histone methylation is the important tran-
scription regulatory system that affects mam-
malian development and cell differentiation. Al-
terations in epigenetic gene regulation are asso-
ciated with disease. Fbx10 (F-box and leucine-
rich repeat protein 10) is a JmjC domain-
containing histone demethylase. Although Fbx10
has been implicated in cell cycle regulation, cell
death, senescence, and tumorigenesis, these
functions are controversial and its physiological
function is unclear. To determine the *in vivo*
function of Fbx10, in this study, we generated a
homozygous mutation in the mouse Fbx10
gene. About half of Fbx10-deficient mice exhibit

failure of neural tube closure, resulting in ex-
encephaly and die shortly after birth. Fbx10 de-
ficiency also causes retinal coloboma and a curled
tail with low penetrances. Fbx10 mRNA is spe-
cifically expressed in the cranial neural folds at
E8.5 embryos, and apoptosis increased in the
neuroepithelium and mesenchyme of Fbx10-
deficient E9.5 embryos, consistent with neural
tube defects found in Fbx10-deficient mice. De-
pletion of Fbx10 induced the increased expres-
sion of p19ARF, an inducer of apoptosis, in E8.5
embryos and mouse embryonic fibroblast cells.
In addition, the number of mitotic neural pro-
genitor cells is significantly increased in the mu-
tant E14.5 brain. Our findings suggest that the
Fbx10 gene makes important contributions to
embryonic neural development by regulating
cell proliferation and cell death in mice.

6. Understanding the mechanism of blood- lymphatic vascular separation

**Taeko Ichise, Nobuaki Yoshida, and Hirotake
Ichise**

The lymphatic vasculature constitutes a highly
specialized vascular system that is essential for
fluid homeostasis, lipid absorption from the in-
testine, and immune cell trafficking. During em-
bryonic development, lymphatic vessels origi-
nate from blood vessels, but become separated
from blood vessels. Lymphatic and blood ves-
sels are connected only in a few sites where
lymph goes back to blood circulation. Recent
studies have demonstrated that hematopoietic
cells play an important role in blood-lymphatic
vascular separation; however, hematopoietic cell
types responsible for the separation have been
debated, and mechanisms underlying the separa-
tion process remain largely unknown.

To gain an understanding of the vascular par-
titioning, we searched for the affected gene in a
spontaneous mouse mutant exhibiting blood-
filled lymphatic vessels, and identified a null
mutation of the *Plcg2* gene, which encodes
phospholipase C γ 2 (PLC γ 2), by positional candi-
date cloning. Aberrant separation of blood and
lymphatic vessels was observed in lethally irra-
diated wild-type mice reconstituted with PLC γ 2-
null bone marrow cells, as well as PLC γ 2-null
mice. These findings indicate that PLC γ 2-express-
ing hematopoietic cells play an essential role in
initiating and maintaining the separation of the
blood and lymphatic vasculature.

We are presently using genetically engineered
mouse models to address the issues of which
type of hematopoietic cells is essential for the
vascular separation, and how PLC γ 2 is involved
in the intracellular signalling which mediates

the separation.

7. Studies on the role of RNA splicing in neural development

Akinori Tokunaga, Takayuki Shibasaki, Reiko Sakamoto, Mamiko Hamano, Nobuaki Yoshida

We focus on analysis of neural development, aiming to understand the molecular mechanism of the maintenance of stemness and neural differentiation and to advance towards cell therapy of the damaged or degenerating nervous system.

i) Analysis of PTB conditional knockout mouse.

