

Program and Abstracts of the 13th Transgenic Technology Meeting (TT2016)

Clarion Congress Hotel, Prague, Czech Republic, 20–23 March 2016



The TT2016 meeting is hosted by: the Czech Centre for Phenogenomics (CCP), BIOCEV, Prumyslova 595, 25242, Vestec, Czech Republic



Biotechnology and Biomedicine Center of the Academy of Sciences and Charles University in Vestec, Prumyslova 595, 252 42, Vestec, Czech Republic



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TT2016 Scientific Program

Sunday 20th March 2016

13:00–20:00 Registration open

Opening of TT2016

17:30–18:00 Welcome address—ISTT president & organizing committee

Session 1: Opening Keynote lecture

18:00–19:00 Andras Nagy (Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, Canada)
Utilising transposon-delivered transgenes for understanding reprogramming
19:00– Come together evening

Monday 21st March 2016

08:00–18:00 Registration open

Session 2: Generation of transgenic models I

09:00–09:30 Charles A. Gersbach (Duke Center for Genomic and Computational Biology, USA)
Genome and Epigenome Editing with CRISPR/Cas9 for Gene Therapy and Disease Modeling
09:30–10:00 Ralf Kühn (Max-Delbrück-Center for Molecular Medicine, Germany)
Direct production of mouse mutants using engineered nucleases in one-cell embryos
10:00–10:30 Lluís Montoliu (National Centre for Biotechnology (CNB), Spain)
CRISPR-ing the non-coding genome
10:30–10:50 TEA & COFFEE

Session 3: Generation of transgenic models II (selected presentations)

10:50–11:05 Séverine Ménoret
Increased efficiency of BAC transgenesis by piggyBac transposition but not by CRISPR/Cas9 targeted integration for the generation of human SIRPalpha rats
11:05–11:20 Grzegorz Kreiner
Targeting nucleolus—a new approach in generating transgenic mouse models of neurodegenerative diseases and their exploitation to study possible neuroprotective
11:20–11:35 Melissa A. Larson
Nuclear Transfer between Strains of Inbred Mice
11:35–11:50 Christian Mosimann
Post-genome editing approaches for recombinase genetics in zebrafish
11:50–12:05 Andrei Golovko
10 Years of TIGM: Important Lessons and Future Perspectives

- 12:05–12:20 Anna Anagnostopoulos
Using the Human–Mouse: Disease Connection to Identify Mouse Models of Human Disease
- 12:20–13:30 LUNCH & POSTERS

Sponsored session: Applied StemCell, Inc

- 12:20–13:20 Ruby Chen-Tsai (Applied StemCell Inc.)
Development of integrase-based TARGATTM method for generating site-specific transgenic rat models

Session 4: Running a Transgenic Service Facility

- 13:30–15:00 Round table discussion
Marina Gertsenstein (Toronto Center for Phenogenomics (TCP), Canada)
Cord Brakebusch (Biotech Research and Innovation Centre (BRIC), Denmark)
Lauryl Nutter (Toronto Center for Phenogenomics (TCP) (Canada)
- 15:00–15:15 TEA & COFFEE

Session 5: Beyond transgenic model generation

- 15:15–15:45 Mary Dickinson (Baylor College of Medicine, USA)
Analysis of embryonic lethal mutations in mice using 3D imaging
- 15:45–16:15 Nicholas Gale (Regeneron Pharmaceuticals, USA)
A large scale mouse phenotyping screen for the discovery of novel biotech targets in oncology and angiogenesis and other therapeutic areas
- 16:15–16:45 Kent Lloyd (University of California, Davis, USA)
An update on progress by the International Mouse Phenotyping Consortium (IMPC)
- 16:45–17:00 TEA & COFFEE

Session 6: World of Nucleases: discovery and development

- 17:00–17:30 Francis Mojica (University of Alicante, Spain)
Taking a look at the CRISPR biology and applications from a historical perspective
- 17:30–18:00 Bernd Zetsche (Broad Institute of MIT and Harvard Cambridge, USA)
Cpf1 is a single-RNA-guided endonuclease of a Class 2 CRISPR-Cas system
- 18:00–18:30 Konstantin Severinov (Skolkovo Institute of Science and Technology, Russia)
A pipeline approach for discovery of novel CRISPR-Cas systems

