

Genome Concept Centennial Conference

Dates: February 15-17, 2021

Purely Online using zoom



Hosted by
National Institute of Genetics
and
MEXT Yaponesia Genome Project



Organizers

IKEO Kazuho, National Institute of Genetics, Mishima, Japan (chair)

SAITOU Naruya, National Institute of Genetics, Mishima, Japan

SATTA Yoko, Graduate University for Advanced Studies, SOKENDAI, Hayama, Japan

TAMURA Koichiro, Tokyo Metropolitan University, Tokyo, Japan

Conference Home Page: http://molevo.sakura.ne.jp/DnaData_lab/GCC2021.html

National Institute of Genetics (NIG) Home Page: <https://www.nig.ac.jp/nig/>

MEXT Yaponesia Genome Project Home Page: http://www.yaponesian.jp/index_e.php

Keynote Speakers (30min talk + 5min discussion)

Dr. GOJOBORI Takashi (Distinguished Professor & Associate Director of Computational Bioscience Research Center, KAUST)

Dr. Dan GRAUR (Moore Professor, Department of Biology and Biochemistry, University of Houston, Houston)

Dr. LI Wen-Hsiung (Distinguished Research Fellow, Biodiversity Research Center, Academia Sinica, Taipei)

Dr. LI Yi-Xue (Director, Shanghai Center for Bioinformation Technology, Shanghai)

Dr. Mark STONEKING (Professor, University of Leipzig, Leipzig)

Invited Speakers oversea (20min talk+ 5 min discussion)

Dr. FU Qiaomei (Professor, CAS Institute of Paleontology and Paleoanthropology, Beijing)

Dr. Aida ANDRES (Professor, University College London, London)

Dr. Arndt von HAESELER (Professor, University of Vienna, Vienna)

Dr. CHAW Shu-Miaw (Research Fellow, Academia Sinica, Taipei)

Dr. Tal DAGAN (Professor, University of Kiel, Kiel)

Dr. Yun-Xin FU (Professor, University of Texas at Houston, Houston)

Dr. MINETA Katsuhiko (Researcher, KAUST, Jedda)

Dr. SHIMIZU Kentaro (Professor, University of Zurich, Zurich)

Dr. SHIMIZU Hiroshi (Researcher, KAUST, Jedda)

Dr. Anne STONE (Professor, Arizona State University, Phoenix)

Dr. SU Bing (Professor, CAS Kunming Institute of Zoology, Kunming)

Invited Speakers from Japan (20min talk+ 5 min discussion)

Dr. FUJIMOTO Akihiro (Professor, University of Tokyo, Tokyo) *

Dr. HANADA Kousuke (Associate Professor, Kyushu Institute of Technology, Tobata) *

Dr. HASEBE Mitsuyasu (Professor, National Institute of Basic Biology, Okazaki)

Dr. IMANISHI Tadashi (Professor, Tokai University, Isehara) *

Dr. INOUE Jun (Assistant Professor, Atmosphere and Ocean Research Institute, The University of Tokyo, Kashiwa)

Dr. ITOH Takeshi (Advanced Analysis Center Leader, The National Agriculture and Food Research Organization, Tsukuba) *

[Dr. KANZAWA-KIRIYAMA Hideaki](#) (Associate Curator, [National Museum of Nature and Science, Tsukuba](#)) *
[Dr. KIMURA Ryosuke](#) (Associate Professor, [University of Ryukyu, Okinawa](#)) *
[Dr. KINOSHITA Tetsu](#) (Professor, [Yokohama City University](#) , Yokohama)
[Dr. OOTA Hiroki](#) (Professor, [University of Tokyo](#), Tokyo) *
[Dr. OSADA Naoki](#) (Associate Professor, [Hokkaido University](#) , Sapporo) *
[Dr. SASAKI Hiroyuki](#) (Professor, [Kyushu University](#), Fukuoka)
[Dr. SATTA Yoko](#) (Professor, [Graduate University for Advanced Studies](#), Hayama)
[Dr. SHINODA Ken-Ichi](#), (Senior Director in Research, [National Museum of Nature and Science](#), Tokyo/Tsukuba) *
[Dr. SHINZATO Chuya](#) (Associate Professor, [University of Tokyo](#), Kashiwa)
[Dr. SUZUKI Hitoshi](#) (Professor, [Hokkaido University](#), Sapporo) *
[Dr. TAKEYAMA Haruko](#) (Professor, [Waseda University](#), Tokyo)
[Dr. TAMURA Koichiro](#) (Professor, [Tokyo Metropolitan University](#), Tokyo)

[Invited Speakers from National Institute of Genetics \(NIG\) \(20min talk+ 5 min discussion\)](#)

[Dr. Hiroshi AKASHI](#) (Professor, Division of Evolutionary Genetics, NIG, Mishima)
[Dr. IKEO Kazuho](#) (Associate Professor, Laboratory for DNA Data Analysis, NIG, Mishima)
[Dr. INOUE Ituro](#) (Professor, Division of Human Genetics, NIG, Mishima) *
[Dr. Timothy A. JINAM](#) (Assistant Professor, Population Genetics Laboratory, NIG, Mishima) *
[Dr. KITANO Jun](#) (Professor, Division of Ecological Genetics, NIG, Mishima)
[Dr. Kirill KRYUKOV](#) (Specially Appointed Associate Professor, Population Genetics Laboratory, NIG, Mishima)
[Dr. NAKAMURA Yasukazu](#) (Professor, Genome Informatics Laboratory, NIG, Mishima)
[Dr. SAITOU Naruya](#) (Professor, Population Genetics Laboratory, NIG, Mishima) *
[Dr. SUZUKI Rumiko](#) (Project Associate Professor, Population Genetics Laboratory, NIG, Mishima)

* Member of Yaponesia Genome Project

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Program Day 1: Monday, February 15, 2021

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13:00 - 13:10 Opening remarks

Dr. IKEO Kazuho, Chair of GCCC, National Institute of Genetics

Dr. HANAOKA Fumio, Director-General, National Institute of Genetics

13:10 - 15:00 **Session 1** (Chair: Dr. SATTA Yoko)

13:10 - 13:45 **Keynote talk 1** by Dr. Wen-Hsiung Li, Taipei

Talk title: Evolutionary insights from microbial genomes

13:45 - 14:10 **Invited talk 1** by Dr. SU Bing, Kunming

Talk title: Comparative brain 3D genome analysis reveals evolutionary innovations of human corticogenesis