PTB is a member of the heterogeneous nuclear ribonucleoprotein family that binds specifically to pyrimidine-rich sequences of RNAs. PTB is a multifunctional protein involved in RNA processing and internal ribosome entry site (IRES)-dependent translation, and preferentially expressed in neural stem cells (NSCs) in the central nervous system. Although RBPs are indispensable for the normal functions and cell migration of neurons, little is known about the role of RBPs in neural stem cells (NSCs). In vitro functional analysis of PTB in vertebrate neural cell have revealed that PTB has important roles on many alternative splicing events during neural cell differentiation. But it is still unknown whether self-renew and/or cell fate of NSCs are regulated by PTB in vivo. To explore the role of PTB in the early development of mouse brain, we inactivated the gene by employing a Nestin promoter-driven Cre-mediated conditional gene targeting system. We found that most mutant mice die by 10 weeks and almost all mutant mice developed a characteristic dome-like appearance of their heads. Histological analyses of PTB mutant brains revealed that these mice develop severe hydrocephalus. The cell polarity and adherens junction (AJ) of the apical ventricular surface in dorsal cortex were lost in a patchy distribution at E15.5. By E16.5, Tbr2-positive neural progenitor cells and neurons were observed in ventricular zone (VZ) of all AJ-negative spots, which leads depletion of VZ by E18.5. Thus postnatal maturation of ependymal cells with ciliary tufts from radial glia cells (RGCs) was disturbed, which may compromise cerebrospinal fluid dynamics and results in hydrocephalus. Our findings suggest that PTB is important for self-renew and/or cell fate of RGCs, through involving in maintenance of cell polarity and AJ in the dorsal neuroepithelium of lateral ventricles.

ii) Analysis of PTB/nPTB conditional knockout mouse.

Neural polypyrimidine-tract-binding protein (nPTB), which is identified as a homologue of PTB, is one of RNA binding protein involved in the heterogeneous nuclear ribonucleoprotein (hnRNP) family. It is common knowledge that many genes are regulated by alternative splicing during neural development, and previous studies suggested that alternative splicing could contribute to the gene expression and functional diversity of isoforms. nPTB is expressed predominantly in the nervous system, muscle and testis. During neural development, expression of PTB is decreased along with differentiation of neural stem cells into neurons. In contrast, expression level of nPTB that was repressed by PTB is accordingly increased. Thus, tissue-specific RNA binding protein, nPTB may play an important role in neural development. But, functional differences between PTB/nPTB and meaning of developmental stage associated expression change from PTB to nPTB remain to be elucidated. In our study, we are generating nPTB conditional knockout mice to shed light on a role of nPTB in vivo. And now we are also analyzing the function of PTB/nPTB in vitro by using knockdown experiment via a formation of embryoid body (EB) from ES cells.

To address the function of PTB/nPTB, we generate and will analyze PTB/nPTB double knockout mouse.

8. Studies on epigenetic gene regulation in neural development

Akinori Tokunaga, Eri Kawakami, Reiko Sakamoto, Nobuaki Yoshida

The polycomb repressive complex (PRC) 1/2 proteins play a critical role in regulation of gene expression through modification of histone and chromatin structure. Histone modification is the important transcription regulatory system that affects mammalian development and cell differentiation. Alterations in epigenetic gene regulation are associated with disease. We aim to determine the mechanisms of epigenetic gene regulation and to understand their roles in neural development, and are focused on the regulatory genes: Fbxl10/11 and RYBP (Ring1A and YY1 binding protein).

We generated a homozygous mutation in the mouse Fbxl10 gene. About half of Fbxl10-deficient mice exhibit failure of neural tube closure, resulting in exencephaly and die shortly after birth. Fbxl10 deficiency also causes retinal coloboma and a curled tail with low pene-

trances. Fbxl10 mRNA is specifically expressed in the cranial neural folds at E8.5 embryos, and apoptosis increased in the neuroepithelium and mesenchyme of Fbxl10-deficient E9.5 embryos, consistent with neural tube defects found in Fbxl10-deficient mice. Depletion of Fbxl10 induced the increased expression of p19ARF, an inducer of apoptosis, in E8.5 embryos and mouse embryonic fibroblast cells. In addition, the number of mitotic neural progenitor cells is significantly increased in the mutant E14.5 brain. Our findings suggest that the Fbxl10 gene makes important contributions to embryonic neural development by regulating cell proliferation and cell death in mice. Fbxl11 is more broadly expressed, we are generating Fbxl10/11 double knockout mouse.

9. Functional analysis of histone demethylase Fbxl10 on male gamete development

Manabu Ozawa, Reiko Sakamoto and Nobuaki Yoshida

Histone methylation is one of the important epigenetic modifications of genome to orchestrate appropriate spatiotemporal gene expression for normal tissue development or differen-

tiation. Fbxl10 is a histone demethylase and catalyzes tri-methylated H3K4 and di-methylated H3K36, either of which modification is believed to repress adjacent gene expressions.