Tuesday 22nd March 2016

Session 7: Advances in animal biotechnology

- 08:30–09:00 Eckhard Wolf (LMU Munich, Germany)
COST Action BM1308 “Sharing Advances on Large Animal Models—SALAAM”
- 09:00–09:30 Yonglun Luo (Aarhus University, Denmark)
Efficient precision gene editing in pigs: Towards a new era in generating genetically designed pigs of human diseases and regenerative medicine
- 09:30–10:00 Chris Proudfoot (The Roslin Institute of the University of Edinburgh, UK)
Genome engineering livestock
- 10:00–10:15 TEA & COFFEE

Session 8: Advances in animal biotechnology (selected presentations)

- 10:15–10:30 Soo Young Yum
Production and Analysis of a multi-copy integrated transgenic cattle via transposon
- 10:30–10:45 Amy Kaucher
Production of germline ablated male pigs via Crispr/Cas editing of the NANOS2 gene
- 10:45–11:00 Sean Stevens
Pig Genome Engineering for Xenotransplantation
- 11:00–11:15 Wiebke Garrels
Multiplex Transgenesis in Cattle via the Sleeping Beauty Transposon System

Parallel sessions

Session 9: Animal Ethics

- 11:20–11:40 Henriette Bout (University of Amsterdam, the Netherlands)
Ethical aspects of the Crispr/Cas9 technology
- 11:40–12:00 Aurora Brønstad (University of Bergen, Norway)
The AALAS-FELASA Working Group on Harm-Benefit analysis of animal studies
- 12:00–12:20 Michelle Stewart (Mary Lyon Centre, Medical Research Council UK)
The Four R's of phenotyping GA mice—Robustness, Reproducibility, Rigorously, and Randomisation

Session 10: Technology development II

- 11:20–11:40 Toru Takeo (Center for Animal Resources and Development (CARD), Japan)
Efficient production of mouse oocytes using superovulation by immunization against inhibin

- 11:40–12:00 Jeff Batton (GeneSearch, Inc., USA)
New Cost-Effective Methods for Stem Cell Procedures on Pre-Implantation Embryos
- 12:00–12:20 Sandra Hope (Brigham Young University, USA)
Microfabricated Lance Array Nanoinjection system delivers CRISPR-Cas9 to Hundreds of Thousands of Cells Simultaneously
- 12:20–14:00 LUNCH & POSTERS

Session 11: Gene manipulation and genome editing and (disease) models I

- 14:00–14:30 Ethan Bier (University of California, USA)
The implications of active genetics
- 14:30–15:00 Didier Stainier (Max Planck Institute for Heart and Lung Research, Germany)
Genetic compensation induced by deleterious mutations but not gene knockdowns

Session 12: Gene manipulation and genome editing and (disease) models II (selected presentations)

- 15:00–15:15 Marie-Christine Birling
Generation of genomic structural variants by CRISPR/Cas9 genome editing in rodents
- 15:15–15:30 Katharina Boroviak
The possibilities and limitations of CRISPR/Cas9 in mouse zygotes
- 15:30–15:45 Kevin A. Peterson
CRISPR/Cas9 mediated gene modification provides a robust platform for modeling developmental disorders
- 15:45–16:00 TEA & COFFEE

Session 13: Orbis pictus lecture

- 16:00–16:45 Richard Behringer (University of Texas MD Anderson Cancer Center, USA)
Transgenic approaches in diverse animals species
- 16:45–18:00 ISTT GENERAL ASSEMBLY
- 19:15– Gala dinner (Zofin Palace)

Wednesday 23rd March 2016

Session 14: Technology development

- 08:30–09:00 Masato Ohtsuka (Tokai University School of Medicine, Japan)
GONAD and Easy (Isi)-CRISPR: novel mouse genome engineering tools
- 09:00–09:30 Haoyi Wang (Institute of Zoology, Chinese Academy of Sciences, China)
CRISPR-Cas9 Application in Mouse Model Creation and Transcription Regulation

- 09:30–10:00 Tomomi Aida (Medical Research Institute (MRI) of Tokyo Medical and Dental University (TMDU), Japan)
Gene cassette knock-in in mice with cloning-free CRISPR/Cas system
- 10:00–10:15 TEA & COFFEE