14:10 - 14:35 **Invited talk 2** by Dr. FU Qiaomei, Beijing

Talk title: The prehistory of East Asian using insights from ancient DNA

14:35 - 15:00 **Invited talk 3** by Dr. CHAW Shu-Miaw, Taipei

Talk title: Stout camphor tree (Laurel family) genome fills gaps in understanding of flowering plant genome evolution

15:00 - 15:20 Tea break

15:20 - 16:45 **Session 2** (Chair: Dr. TAMURA Koichiro)

15:20 - 15:55 **Keynote talk 2** by Dr. GOJOBORI Takashi, KAUST

Talk title: Genome evolution in Asian rice domestication

15:55 - 16:20 **Invited talk 4** by Dr. SHIMIZU Hiroshi, KAUST

Talk title: Behavior of cnidarian hydra : dominance of foot nervous system in behavioral regulation

16:20 - 16:45 **Invited talk 5** by Dr. MINETA Katsuhiko, KAUST

Talk title: Population genomics of indigenous inhabitants of Arabia

16:45 - 17:05 Tea break

17:05 - 18:30 **Session 3** (Chair: Dr. SAITOU Naruya)

17:05 - 17:40 **Keynote talk 3** by Dr. Mark STONEKING, Leipzig

Talk title: Genes, Culture, and Human Evolution

17:40 - 18:05 **Invited talk 6** by Dr. SHINODA Ken-ichi, Tsukuba

Talk title: Contribution of ancient genome analysis to the origin of the Japanese - Looking back on the research history of the past 30 years

18:05 - 18:30 [Invited talk 7](#) by Dr. Arndt von HAESELER, Vienna
Talk title: Lineage size evolution in developing organoids

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Program Day 2: Tuesday, February 16, 2021

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9:00 - 10:25 [Session 4](#) (Chair: Dr. IKEO Kazuho)

9:00 - 9:35 [Keynote talk 4](#) by Dr. Dan GRAUR, Houston

Talk title: The selectionist pandemic and the emperor's new clothes: examining the evidence for soft selective sweeps in humans

9:35 - 10:00 [Invited talk 8](#) by Dr. Anne STONE, Phoenix

Talk title: Mycobacterium leprae genomic variation and evolutionary history in the Pacific

10:00 - 10:25 [Invited talk 9](#) by Dr. Yun-Xin FU, Houston

Talk title: Tetrahymena amitosis strategy: from sex determination to whole genome sequencing

10:25 - 10:45 Tea break

10:45 - 12:10 [Session 5](#) (Chair: Dr. KITANO Jun)

10:45 - 11:20 [Keynote talk 5](#) by Dr. LI Yi-Xue, Shanghai

Talk title: A pharmaco-genomic landscape in human liver cancers

11:20 - 11:45 [Invited talk 10](#) by Dr. KINOSHITA Tetsu, Yokohama

Talk title: Overcoming the species hybridization barrier by ploidy manipulation in the genus Oryza

11:45 - 12:10 [Invited talk 11](#) by Dr. HASEBE Mitsuyasu, Okazaki

Talk title: Evolution of carnivory and movement in plants

12:10 - 13:30 Lunch

13:30 - 14:45 [Session 6](#) (Chair: Dr. NAKAMURA Yasukazu)

13:30 - 13:55 [Invited talk 12](#) by Dr. SASAKI Hiroyuki, Fukuoka

Talk title: DNA methylation in development and disease

13:55 - 14:20 [Invited talk 13](#) by Dr. INOUE Jun, Kashiwa

Talk title: dbCNS: a new database for conserved non-coding sequences

14:20 - 14:45 [Invited talk 14](#) by Dr. SHINZATO Chuya, Kashiwa

Talk title: Using genomics to reveal novel insights into coral biology

14:45 - 15:05 Tea break

15:05 - 16:45 **Session 7** (Chair: Dr. SUZUKI Rumiko)

15:05 - 15:30 **Invited talk 15** by Dr. Hiroshi AKASHI, NIG

Talk title: Population genomics of weak evolutionary forces: Base composition evolution in *Drosophila*

15:30 - 15:55 **Invited talk 16** by Dr. NAKAMURA Yasukazu, NIG

Talk title: A chromosome-level assembly of a domestic cat of American Shorthair

15:55 - 16:20 **Invited talk 17** by Dr. KITANO Jun, NIG

Talk title: Genetics of adaptive radiation in stickleback and medaka fishes

16:20 - 16:45 **Invited talk 18** by Dr. INOUE Ituro, NIG

Talk title: Genomics and cultivation of new virus world

16:45 - 17:05 Tea break

17:05 - 18:45 **Session 8** (Chair: Dr. AKASHI Hiroshi)

17:05 - 17:30 **Invited talk 19** by Dr. TAMURA Koichiro, Tokyo

Talk title: Genome evolution for cold adaptation in experimental populations of *Drosophila albomicans*

17:30 - 17:55 **Invited talk 20** by Dr. Tal DAGAN, Kiel

Talk title: Plasmids as turtles in an evolutionary race

17:55 - 18:20 **Invited talk 21** by Dr. SHIMIZU Kentaro, Zurich

Talk title: Polyploid wheat as the traditional model of genome analysis and the last frontier of genome sequencing

18:20 - 18:45 **Invited talk 22** by Dr. Aida ANDRES, London

Talk title: Dissecting genomes to identify local adaptations in humans and other primates

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Program Day 3: Wednesday, February 17, 2021

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9:00 - 10:40 **Session 9** (Chair: Dr. IMANISHI Tadashi)

9:00 - 9:25 **Invited talk 23** by Dr. SATTA Yoko, Hayama

Talk title: Population genomics on the origin of lactase persistence in Europe and South Asia

9:25 - 9:50 **Invited talk 24** by Dr. IKEO Kazuho, NIG

Talk title: Reconstruction of cell lineage trees by using single-cell RNA sequence data

9:50 - 10:15 **Invited talk 25** by Dr. OSADA Naoki, Sapporo

Talk title: Genome-wide genetic diversity of wild house mice across Eurasia

10:15 - 10:40 [Invited talk 26](#) by Dr. KIMURA Ryosuke, Okinawa
Talk title: Pleiotropic effects of the EDAR 370V/A variant on East Asian phenotypes