Gametogenesis is also under control of epigenetic modification, and status of DNA or histone modifications changes drastically during the development. Some previous studies using epigenetic gene-null mice showed infertile phenotypes. These results make us hypothesize that Fbxl10 null mice show abnormal gametogenesis. To test the hypothesis, we, in this year, have determined spermatogenesis in testis of the gene knockout mice (KO mice). KO mice at younger age (< 6month-old) have comparable number of sperms in epididymis as wild type control, whereas aged male (>1 year old) has lower number of sperms (almost 4-folds less than control). Layers of testicular germ cells in seminiferous tube are quite poor and spermatocytes after first meiosis are almost missing in the aged null mice. Layer of germ cells in seminiferous tube in the younger mice looks similar to the control, whereas distribution patterns of immature or meiotic germ cells are distinct from the control. We are now determining molecular mechanisms which cause the abnormal phenotype in the testis of Fbxl10 null mice.

Publications

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Center for Experimental Medicine and Systems Biology

Laboratory of Innate Immunity

自然免疫研究分野

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Pathogen sensors, such as Toll-like receptor (TLR), play sentinel roles in detecting pathogenic ligands during infection and induce both innate and acquired immune responses. Meanwhile, excessive TLR responses are strongly associated with septic shock and autoimmune diseases. Immune system must strictly control TLR responses to avoid disruption of homeostasis, although molecular mechanisms involved in regulating those responses remain unclear. We have previously shown that TLR associating molecules, including MD-2, PRAT4A and Unc93B1, are essential for controlling TLR responses. To correctly understand coordinated TLR responses, our goal is to elucidate unknown molecular mechanism which is indispensable for appropriate TLR responses using genetically engineered mice.

1. Roles of PRAT4A (PRotein Associated with Toll-like receptor 4) in immune modulation.

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TLRs induce complex inflammatory responses that functions to protect the host from invading pathogens. But, in excessive or persistent inflammatory responses, hosts suffer the disadvantage of septic shock, delayed tissue repair and autoimmune diseases. To control the extent and dilated inflammation by TLRs, hosts evolved the multiple regulatory mechanisms, called tolerance.

We have previously reported that a novel TLR associating protein 'PRotein Associated with TLR4 (PRAT4A)', an endoplasmic reticulum resident protein, controls maturation and intracellular trafficking of multiple TLRs. PRAT4

A deficient Macrophages/Dendritic cells (DCs), with abnormal TLR distribution, showed impaired immune responses to TLR2/4/7/9 ligands, except to TLR3 ligand. As mRNA level of PRAT4A significantly decreased after stimulation by various TLR ligands in physiological state, PRAT4A deficiency presumably mimicked the tolerant state. These facts raised the possibility that PRAT4A play a central role in tolerance suppressing excessive inflammation by TLRs. Overexpression studies may be helpful in evaluating the tolerant effect of PRAT4A.

Furthermore, using established anti-PRAT4A monoclonal antibodies, we found secreted PRAT4A which was detected in the serum for wild mice and the culture supernatant of Macrophages. There is another possibility that PRAT4A is not only a TLR associating chaperone but also another immune modulator.

To further address PRAT4A function, we constructed Cre/loxP conditional transgenic mice by targeting ROSA26 locus which enables us to analyze cell type-specific overexpression studies *in vitro* and *in vivo*. Now we start to analyze conventional and conditional PRAT4A transgenic lines.

2. The meaning of intracellular localization of TLRs.

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TLR4/MD-2, a sensor for LPS, delivers the MyD88-dependent signal from the cell surface, then traffics to endolysosomes, and delivers the TRIF/TICAM-1-dependent signal. Both signals are thought to be dependent on cell surface TLR4/MD-2. Although TLR4/MD-2 is located also in the recycling endosomes, the Golgi apparatus, or the endoplasmic reticulum (ER), little is known about what role for intracellular TLR4/MD-2 may play in LPS responses. Here we studied intracellular LPS-sensing in macrophages.