Session 15: Genetics, Epigenetics, Stem cell manipulation

- 10:15–10:45 Robin Lovell-Badge (Francis Crick Institute, UK)
Regulation of Sox9 in the gonad during sex determination
- 10:45–11:15 F. Kent Hamra (University of Texas Southwestern Medical Center, USA)
Rat Germline Editing in Donor Spermatogonial Stem Cells
- 11:15–11:45 John Schimenti (Cornell University, USA)
GWIS: Genetics with Interrogation of SNPs
- 11:45–13:30 LUNCH & POSTERS

Session 16: Generation of transgenic models I: Models of diseases and applications (selected presentations)

- 13:30–13:45 Yann Herault
Modelling and understanding rare genetic diseases with intellectual disabilities for tomorrow's treatment
- 13:45–14:00 Petr Kasparek
TALEN-mediated inactivation of Klk5 and Klk7 rescues lethal phenotype of Netherton syndrome mouse model
- 14:00–14:15 Javier Martín-González
A powerful new tool to improve immune-compromised mouse models: derivation of NRG embryonic stem cell lines.
- 14:15–14:30 Prem Premririt
RNAi and CRISPR/Cas9 based In Vivo Models for Drug Discovery
- 14:30–14:45 TEA & COFFEE

Session 17: Orbis pictus lecture II

- 14:45–15:30 Thomas Boehm (Max Planck Institute of Immunology and Epigenetics, Germany)
Genetic basis of lymphoid organ formation

Session 18: Genetics & models pluripotency/iPS cells

- 15:30–16:00 Rene Maehr (UMass Medical School, USA)
Towards using pluripotent stem cell-based disease models to study immune syndromes
- 16:00–16:30 Ron Weiss (Massachusetts Institute of Technology, USA)
Mammalian Synthetic Biology: From Parts to Modules to Therapeutic Systems

16:30–16:45 TEA & COFFEE

Session 19: Award session

16:45–16:50 3rd ISTT Young Investigator Award
 16:50–17:10 Pablo Ross
Embryonic stem cells and interspecies blastocyst complementation in farm animals

Session 20: Closing Keynote Lecture

17:10–17:55 Denis Duboule (University of Geneva, Switzerland)
A Genetic Approach of Long-range Gene Regulation During Development and Evolution
 17:55–18:10 Close of Meeting

TT2016 Hands-on Workshops

Workshop organization committee

Radislav Sedlacek (CCP, Prague, Czech Republic)
Martin Fray (MRC, Harwell, UK)
Petr Bartunek (IMG, Prague, Czech Republic)
Bjoern Schuster (CCP, Prague, Czech Republic)
Inken M. Beck (CCP, Prague, Czech Republic)
Nicole Chambers (CCP, Prague, Czech Republic)

INFRAFRONTIER-I3—Mouse cryopreservation workshop

Day 1—Wednesday 16th March 2016

08:30–09:00 Arrival and registration
 09:00–09:15 Welcome and introduction to the IMG and CCP
 Radislav Sedlacek, IMG, Prague, Czech Republic
 09:15–09:25 Introduction to the course and the teaching material
 09:25–10:45 Principles and benefits of cryobiology
 Martin Fray, Medical Research Council, Harwell, UK
 10:45–11:00 **TEA and COFFEE**
 11:00–12:00 New approaches to exchanging mouse strains
 Lluís Montoliu, National Centre of Biotechnology, Madrid, Spain
 12:00–13:00 **LUNCH**
 13:00–15:00 Sperm Harvesting/Freezing Introduction
 A. Sperm freezing—(Practical)
 B. Preparing epididymides held for refrigerated transportation in Lifer (Practical)
 C. Sperm held on dry-ice (Demonstration)

15:00–15:15 **TEA and COFFEE**
 15:15–16:00 Preparation for Thursday's IVF Media preparation
 A. Pre-incubation dish containing MBCD
 B. Fertilisation drops containing GSH
 C. Wash dish containing mHTF
 16:00–16:30 Animal welfare aspects on cryopreservation
 Marcello Raspa, CNR-IBCN, Monterotondo, Italy
 16:30–17:00 Recap/Review
 19:30 **MEET IN PRAGUE FOR BAR DINNER**