10:40 - 11:00 Tea break

11:00 - 12:15 [Session 10](#) (Chair: Dr. INOUE Ituro)

11:00 - 11:25 [Invited talk 27](#) by Dr. TAKEYAMA Haruko, Tokyo

Talk title: high-resolution analysis of environmental microbes by massively parallel single-cell genome sequencing

11:25 - 11:50 [Invited talk 28](#) by Dr. FUJIMOTO Akihiro, Tokyo

Talk title: Whole genome sequencing with long-reads reveals complex structure and origin of structural variation in human genetic variations and somatic mutations in cancer

11:50 - 12:15 [Invited talk 29](#) by Dr. OOTA Hiroki, Tokyo

Talk title: Genome of Jomon people and peopling history of East Eurasians

12:15 - 13:30 Lunch

13:30 - 14:45 [Session 11](#) (Chair: Dr. OSADA Naoki)

13:30 - 13:55 [Invited talk 30](#) by Dr. SUZUKI Hitoshi, Sapporo

Talk title: Geographic shift of the house mouse *Mus musculus* following humans during the past 15,000 years

13:55 - 14:20 [Invited talk 31](#) by Dr. ITOH Takeshi, Tsukuba

Talk title: Genomics of plants: the genome concept made real

14:20 - 14:45 [Invited talk 32](#) by Dr. HANADA Kousuke, Tobata

Talk title: Positive selective sweeps of epigenetic mutations regulating specialized metabolites in plants

14:45 - 15:05 Tea break

15:05 - 16:20 [Session 12](#) (Chair: Dr. FUJIMOTO Akihiro)

15:05 - 15:30 [Invited talk 33](#) by Dr. IMANISHI Tadashi, Isehara

Talk title: Rapid profiling of drug-resistant bacteria using a single-molecule DNA sequencer

15:30 - 15:55 [Invited talk 34](#) by Dr. KANZAWA-KIRIYAMA Hideaki, Tsukuba

Talk title: Genome from the initial to final Jomon: Genetic history throughout the Jomon period

15:55 - 16:20 [Invited talk 35](#) by Dr. Timothy A. JINAM, NIG

Talk title: Population substructure within mainland Japanese suggests multiple waves of migration

16:20 - 16:40 Tea break

16:40 - 17:55 **Session 13** (Chair: Dr. Timothy A. JINAM)

16:40 - 17:05 **Invited talk 36** by Dr. SUZUKI Rumiko, NIG

Talk title: Genome mapping of F1 hybrid camels

17:05 - 17:30 **Invited talk 37** by Dr. Kirill KRYUKOV, NIG

Talk title: GenomeSync: streamlining access to current genome data

17:30 - 17:55 **Invited talk 38** by Dr. SAITOU Naruya, NIG

Talk title: AGTC, iDarwin, and Yaponesia Genome Project

17:55 - 18:00 Closing Remarks

SATTA Yoko, Graduate University for Advanced Studies, SOKENDAI, Hayama, Japan

TAMURA Koichiro, Tokyo Metropolitan University, Tokyo, Japan

Profile of **Keynote talk 1** Speaker: Dr. Wen-Hsiung Li, Taipei

Talk time: Monday, February 15, 13:10 - 13:45 (12:10-12:45 Taipei time)

Talk title: Evolutionary insights from microbial genomes



Academician and Distinguished Research Fellow at the Biodiversity Research Center, Academia Sinica, Taipei
James D. Watson Professor emeritus, University of Chicago, Chicago

Recent publications

1. Li W.-H. (2021) Adventures of a Mathematician in Evolutionary Biology. *Genome Biology and Evolution*. <https://doi.org/10.1093/gbe/evab012>
2. Liu W.-Y. et al. (2020) Maize ANT1 modulates vascular development, chloroplast development, photosynthesis, and plant growth. *Proc. Natl. Acad. Sci. USA* 117 (35): 21747-21756. <https://doi.org/10.1073/pnas.2012245117>
3. Anandharaj M. et al. (2020) Constructing a yeast to express the largest cellulosome complex on the cell surface. *Proc. Natl. Acad. Sci. USA* 117 (5): 2385-2394. <https://doi.org/10.1073/pnas.1916529117>

Profile of **Keynote talk 2** Speaker: Dr. GOJOBORI Takashi, KAUST

Talk time: Monday, February 15, 15:20 - 15:55 (9:20-9:55 Jedda time)

Talk title: Genome evolution in Asian rice domestication



Distinguished Professor of Bioscience, King Abdullah University of Science and Technology
Acting Director, Computational Bioscience Research Center, King Abdullah University of Science and Technology
Professor emeritus, National Institute of Genetics, Mishima

Recent publications

1. Mineta K. et al. (2021) Population structure of indigenous inhabitants of Arabia. *Plos Genetics* 17 (1) e1009210. <https://doi.org/10.1371/journal.pgen.1009210>
2. Gojobori T. et al. (2019) *Marine Metagenomics: Technological Aspects and Applications*. Springer. <https://doi.org/10.1007/978-981-13-8134-8>
3. Behzad H., Mineta K., and Gojobori T. (2018) Global ramifications of dust and sandstorm microbiota. *Genome Biology and Evolution* 10 (8): 1970-1987. <https://doi.org/10.1093/gbe/evy134>

Profile of **Keynote talk 3** Speaker: Dr. Mark STONEKING, Leipzig

Talk time: Monday, February 15, 17:05 - 17:40 (9:05 - 9:40 Leipzig time)

Talk title: Genes, Culture, and Human Evolution



Group Leader, Max Planck Institute for Evolutionary Anthropology, Leipzig
Honorary Professor of Biological Anthropology, University of Leipzig, Leipzig

Recent publications

1. Pugach I. et al. (2021) Ancient DNA from Guam and the peopling of the Pacific. **Proc. Natl. Acad. Sci. USA** 118 (1) e2022112118. <https://doi.org/10.1073/pnas.2022112118>
2. Yang M. A. et al. (2020) Ancient DNA indicates human population shifts and admixture in northern and southern China. *Science* 369 (6501): 282-288. DOI: 10.1126/science.aba0909
3. Liu D. et al. (2020) Extensive ethnolinguistic diversity in Vietnam reflects multiple sources of genetic diversity. *Molecular Biology and Evolution* 37 (9): 2503–2519. <https://doi.org/10.1093/molbev/msaa099>