PRAT4A (protein associated with TLR4 A) is a cochaperone for the general chaperone gp96 and is required for cell surface expression of TLR4/MD-2. Cell surface TLR4/MD-2 was undetectable on either PRAT4A^{-/-} thioglycollate-elicited peritoneal macrophages (P-Macs) or bone marrow derived macrophages (BM-Macs). LPS responses were all abolished in PRAT4A^{-/-} P-Macs, whereas some LPS responses remained detectable in PRAT4A^{-/-} BM-Macs. Of note, LPS responses in PRAT4A^{-/-} BM-Macs were not necessarily dependent on TRIF/TICAM-1-signaling. PRAT4A^{-/-} BM-Macs showed unimpaired production of both TRIF/TICAM-1-dependent chemokine RANTES (CCL5) and of MyD88-dependent chemokine MCP-1 (CCL2). Moreover, upregulation of the costimulatory molecules CD40 and CD86 was not altered. In contrast, TRIF/TICAM-1-dependent production of type I interferon was profoundly impaired. In response to heat-killed *E. coli* bacteria, BM-Macs also required PRAT4A independent TLR4/MD-2 for production of MCP-1 (CCL2) and RANTES (CCL5) and for upregulation of CD40 and CD86, indicating that intracellular TLR4/MD-2 is able to sense phagocytosed bacteria and activate immune responses. These results demonstrate that intracellular TLR4/MD-2 is responsible for a unique set of LPS responses.

3. Finding a novel tetraspanin protein involved in the negative regulation of multiple TLR responses.

Takuma Shibata^{1,2}, Nobuaki Yoshida² and Kensuke Miyake^{1,2}

Multiple TLRs work in concert to sense a pathogen and mount defense responses. Little is known, however, about a mechanism coordinating multiple TLRs responses.

Under the screening of TLR2 regulating molecules, we found a novel tetraspanin protein which co-precipitated with TLR2 in immunoprecipitation assay.

Conditional knock out and Conditional transgenic mice using ROSA26 locus of this novel tetraspanin protein have been generated to allow rigorous assessment of its function. Further study is under way to reveal a role of this gene in immune responses.

4. Characterization of cleaved forms of TLR7 and TLR9

Takuma Shibata^{1,2}, Atsuo Kanno¹, Masahiro Onji¹, Yuji Motoi¹, Ryutaro Fukui¹, Shin-Ichiroh Saitoh¹, Nobuaki Yoshida² and Kensuke Miyake^{1,2}

Vertebrates have TLR3, 7, 8 and 9 as sensors of microbial nucleic acids, however it is suggested that TLR7/9 responses strongly associate with autoimmune diseases owing to inappropriate recognition of self nucleic acid. In endolysosome, TLR7 and TLR9 recognize a single-stranded RNA and an unmethylated CpG motif in microbial DNA, respectively. TLR7/9 ordinarily reside in Endoplasmic Reticulum, and ligand stimulation enhance the trafficking of TLR7/9 to endolysosome. Such strict regulation of TLR7/9 subcellular localization seems to have a role for blocking self nucleic acid recognition. Previous reports indicated novel posttranscriptional modification in TLR7/9 that ectodomains of TLR7/9 were cleaved in endolysosome. It seemed that ectodomain cleavage in TLR7/9 represents another strategy to restrict excessive TLR7/9 activation.

Recently, we originally identified cleavage sites in TLR7 and TLR9. To clarify the meaning of ectodomain cleavage in TLR7/9, we constructed knock-in mice which load TLR7/9 without cleavage site. Now we start to analyze those Knock-in mice to reveal the meaning of cleavage in TLR7/9.

5. Roles for Unc93 homolog B1-dependent TLR7/9 balance in vivo

Atsuo Kanno¹, Ryutaro Fukui¹, Shin-Ichiroh Saitoh¹, Takuma Shibata^{1,2}, Yuji Motoi¹, Nobuaki Yoshida² and Kensuke Miyake^{1,2}

Nucleic acid sensing Toll-like receptor 7 (TLR7) and TLR9 recognize microbial RNA and

DNA, respectively. These TLRs potentially recognize self-derived nucleic acid and have been shown to have a role in autoimmune diseases. For maintenance of homeostasis, it is important to keep the responsiveness of the nucleic acid-sensing TLRs under the tight control.