Day 2—Thursday 17th March 2016

07:30–10:30 IVF Introduction
 (a) Set up an IVF using freshly harvested sperm and vitrified oocytes—(Demonstration)
 (b) Set up an IVF using sperm held on dry ice—(Demonstration)
 (c) Set up an IVF using sperm harvested from epididymides held overnight in Lifer—(Practical)
 (d) Set up an IVF using sperm frozen in LN₂—(Practical)
 10:30–11:00 **TEA AND COFFEE**
 11:00–12:00 New development and ideas in sperm freezing techniques—Toru Takeo, CARD, Kumamoto University, Japan
 12:00–13:00 **LUNCH**
 13:00–15:30 Wash IVF—(Demonstration followed by practical training)
 15:30–16:00 INFRAFRONTIER-EMMA resource, principles to efficiently share mouse models—Susan Marschall (Helmholtz Zentrum Munich, Germany)
 16:00–16:15 Recap/Review
 16:15–17:00 CRISPR technology (joint lecture)
 Lluís Montoliu, National Centre of Biotechnology, Madrid, Spain

Day 3—Friday 18th March 2016

08:30–10:00 Assess IVF dishes—(Demonstration followed by practical)
 10:00–10:15 **TEA AND COFFEE**
 10:15–12:00 Embryo vitrification—(Demonstration followed by practical)
 12:00–13:00 Thawing vitrified embryos—(Demonstration followed by practical)
 13:00–14:00 **LUNCH**
 14:00–16:00 Non-surgical embryo transfer—Barbara Stone, Paratechs Corporation
 16:00–16:15 **TEA and COFFEE**
 16:15–17:15 Preparing frozen samples for shipment—Soren Knudsen—Cryoport
 17:15–17:30 Wrap up presentation and closure of the course

CCP programmable nucleases (CRISPR/Cas9) Transgenesis Course

Day 1—Wednesday 16th March 2016

- 08:30–09:00 Arrival and Registration
 09:00–09:15 Welcome and Introduction to IMG and CCP
Radislav Sedlacek (IMG/CCP)
 09:15–09:25 Introduction to the Course and the Teaching Material
Björn Schuster (IMG/CCP)
 09:25–10:00 Lecture: Mouse transgenesis: *Pros-and-cons* of programmable nucleases
Radislav Sedlacek
 10:00–10:45 Sponsored lecture: Guide design and demonstration of web based tool
Leigh Brody—Desktop Genetics
 10:45–11:00 **TEA and COFFEE**
 11:00–13:00 Practical training session I.
 A. CRISPR/Cas9 Zygote injection—*Ronald Naumann*
 B. Electroporation of zygotes—*Haoyi Wang*
 C. Bioinformatics, experimental design & targeting & genotyping—*Björn Schuster*
 13:00–14:00 **LUNCH**
 14:00–14:30 Targeting design—validation of the tools—genotyping
Björn Schuster (IMG/CCP)
 14:30–16:00 CRISPR validation practical (cell culture & transfection)
Björn Schuster & Jana Kopkanova (IMG/CCP)
 16:00–16:15 **TEA and COFFEE**
 16:15–17:00 Lecture: oocyte—embryo transition in mammals
Petr Svoboda—Institute of Molecular Genetics, CZ
 19:30 **MEET IN PRAGUE FOR DINNER**

Day 2—Thursday 17th March 2016

- 09:00–09:15 Recap/Review
 09:15–10:00 Lecture: Genotyping strategies and tools
Jana Kopkanova & Björn Schuster (IMG/CCP)
 10:00–10:45 Sponsored Lecture: CRISPR genome editing workflow
Caroline Becket—Merck Millipore Sigma
 10:45–11:00 **TEA AND COFFEE**
 11:00–13:00 Practical training session II.
 A. CRISPR/Cas9 Zygote injection—*Ronald Naumann*
 B. Electroporation of zygotes—*Haoyi Wang*
 C. Bioinformatics, experimental design & targeting & genotyping—*Björn Schuster*
 13:00–14:00 **LUNCH**
 14:00–14:20 Targeting design—validation of the tools—genotyping
Björn Schuster (IMG/CCP)
 14:20–16:00 CRISPR validation practical (DNA isolation and PCR based genotyping I)
Jana Kopkanova & Björn Schuster (IMG/CCP)
 16:00–16:15 **TEA & COFFEE**

- 16:15–17:00 Lecture—CRISPR technology
Lluis Montoliu—CNB, Spain
This lecture will be a joint lecture with the Cryopreservation workshop
 19:30 **DINNER**