Profile of **Keynote talk 4** Speaker: Dr. Dan GRAUR, Houston

Talk time: Tuesday, February 16, 9:00 - 9:35 (Monday, February 15, 18:00 - 18:35 Houston time)

Talk title: The selectionist pandemic and the emperor's new clothes: examining the evidence for soft selective sweeps in humans



John and Rebecca Moores Professor, Department of Biology and Biochemistry, University of Houston, Houston
Professor, Department of Biomedical Engineering, Cullen College of Engineering, University of Houston
Professor emeritus of Zoology, Tel Aviv University, Tel Aviv

Recent publications

1. Zheng Y., Graur D., and Azevedo R. B. R. (2018) Correlated selection on amino acid deletion and replacement in mammalian protein sequences. **Journal of Molecular Evolution** 86: 365-378.
2. Graur D. (2017) An upper limit on the functional fraction of the human genome. **Genome Biology and Evolution** 9 (7): 1880-1885. <https://doi.org/10.1093/gbe/evx121>
3. Graur D. (2017) Rubbish DNA: The functionless fraction of the human genome. Pp. 19-60, **Evolution of the Human Genome** I. Springer.

Profile of **Keynote talk 5** Speaker: Dr. LI Yi-Xue, Shanghai

Talk time: Tuesday, February 16, 10:45 - 11:20 (9:45-10:20, Shanghai time)

Talk title: A pharmaco-genomic landscape in human liver cancers



Professor, Institute of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Shanghai
Director, Department of Bioinformatics and Biostatistics, Shanghai Jiaotong University, Shanghai
Director, Shanghai Center for Bioinformation Technology, Shanghai

Recent publications

1. Li C. et al. (2020) Integrated omics of metastatic colorectal cancer. **Cancer Cell** 38 (5) 734-747. <https://doi.org/10.1016/j.ccell.2020.08.002>
2. Li Q. et al. (2020) DysRegSig: an R package for identifying gene dysregulations and building mechanistic signatures in cancer. **Bioinformatics** btaa688. <https://doi.org/10.1093/bioinformatics/btaa688>
3. Chen X.-M. et al. (2019) A novel mutation *KCNQ1p.Thr312del* is responsible for long QT syndrome type 1. **Heart and Vessels** 34: 177–188.

Profile of **Invited talk 1** Speaker: Dr. SU Bing, Kunming

Talk time: Monday, February 15, 13:45 - 14:10 (12:45 - 13:10 Kunming Time)

Talk title: Comparative brain 3D genome analysis reveals evolutionary innovations of human corticogenesis



Professor, State Key Laboratory of Genetic Resources and Evolution, CAS Kunming Institute of Zoology, Kunming

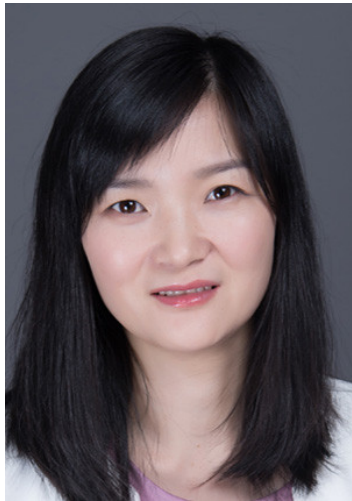
Recent publications

1. He Y. et al. (2019) Long-read assembly of the Chinese rhesus macaque genome and identification of ape-specific structural variants. **Nature Communications** 10, 4233.
2. Shi L. et al. (2019) Transgenic rhesus monkeys carrying the human *MCPHI* gene copies show human-like neoteny of brain development. **National Science Review** 6 (3): 480-493.
3. Peng Y. et al. (2017) Down-regulation of *EPAS1* transcription and genetic adaptation of Tibetans to high-altitude hypoxia. **Molecular Biology and Evolution** 34 (4): 818-830.

Profile of [Invited talk 2](#) Speaker: Dr. FU Qiaomei, Beijing

Talk time: Monday, February 15, 14:10 - 14:35 (13:10 - 13:35 Beijing Time)

Talk title: The prehistory of East Asian using insights from ancient DNA



Professor, CAS Institute of Vertebrate Paleontology and Paleoanthropology, Beijing

Recent publications

1. Yang M. A. et al. (2020) Ancient DNA indicates human population shifts and admixture in northern and southern China. **Science** 369 (6501): 282-288.
2. Ding M. et al. (2020) Ancient mitogenomes show plateau populations from last 5200 years partially contributed to present-day Tibetans. **Proceedings of the Royal Society B** 287: 20192968.
3. Yang M. A. et al. (2017) 40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. **Current Biology** 27 (20): 3202-3208.

Profile of [Invited talk 3](#) Speaker: Dr. CHAW Shu-Miaw, Taipei

Talk time: Monday, February 15, 14:35 - 15:00 (13:35 - 14:00 Taipei Time)

Talk title: Stout camphor tree (Laurel family) genome fills gaps in understanding of flowering plant genome evolution



Distinguished Research Fellow, Biodiversity Research Center, Academia Sinica, Taipei

Recent publications

1. Wu C.-S. et al. (2020) Genome skimming and exploration of DNA barcodes for Taiwan endemic cypresses. **Scientific Reports** 10 (1) 20650.
2. Sudianto E., Wu C.-S., and Chaw S. M. (2020) The origin and evolution of plastid genome downsizing in Southern Hemispheric cypresses (Cupressaceae). **Frontiers in Plant Science** 11, 901.
3. Chaw S.-M. et al. (2020) The origin and underlying driving forces of the SARS-CoV-2 outbreak. **Journal of Biomedical Science** 27 (1) 73.

Profile of [Invited talk 4](#) Speaker: Dr. SHIMIZU Hiroshi, KAUST

Talk time: Monday, February 15, 15:55 - 16:20 (9:55 - 10:20 Jeddah time)

Talk title: Behavior of cnidarian hydra : dominance of foot nervous system in behavioral regulation



Senior Research Scientist, Gojobori Group, King Abdullah University of Science and Technology

Recent publications

1. Noro Y. et al. (2020) A single neuron subset governs a single coactive neuron circuit in *Hydra vulgaris*, representing a prototypic feature of neural evolution. **bioRxiv** <https://doi.org/10.1101/2020.11.22.392985>
2. Noro Y. et al. (2019) Regionalized nervous system in *Hydra* and the mechanism of its development. **Gene Expression Patterns** 31: 42-59.
3. Ishikawa M. et al. (2016) Different endosymbiotic interactions in two hydra species reflect the evolutionary history of endosymbiosis. **Genome Biology and Evolution** 8 (7): 2155-2163.