Unc93 homolog B1 (Unc93B1) is reported to be indispensable for TLR7/9 responses. We have previously found that the alanine substitution for the 34th aspartic acid (D34A) of Unc93B1 enhanced TLR7 response but downregulated TLR9 response. These results suggest that TLR7 and TLR9 are reciprocally linked by Unc93B1, and the TLR7/TLR9 balance is biased towards TLR9 in the steady state.

To further clarify a role for Unc93B1-dependent TLR7/TLR9 balance *in vivo*, we started to generate knock-in mice harboring various types of mutations around D34 locus in the Unc93B1 gene which showed more accelerated phenotypes than D34A mutant mice. So far, we have finished germ line transmission for

this knock in mice.

6. Identification of regulatory molecules for TLR responses and constructing genetically altered mice.

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Except above projects, we try functional clonings and co-immunoprecipitation assay to comprehensively identify regulatory molecules associating with TLR responses. After simple screenings in cell lines, we constructed conditional knock out mice to reveal the physiological function of found novel molecules *in vivo*. So far, we found more than 20 candidate genes, and continued or finished to construct conditional knock out mice.

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Center for Experimental Medicine and Systems Biology

Laboratory of Cancer Cell signaling

発癌機構研究分野

| Professor Tadashi Yamamoto, Ph.D

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Protein-tyrosine kinases are important not only for the development of malignant tumors but also for the regulation of growth and function of normal cells. We are interested in characterizing signal transduction downstream of protein-tyrosine kinases that are relevant to cancer development and to neuronal function.

Roles of Fyn kinase signaling in the brain development

Naosuke Hoshina, Toru Suzuki*, Tadashi Yamamoto (*Division of Oncology)

During the course of Fyn substrate screening, we have identified Protocadherin17 (PCDH17) as a potential target of the Fyn tyrosine kinase. Although several protocadherin members are involved in cancer progression, its physiological roles are largely unknown. To analyze physiological roles of specific protocadherin members *in vivo*, we focused on PCDH17. PCDH17 was specifically expressed in the brain, with high expression in the basal ganglia including striatum, globus pallidus, and substantia nigra. Developmentally, PCDH17 was highly expressed at the stage of synaptogenesis. Furthermore, PCDH17 and its family member, PCDH10 exhibited totally complementary expression patterns in the basal ganglia. At synapses, PCDH17 was localized in perisynaptic regions and showed calcium-dependent homophilic binding, but not heterophilic binding to PCDH10. To elucidate the function of PCDH17 *in vivo*, we generated

PCDH17 knockout mice. With these mice, we are now studying the roles of PCDH17 in the basal ganglia circuitry using morphological, electrophysiological and behavioral approaches.

Expression levels of cadherin family proteins have been implicated in the progression of various cancers. Generally, tumors expressing lower levels of cadherin tended to exhibit higher invasive potentials. Recent reports suggested that silencing of PCDH17 or its closely related family member PCDH10 is involved in cancer malignancy. Therefore, we would like to examine whether mice lacking expression of PCDH17 are prone to develop tumors and/or whether deficiency of PCDH17 could promote tumor progression by introducing *pcdh17* homo-deficiency into cancer-prone mice harboring oncogenically mutated K-*ras*.

Database screening of the possible target of Src-family kinases identified a yet uncharacterized protein which we tentatively termed Bst. Bst specifically expressed in the brain and is well tyrosine phosphorylated in the basal ganglia. Physiological studies that include analysis of *bst* targeted mice are in progress.

Center for Experimental Medicine and Systems Biology

Laboratory of Systems Biology

システムズバイオロジー研究分野

Project Associate Professor Susumu Nakae, Ph.D. | 特任准教授 農学博士 中江 進

Gene-modified mice are considered to be powerful tools for understanding of pathophysiological function of the targeted gene(s) in vivo. Our research focus is the understanding of pathogenesis of rejection and immune disorders such as allergy and autoimmunity using gene-modified mice.

Interleukin-17 accelerates allograft rejection by suppressing regulatory T cell expansion.