Day 3—Friday 18th March 2016

- 09:00–09:45 Development CRISPR-Cas9 technology & Cpf1
Bernd Zetsche—Broad Institute, USA
 09:45–10:00 **TEA AND COFFEE**
 10:00–12:00 Practical training session III.
 A. CRISPR/Cas9 Zygote injection—*Ronald Naumann*
 B. Electroporation of zygotes—*Haoyi Wang*
 C. Bioinformatics, experimental design & targeting & genotyping—*Björn Schuster*
 12:00–13:00 **LUNCH**
 13:00–15:00 CRISPR validation practical (PCR based genotyping)
Jana Kopkanova & Björn Schuster (IMG/CCP)
 15:00–15:15 **TEA and COFFEE**
 15:15–16:00 Collection of results and preparation of short presentations
 16:00–17:15 Short group presentations and discussion
 17:15–17:30 Summary & Conclusions
Radislav Sedlacek
 17:30 End of course

Zebrafish Genome Editing

Day 1—Wednesday 23rd March 2016

- 18:00–18:45 Registration (Clarion Congress Hotel, Prague)
 18:45–19:00 Welcome and Introduction (P. Bartunek and Z. Kozmik)
 19:00–19:45 Talk-Zebrafish transgenesis and genome editing: state-of-the-art (C. Mosimann)
 20:00–22:00 Get together/roundtable discussion/course expectations and **LIGHT DINNER**

Day 2—Thursday 24th March 2016

- 08:30–09:00 Arrival at Institute of Molecular Genetics, Prague—**TEA/COFFEE**
 09:00–12:30 Collection of embryos, microinjections—morpholino oligonucleotides, CRISPR-Cas9 (mRNA and protein)
 12:30–13:30 **LUNCH**
 13:30–14:00 Talk-sgRNA design, genotyping and analysis of results (C. Mosimann)
 14:00–15:30 *in vitro* transcription and purification of sgRNA, discussion of alternative methods
 16:00–16:30 **TEA and COFFEE**
 16:30–18:00 Embryo manipulations, mounting, imaging, analysis (stereo, microscope)
 18:00–18:30 Setup of adult zebrafish to generate injection-ready embryos
 19:00 **DINNER**

Day 3—Friday 25th March 2016

09:00–12:00	Collection of embryos, microinjections (To12 transposase, fluorescent constructs)
12:00–13:00	LUNCH
13:15–14:00	Special lecture (G. Lieschke)
14:00–15:00	Molecular analysis of mutagenesis efficiency (T7 endo assay, gel electrophoresis)
15:00–15:30	TEA and COFFEE
15:30–17:30	Embryo manipulations, mounting, imaging, analysis (time-lapse, confocal)
17:30–18:00	Discussion and closing remarks
18:00	End of workshop

Oral Presentations**Utilising transposon-delivered transgenes for understanding reprogramming****Andras Nagy**

Lunenfeld-Tanenbaum Research Institute, Mount Sinai Hospital, Toronto, Canada; Department of Obstetrics & Gynaecology and Institute of Medical Science, University of Toronto, Toronto, Canada

The discovery of a defined set of transcription factors that can induce reprogramming of somatic cells to pluripotent stem cells (iPSCs) has had an unprecedented impact on our view on future cell transplantation-based tissue repair and restoration of faulty physiological functions. Somatic cell reprogramming is a several weeks long process through which cells reach pluripotency, the developmental state similar to embryonic stem cells. This cascade of events and the driving forces behind the phenomenon are very poorly understood. It is, however, crucial to uncover the fine details of this process in order to comprehend the true properties of iPSCs and so better tailor their future therapeutic use.

To address this need we utilized the unique property of the transposon-mediated transgene delivery system combined with doxycycline inducible expression of the reprogramming factors. The transposon ITR-flanked transgenes were seemingly much less subjected to silencing than the virus-delivered ones. Therefore, we were able to generate highly efficient secondary reprogramming systems, allowing us a comprehensive molecular description of the reprogramming cascade toward two distinct pluripotent states. We explored alternative outcomes of somatic reprogramming by fully characterizing reprogrammed cells independent of preconceived definitions of reprogrammed iPSC states. We demonstrate that manipulating the expression level of the reprogramming factor influences the arrival of cells to a non-ES cell-like or ES cell like pluripotent state. This bifurcated process has been characterized with multiple “omic” platforms, consisting of the transcriptome (microRNA, lncRNA and mRNA), CpG methylation, ChIP-sequencing (for chromatin marks: H3K4me3, H3K27me3 and H3K36me3), in addition to quantitative mass spectrometry profiling of the global and cell surface proteome. This dataset enables cross-referencing between “omic” platforms, which facilitates deeper understanding of the cascade of molecular events and

the dynamics of the epigenome driving the generation of pluripotent cells.