Profile of [Invited talk 5](#) Speaker: Dr. MINETA Katsuhiko, KAUST

Talk time: Monday, February 15, 16:20 - 16:45 (10:20 - 10:45 Jeddah time)

Talk title: Population genomics of indigenous inhabitants of Arabia



Principal Research Scientist, Computational Bioscience Research Center, King Abdullah University of Science and Technology

Recent publications

1. Mineta K. et al. (2021) Population structure of indigenous inhabitants of Arabia. **Plos Genetics** 17 (1) e1009210.
2. Mineta K. et al. (2020) Indigenous Arabs have an intermediate frequency of a Neanderthal-derived COVID-19 risk haplotype compared with other world populations. **Clinical Genetics** 10, 1111.
3. Behzad H., Mineta K., and Gojobori T. (2018) Global ramifications of dust and sandstorm microbiota. **Genome Biology and Evolution** 10 (8): 1970-1987.

Profile of [Invited talk 6](#) Speaker: SHINODA Ken-ichi, Tokyo

Talk time: Monday, February 15, 17:40 - 18:05

Talk title: Contribution of ancient genome analysis to the study of the origin of the Japanese - Looking back on the research history of the past 30 years



Senior Director in Research, National Museum of Nature and Science, Tokyo
Chair, Department of Anthropology, National Museum of Nature and Science, Tsukuba

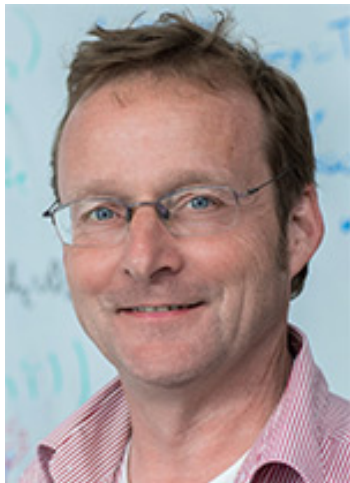
Recent publications

1. Eisenhower R., Kanzawa-Kiriyama H., Shinoda K., and Weyrich L. S. (2020) Investigating the demographic history of Japan using ancient oral microbiota. **Proceedings of the Royal Society B** 287. <https://doi.org/10.1098/rstb.2019.0578>
2. Kanzawa-Kiriyama H. et al. (2019) Late Jomon male and female genome sequences from the Funadomari site in Hokkaido, Japan. **Anthropological Science** 127(2): 83-108.
3. Adachi N., Kakuda T., Takahashi R., Kanzawa-Kiriyama H., and Shinoda K. (2017) Ethnic derivation of the Ainu inferred from ancient mitochondrial DNA data. **American Journal of Physical Anthropology** 165:139–148.

Profile of [Invited talk 7](#) Speaker: Dr. Arndt von HAESELER, Vienna

Talk time: Monday, February 15, 18:05 - 18:30 (10:05 - 10:30 Vienna time)

Talk title: Lineage size evolution in developing organoids



Dean, Center of Molecular Biology at the University of Vienna, Vienna
Head, Center for Medical Biochemistry, Medical University of Vienna, Vienna
Professor, University of Vienna and Medical University of Vienna, Vienna
Scientific Director, Center for Integrative Bioinformatics, Vienna

Recent publications

1. Leuchtenberger A. F. et al. (2020) Distinguishing Felsenstein zone from Farris zone using neural networks. **Molecular Biology and Evolution** 37 (12): 3632–3641.
2. Jain A. et al. (2019) The evolutionary traceability of a protein. **Genome Biology and Evolution** 11 (2): 531-545.
3. Plug F. G. And von Haeseler A. (2018) TRUniCount: correctly counting absolute numbers of molecules using unique molecular identifiers. **Bioinformatics** 34 (18): 3137-3144.

Profile of [Invited talk 8](#) Speaker: Dr. Anne STONE, Phoenix

Talk time: Tuesday, February 16, 9:35 - 10:00 (Monday, February 15, 17:35 - 18:00 Phoenix time)

Talk title: *Mycobacterium leprae* genomic variation and evolutionary history in the Pacific



Regents Professor, School of Human Evolution and Social Change, Arizona State University, Phoenix

Recent publications

1. Housman G. et al. (2018) Assessment of DNA methylation patterns in the bone and cartilage of a nonhuman primate model of osteoarthritis. **Cartilage** 10 (3): 335-345.
2. Honap T. et al. (2018) *Mycobacterium leprae* genomes from naturally infected nonhuman primates. **PLoS Neglected Tropical Diseases** 12 (1): e0006190.
3. Nieves-Colón M. A. et al. (2018) Comparison of two ancient DNA extraction protocols for skeletal remains from tropical environments. **American Journal of Physical Anthropology** 166: 824–836.

Profile of [Invited talk 9](#) Speaker: Dr. Yun-Xin FU, Houston

Talk time: Tuesday, February 16, 10:00 - 10:25 (Monday, February 15, 19:00 - 19:25 Houston time)

Talk title: Tetrahymena amitosis strategy: from sex determination to whole genome sequencing



Director and Professor, Computational Genomics Section, Human Genetics Center and Division of Biostatistics School of Public Health, The University of Texas at Houston, Houston
Visiting Professor, National Institute of Genetics, Mishima

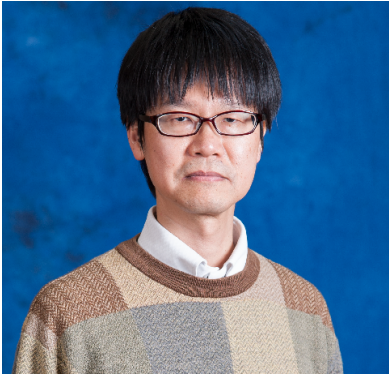
Recent publications

1. Fu Y.-X. et al. (2020) Amitosis as a strategy of cell division - Insight from the proliferation of *Tetrahymena thermophila* macronucleus. **bioRxiv** <https://doi.org/10.1101/2020.08.11.247031>
2. Liu X. And Fu Y.-X. (2020) Stairway Plot 2: demographic history inference with folded SNP frequency spectra. **Genome Biology** 21, 280.
3. Liu Q. et al. (2020) *Mycobacterium tuberculosis* clinical isolates carry mutational signatures of host immune environments. **Science Advances** 6 (22) eaba4901.