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Interleukin-17 (IL-17), which is predominantly produced by Th17 cells distinct from Th1 or Th2 cells, participates in the pathogenesis of infectious, autoimmune and allergic disorders. How-

ever, the precise role in allograft rejection remains uncertain. In the present study, we investigated the role of IL-17 in acute allograft rejection using IL-17-deficient mice. Donor hearts from FVB mice were heterotopically transplanted into either C57BL/6J-IL-17-deficient (IL-17^{-/-}) or -wild-type (WT) mice. Allograft survival was significantly prolonged in IL-17^{-/-} recipient mice due to reduced local inflammation accompanied by decreased inflammatory cell recruitment and cytokine/chemokine expression. IL-17^{-/-} recipient mice exhibited decreased IL-6 production and reciprocally enhanced regulatory T cell (Treg) expansion, suggesting a contribution of Tregs to prolonged allograft survival. Indeed, allografts transplanted into anti-CD25 mAb-treated IL-17^{-/-} recipient mice (Treg-depleted) developed acute rejection similar to WT recipient mice. Surprisingly, we found that gamma delta T cells rather than CD4⁺ and CD8⁺ T cells were key IL-17 producers in the allografts. In support, equivalent allograft rejection was observed in Rag-2^{-/-} recipient mice engrafted with either WT or IL-17^{-/-} CD4⁺ and CD8⁺ T cells. Finally, hearts transplanted into $\gamma\delta$ T cell deficient mice resulted in decreased allograft rejection compared to WT control. In summary, during heart transplantation, (1) IL-17 is crucial for acceleration of acute rejection, (2)

IL-17-deficiency enhances Treg expansion, and (3) $\gamma\delta$ T cells rather than CD4⁺ and CD8⁺ T cells are a potential source of IL-17. IL-17-neutralization may provide a potential target for novel therapeutic treatment for cardiac allograft rejection.

Interleukin-16 deficiency suppresses the development of chronic rejection in murine cardiac transplantation model

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Interleukin-16 (IL-16), originally identified as a T cell chemoattractant factor, promotes the recruitment of various cells expressing CD4, a receptor for IL-16. The precise role of IL-16 in transplant rejection remains unknown. Therefore, the goal of the present study is to determine the contribution of IL-16 to the development of chronic rejection in heart transplants. Utilizing a murine heterotopic heart transplant model, C-H-2^{bm12}KhEg (H-2^{bm12}) donor hearts were transplanted into either (a) IL-16-deficient (IL-16^{-/-}) C57BL/6J or (b) wild type control recipients (MHC class II mismatch). Grafts were harvested 52 days after transplantation and then quantified morphometrically for GCAD. Graft infiltrating cells were detected 10 days and 52 days after transplantation, by flow cytometry and by immunohistochemistry, respectively. Intragraft cytokine and chemokine profiles were assessed with luminex technique. GCAD, or chronic rejection was significantly attenuated in donor hearts transplanted into IL-16^{-/-} recipient mice compared with wild-type controls. More specifically, donor hearts transplanted into IL-16^{-/-} recipients had a significant reduction in coronary artery luminal occlusion, intima-to-

media ratio, and percentage of diseased vessels. GCAD reduction was associated with decreased donor organ inflammation, as well as donor organ cytokine (IL-1 β and IL-6) and chemokine (MCP-1 and KC) protein expression. In summary, IL-16-deficiency resulted in the reduction of chronic rejection, graft inflammatory cell recruitment, and allograft inflammatory cytokine and chemokine production. Therefore, IL-16 neutralization may provide a potential target for novel therapeutic treatment for cardiac allograft rejection.

N-acetylglucosaminyltransferase V-deficiency increases susceptibility to murine malaria

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It is considered that several glycoproteins on erythrocytes in mammalian species are involved in malaria parasite infection. To elucidate the role of N-glycans on malaria parasite infection, we induced experimental murine malaria infection (using *Plasmodium berghei* ANKA) in mice deficient in N-acetylglucosaminyltransferase V (Mgat5), which is one of the enzymes involved in β 1,6-GlcNAc N-glycan biosynthesis. After infection, *Mgat5*^{-/-} mice showed severe body weight loss and parasitemia compared with wild-type mice. The *Mgat5*^{-/-} mice, but not wild-type mice, also showed severe pathology accompanied by marked infiltration of plasma cells into the lungs and liver. These results suggest that β 1,6 GlcNAc N-glycans on/in host erythrocytes may interfere with invasion of the parasites and progression to severe malaria.

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