Keywords: stem cells, pluripotency, somatic cell reprogramming, epigenetics of stem cells

Genome and epigenome editing with CRISPR/Cas9 for gene therapy and disease modeling**Charles A. Gersbach**

Department of Biomedical Engineering, Duke University, Durham, USA

The advent of genome engineering technologies, including the RNA-guided CRISPR/Cas9 system, has enabled the precise editing and regulation of endogenous human genes and epigenetic states. We have applied these tools to the correction of mutations that cause genetic disease and also adapted them to manipulate the epigenome and control cell fate decisions. For example, we engineered CRISPR/Cas9-based nucleases to correct the human dystrophin gene that is mutated in Duchenne muscular dystrophy patients. When we delivered these nucleases to cells from patients with this disease, the correct gene reading frame and expression of the functional dystrophin protein were restored *in vitro* and following cell transplantation into mouse models *in vivo*. When delivered directly to a mouse model of this disease, gene editing by the CRISPR/Cas9 system led to gene restoration and improvement of biochemical and mechanical muscle function. In other studies, we have engineered CRISPR/Cas9-based tools to regulate the expression of endogenous genes and applied these tools to control diverse genes relevant to disease, development, and differentiation. Genome-wide analysis of the DNA-binding, gene regulation, and chromatin remodeling by these targeted epigenome modifiers has demonstrated their exceptional specificity. We have recently applied these technologies to control the decisions of stem cells to become specific cell fates and reprogram cell types into other lineages that could be used for drug screening and disease modeling. Incorporating methods to dynamically control the activity of these proteins, such as optogenetic control of the proteins with light, has allowed us to pattern gene expression both temporally and spatially. Ongoing efforts include designing strategies to manipulate specific epigenetic marks that would enable deciphering the influence of epigenetics on gene regulation and disease states. Collectively, these studies demonstrate the potential of modern genome engineering technologies to capitalize on the products of the Genomic Revolution and transform medicine, science, and biotechnology.

Keywords: genome editing, epigenome editing, CRISPR, gene therapy

Direct production of mouse mutants using engineered nucleases in one-cell embryos**Ralf Kühn**

Max-Delbrück Center for Molecular Medicine, Berlin, Germany

School of Medicine, Isehara, Kanagawa, Japan; ²Department of Regenerative Medicine, Basic Medical Science, Tokai University School of Medicine, Isehara, Kanagawa, Japan; ³Department of Bioproduction, Tokyo University of Agriculture, 196 Yasaka, Abashiri, Hokkaido, 099-2493, Japan; ⁴Mouse Genome Engineering Core Facility, University of Nebraska Medical Center, Omaha, NE, USA; ⁵Section of Gene Expression Regulation, Frontier Science Research Center, Kagoshima University, Kagoshima, Kagoshima, Japan; ⁶Developmental Neuroscience, Munroe Meyer Institute for Genetics and Rehabilitation, University of Nebraska Medical Center, Omaha, NE, USA

The CRISPR/Cas9 system has emerged as a popular genome editing method because of its technical simplicity and robustness. It can be widely applied to generate genome editing animals including mice. In this talk I will present our recently developed *add-on* tools for CRISPR/Cas9 system: GONAD and Easy (*Isi*)-CRISPR.