Profile of [Invited talk 10](#) Speaker: Dr. KINOSHITA Tetsu, Yokohama

Talk time: Tuesday, February 16, 11:20 - 11:45

Talk title: Overcoming the species hybridization barrier by ploidy manipulation in the genus *Oryza*



Professor, Epigenome Laboratory, Kihara Institute for Biological Research, Yokohama City University, Yokohama

Recent publications

1. Ohnishi Y. et al. (2019) Sperm Entry into the Egg Cell Induces the Progression of Karyogamy in Rice Zygotes. **Plant & cell physiology** 60 (8):1656 – 1665.
2. Kim M. Y. et al. (2019) DNA demethylation by ROS1a in rice vegetative cells promotes methylation in sperm. **Proc. Natl. Acad. Sci. USA** 116: 9652-9657.
3. Kinoshita T. (2018) A parental tug-of-war. **Nature Plants** 4:329–330.

Profile of [Invited talk 11](#) Speaker: Dr. HASEBE Mitsuyasu, Okazaki

Talk time: Tuesday, February 16, 11:45 - 12:10

Talk title: Evolution of carnivory and movement in plants



Professor, Division of Evolutionary Biology, National Institute of Basic Biology, Okazaki

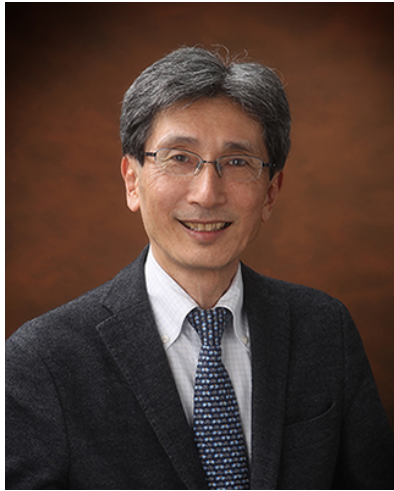
Recent publications

1. Suda H. et al. (2020) Calcium dynamics during trap closure visualized in transgenic Venus flytrap. **Nature Plants** 6:1219–1224.
2. Gu N. et al. (2020) DNA damage triggers reprogramming of differentiated cells into stem cells in *Physcomitrella*. **Nature Plants** 6:1098–1105.
3. Palfalvi G. et al. (2020) Genomes of the Venus flytrap and close relatives unveil the roots of plant carnivory. **Current Biology** 30: 1-9.

Profile of [Invited talk 12](#) Speaker: Dr. SASAKI Hiroyuki, Fukuoka

Talk time: Tuesday, February 16, 13:30 - 13:55

Talk title: DNA methylation in development and disease



Dean, Kyushu University Institute for Advanced Study, Fukuoka

Professor, Medical Institute of Bioregulation, Kyushu University, Fukuoka

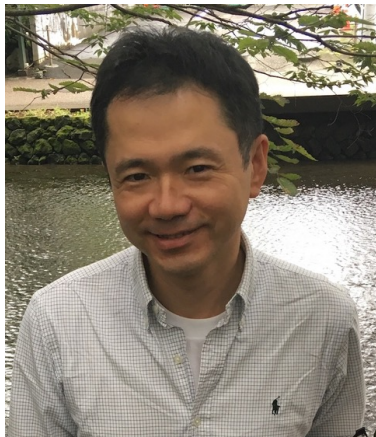
Recent publications

1. Albert J. R. et al. (2020) Maternal DNMT3A-dependent de novo methylation of the paternal genome inhibits gene expression in the early embryo. **Nature Communications** 11: 5417.
2. Ishiuchi T. et al. (2020) Reprogramming of the histone H3.3 landscape in the early mouse embryo. **Nature Structural and Molecular Biology** 28: 38–49.
3. Yeung W. K. A. et al. (2019) Histone H3K9 methyltransferase G9a in oocytes is essential for preimplantation development but dispensable for CG methylation protection. **Cell Reports** 27 (1): 282-293.

Profile of [Invited talk 13](#) Speaker: Dr. INOUE Jun, Kashiwa

Talk time: Tuesday, February 16, 13:55 - 14:20

Talk title: dbCNS: a new database for conserved non-coding sequences



Assistant Professor, Atmosphere and Ocean Research Institute, University of Tokyo, Kashiwa

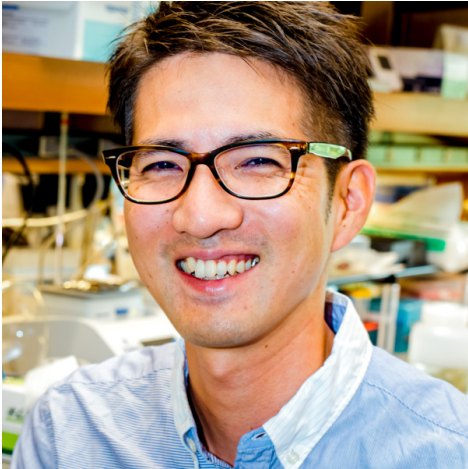
Recent publications

1. Inoue J. and Saitou N. (2020) dbCNS: a new database for conserved noncoding sequences. **Molecular Biology and Evolution** doi:10.1093/molbev/msaa29
2. Inoue J. and Satoh N. (2019) ORTHOSCOPE: an automatic web tool for phylogenetically inferring bilaterian orthogroups with user-selected taxa. **Molecular Biology and Evolution** 36 (3): 621-631.
3. Inoue J. and Satoh N. (2018) Deuterostome Genomics: Lineage-Specific Protein Expansions That Enabled Chordate Muscle Evolution. **Molecular Biology and Evolution** 35 (4): 914-924.