GONAD: Animal transgenesis involves three major technical steps; isolation of fertilized eggs, microinjection and subsequent transfer of eggs into recipient females. Of these, the microinjection is the most tedious step that requires sophisticated equipment as well as highly skilled personnel to perform the task. Using CRISPR system, some groups recently demonstrated that *microinjection* can be replaced with electroporation of eggs. Such *ex vivo* electroporation helped handling of many eggs simultaneously but it did not exclude other two steps of animal transgenesis. We developed a new system called Genome-editing via Oviductal Nucleic Acids Delivery (GONAD) method that could bypass all three critical steps of traditional genome engineering methods. The GONAD strategy allows electroporation to deliver nucleic acids (NAs) to the zygotes within the intact mouse oviduct *in situ*. With this method (instillation of NA solution into the oviductal lumen of pregnant females and following electroporation to the oviducts), we successfully delivered NAs into the day 0.7 and day1.5 zygotes and obtained gene-disrupted embryos/pups when delivered CRISPR/Cas9 genome editing components. The GONAD method can also be potentially applied to generate genetically engineered models in other species.

Easy-CRISPR: One of the major challenges of CRISPR/Cas9 system is very poor efficiency of insertion of longer DNA cassettes at the Cas9 cut sites. Because smaller single-stranded OligoDeoxyNucleotides (ssODNs) get inserted at relatively higher efficiency than the longer double-stranded DNA cassettes, we hypothesized that longer single-stranded DNAs (ssDNAs) could also get inserted efficiently. Because longer ssDNAs (>200-bases long) cannot be readily synthesized commercially, such strategies require the use of dsDNAs (plasmid-based constructs) even though the dsDNA repair templates generally require long homology arms and are inserted with lower efficiency compared to ssDNA. We synthesized ssDNA donors of 0.2 to 0.5-kb or longer, using a standard molecular biology technique; *in vitro* Transcription and Reverse Transcription (*iv*TRT) that were then used in CRISPR/Cas9-mediated targeted insertion experiments (pronuclear and cytoplasmic injection of ssDNA together with CRISPR/Cas9 genome editing components). As a result, we routinely obtained knock-in mice with an insertion efficiency

of up to 83 %. We named this new method as (*Isi*)-CRISPR: *iv*TRT-ssDNA insertion CRISPR (pronounced *Easy*-CRISPR). **Keywords:** CRISPR/Cas9, *in vivo* electroporation, GONAD, ssDNA, knock-in, Easy-CRISPR

CRISPR-Cas9 application in mouse model creation and transcription regulation

Haoyi Wang^{1,2}

¹Institute of Zoology, Chinese Academy of Sciences, Beijing, China; ²The Jackson Laboratory, Bar Harbor, Maine, USA

CRISPR-Cas9 system has become the tool of choice for genome engineering. Previously we established the method of microinjecting CRISPR-Cas9 system into zygotes to generate mouse models. To overcome the technically demanding and inherently low throughput method of microinjection, we devised the Zygote Electroporation of Nuclease (ZEN) technology, which employs electroporation to deliver CRISPR-Cas9 reagents to the zygotes and generated live mice carrying targeted NHEJ and HDR mutations. The general principles discovered and described in this study have implications for high efficiency, high throughput genome engineering in animals.

To extend the utility of the CRISPR-Cas9 system, we have taken advantage of the ability of Pumilio PUF domains to bind specific 8-mer RNA sequences. By combining these two systems, we established the Casilio system, which allows for specific and independent delivery of effector proteins to specific genomic loci. We demonstrated that the Casilio system enables independent up- and down-regulation of multiple genes, as well as live-cell imaging of multiple genomic loci simultaneously. Importantly, multiple copy of PUF binding sites can be incorporated on sgRNA backbone, therefore allowing for local multimerization of effectors. In addition, the PUF domain can be engineered to recognize any 8-mer RNA sequence, therefore enabling the generation and simultaneous operation of many Casilio modules.

Keywords: Genome editing, CRISPR-Cas9, mouse model, transcription regulation

Gene cassette knock-in in mice with cloning-free CRISPR/Cas system

Tomomi Aida¹, Tetsushi Sakuma², Shota Nakade², Takashi Yamamoto², Kohichi Tanaka¹

¹Laboratory of Molecular Neuroscience, Medical Research Institute (MRI), Tokyo Medical and Dental University (TMDU), Tokyo, Japan; ²Department of Mathematical and Life Sciences, Graduate School of Science, Hiroshima University, Hiroshima, Japan

Knock-in mice carrying functional gene cassettes have provided invaluable opportunities for *in vivo* functional analysis of genes, cells, and circuits in mammalian organisms. Although the CRISPR/Cas system has enabled one-step generation of knockout mice with high efficiency, relatively low success rates of gene cassette knock-in limit its application range. We