Profile of [Invited talk 14](#) Speaker: Dr. SHINZATO Chuya, Kashiwa

Talk time: Tuesday, February 16, 14:20 - 14:45

Talk title: Using genomics to reveal novel insights into coral biology



Associate Professor, Atmosphere and Ocean Research Institute, University of Tokyo, Kashiwa

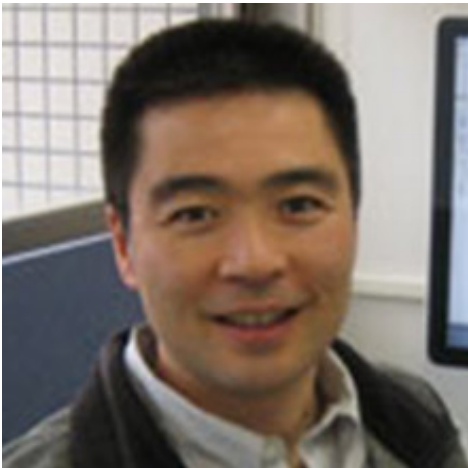
Recent publications

1. Sinzato C. et al. (2020) Eighteen coral genomes reveal the evolutionary origin of Acropora strategies to accommodate environmental changes. **Molecular Biology and Evolution** 38 (1): 16-30.
2. Yoshioka Y. Et al. (2020) Whole-genome transcriptome analyses of native symbionts reveal host coral genomic novelties for establishing coral-algae symbioses. **Genome Biology and Evolution** 13 (1) doi:10.1093/gbe/evaa24
3. Sinzato C. et al. (2018) Using seawater to document coral-zooxanthella diversity: A new approach to coral reef monitoring using environmental DNA. **Frontiers in Marine Science** 5, 28.

Profile of [Invited talk 15](#) Speaker: Dr. Hiroshi AKASHI, NIG

Talk time: Tuesday, February 16, 15:05 - 15:30

Talk title: Population genomics of weak evolutionary forces: Base composition evolution in *Drosophila*



Professor, Evolutionary Genetics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Matsumoto T. and Akashi H. (2018) Distinguishing Among Evolutionary Forces Acting on Genome-Wide Base Composition: Computer Simulation Analysis of Approximate Methods for Inferring Site Frequency Spectra of Derived Mutation. **G3** 8: 1755-1769.
2. Matsumoto T. et al. (2016) Codon usage selection can bias estimation of the fraction of adaptive amino acid fixations. **Molecular Biology and Evolution** 33: 1580-1589.
3. Matsumoto T., Akashi H., and Yang Z. (2015) Evaluation of Ancestral Sequence Reconstruction Methods to Infer Nonstationary Patterns of Nucleotide Substitution. **Genetics** 200: 873-890.

Profile of [Invited talk 16](#) Speaker: Dr. NAKAMURA Yasukazu, NIG

Talk time: Tuesday, February 16, 15:30 - 15:55

Talk title: A chromosome-level assembly of a domestic cat of American Shorthair



Professor, Genome Informatics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Montgomery S. A. et al. (2020) Chromatin organization in early land plants reveals an ancestral association between H3K27me3, transposons, and constitutive heterochromatin. **Current Biology** 30 (4): R161-R163.
2. Isobe S. et al. (2020) AnAms1.0: A high-quality chromosome-scale assembly of a domestic cat *Felis catus* of American Shorthair breed. **bioRxiv** <https://doi.org/10.1101/2020.05.19.103788>
3. Tanizawa Y., Fujisawa T., and Nakamura Y. (2018) DFAST: a flexible prokaryotic genome annotation pipeline for faster genome publication. **Bioinformatics** 36 (6): 1037–1039.

Profile of [Invited talk 17](#) Speaker: Dr. KITANO Jun, NIG

Talk time: Tuesday, February 16, 15:55 - 16:20

Talk title: Genetics of adaptive radiation in stickleback and medaka fishes



Professor, Ecological Genetics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Ansai. S. et al. (2021) Genome editing reveals fitness effects of a gene for sexual dichromatism in Sulawesian fishes. **Nature Communications** (in press).
2. Yamasaki Y. Y. et al. (2020) Genome-wide patterns of divergence and introgression after secondary contact between *Pungitius* sticklebacks. **Philosophical Transactions of the Royal Society B** 375, 20190548.
3. Ishikawa A. et al. (2019) A key metabolic gene for recurrent freshwater colonization and radiation in fishes. **Science** 364: 886-889.

Profile of [Invited talk 18](#) Speaker: Dr. INOUE Ituro, NIG

Talk time: Tuesday, February 16, 16:20 - 16:45

Talk title: Genomics and cultivation of new virus world



Professor, Human Genetics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Nishimura L. et al. (2020) Identification of ancient viruses from metagenomic data of the Jomon people. **Journal of Human Genetics** 66: 287–296
2. Sugimoto R. et al. (2020) De novo virus inference and host prediction from metagenome using CRISPR spacers. **bioRxiv** <https://doi.org/10.1101/2020.09.04.282665>
3. Romero V. et al. (2018) High order formation and evolution of hornerin in primates. **Genome Biology and Evolution** 10 (12): 3167–317.

Profile of [Invited talk 19](#) Speaker: Dr. TAMURA Koichiro, Tokyo

Talk time: Tuesday, February 16, 17:05 - 17:30

Talk title: Genome evolution for cold adaptation in experimental populations of *Drosophila albomicans*



Director, Research Center for Genomics and Bioinformatics, Tokyo Metropolitan University, Tokyo
Professor, Department of Biological Sciences, Tokyo Metropolitan University, Tokyo

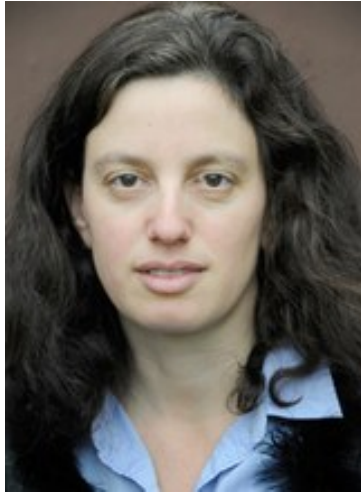
Recent publications

1. Moriguchi N. et al. (2019) Inferring the demographic history of Japanese cedar, *Cryptomeria japonica*, using amplicon sequencing. **Heredity** 123: 371-383.
2. Tamura K., Qiqing Tao, and Kumar S. (2018) Theoretical foundation of the RelTime method for estimating divergence times from variable evolutionary rates. **Molecular Biology and Evolution** 35 (7): 1770-1782.
3. Kumar S. et al. (2018) MEGA X: molecular evolutionary genetics analysis across computing platforms. **Molecular Biology and Evolution** 35 (6): 1547-1549.

[Profile of Invited talk 20](#) Speaker: Dr. Tal DAGAN, Kiel

Talk time: Tuesday, February 16, 17:30 - 17:55 (9:30 - 9:55 Kiel time)

Talk title: Plasmids as turtles in an evolutionary race



Professor, Institute of Microbiology, University of Kiel, Kiel

Recent publications

1. Yu L. et al. (2020) Somatic genetic drift and multilevel selection in a clonal seagrass. **Nature Ecology and Evolution** 4 (7): 952-962.
2. Hammerschmidt K. et al. (2020) The order of trait emergence in the evolution of cyanobacterial multicellularity. **Genome Biology and Evolution**, evaa249.
3. Ilhan J. et al. (2019) Segregational drift and the interplay between plasmid copy number and evolvability. **Molecular Biology and Evolution** 36 (3): 472-486.

[Profile of Invited talk 21](#) Speaker: Dr. SHIMIZU Kentaro, Zurich

Talk time: Tuesday, February 16, 17:55 - 18:20 (9:55 - 10:20 Zurich time)

Talk title: Polyploid wheat as the traditional model of genome analysis and the last frontier of genome sequencing



Professor, Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich

Recent publications

1. Walkowiak S. et al. (2020) Multiple wheat genomes reveal global variation in modern breeding. **Nature** 588: 277–283.
2. Hatakeyama M. et al. (2018) Multiple hybrid de novo genome assembly of finger millet, an orphan allotetraploid crop. **DNA Research**, 25(1):39-47.
3. Paape T. et al. (2018) Patterns of polymorphism and selection in the subgenomes of the allopolyploid *Arabidopsis kamchatica*. **Nature Communications** 9: 3909.

Profile of Invited talk 22 Speaker: Dr. Aida ANDRES, London

Talk time: Tuesday, February 16, 18:20 - 18:45 (9:20 - 9:45 London time)

Talk title: Dissecting genomes to identify local adaptations in humans and other primates



Associate Professor, Division of Biosciences, University College London, London

Recent publications

1. Rees J. S., Castellano S., and Andrés A. M. (2020) The genomics of human local adaptation. **Trends in Genetics** 36 (6): 415-428.
2. Giner-Delgado C. et al. (2019) Evolutionary and functional impact of common polymorphic inversions in the human genome. **Nature Communications** 10 (1): 1-14.
3. Key F. M. et al. (2018) Human local adaptation of the TRPM8 cold receptor along a latitudinal cline. **PLoS Genetics** 14 (5), e1007298.

Profile of Invited talk 23 Speaker: Dr. SATTA Yoko, Hayama

Talk time: Wednesday, February 17, 9:00 - 9:25

Talk title: Population genomics on the origin of lactase persistence in Europe and South Asia



Professor, School of Advanced Sciences, Graduate University for Advanced Studies, Hayama

Recent publications

1. Iwasaki R. L. et al. (2020) Evolutionary history of the risk of SNPs for diffuse-type gastric cancer in the Japanese population. **Genes** 11 (7), 775. <https://doi.org/10.3390/genes11070775>
2. Satta Y. et al. (2019) Two-dimensional site frequency spectrum for detecting, classifying and dating incomplete selective sweeps. **Genes and Genetic Systems** 94: 283-300. <https://doi.org/10.1266/ggs.19-00012>
3. Fujito N. T. et al. (2018) Positive selection on schizophrenia-associated ST8SIA2 gene in post-glacial Asia. **PLoS ONE** 13 (7): e0200278. <https://doi.org/10.1371/journal.pone.0200278>.

Profile of [Invited talk 24](#) Speaker: Dr. IKEO Kazuho, NIG

Talk time: Wednesday, February 17, 9:25 - 9:50

Talk title: Reconstruction of cell lineage trees by using single-cell RNA sequence data



Associate Professor, DNA Data Analysis Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Yaguchi S. et al. (2020) Establishment of homozygous knock-out sea urchins. **Current Biology** 30 (10): R427-R429.
2. Sun J. et al. (2020) The Scaly-foot Snail genome and implications for the origins of biomineralised armour. **Nature Communications** 11, 1657.
3. Kinjo S. et al. (2018) Maser: one-stop platform for NGS big data from analysis to visualization. **Database** 2018, bay027.

Profile of [Invited talk 25](#) Speaker: Dr. OSADA Naoki, Sapporo

Talk time: Wednesday, February 17, 9:25 - 9:50

Talk title: Genome-wide genetic diversity of wild house mice across Eurasia



Associate Professor, Division of Bioengineering and Bioinformatics, Graduate School of Information Science and Technology, Hokkaido University, Sapporo

Recent publications

1. Osada N. and Kawai Y. (2021) Exploring models of human migration to the Japanese archipelago using genome-wide genetic data. **Anthropological Science** 129 (in press).
2. Li Y. et al. (2020) House mouse *Mus musculus* dispersal in East Eurasia inferred from 98 newly determined complete mitochondrial genome sequences. **Heredity** 126: 132-147.
3. Satomura K., Osada N., and Endo T. (2019) Achiasmy and sex chromosome evolution. **Ecological Genetics and Genomics** 13, 100046.

Profile of [Invited talk 26](#) Speaker: Dr. KIMURA Ryosuke, Okinawa

Talk time: Wednesday, February 17, 10:15 - 10:40

Talk title: Pleiotropic effects of the EDAR 370V/A variant on East Asian phenotypes



Associate Professor, Department of Human Biology and Anatomy, Graduate School of Medicine, University of the Ryukyu, Okinawa

Recent publications

1. Matsunami M. et al. (2021) Fine-scale genetic structure and demographic history in the Miyako Islands of the Ryukyu Archipelago. **Molecular Biology and Evolution** msab005 published online.
2. Gakuhari T. et al. (2020) Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. **Communications Biology** 3, 437.
3. Gamage C. et al. (2020) Understanding leptospirosis eco-epidemiology by environmental DNA metabarcoding of irrigation water from two agro-ecological regions of Sri Lanka. **PLoS Neglected Tropical Diseases** 14(7): e0008437.

Profile of [Invited talk 27](#) Speaker: Dr. TAKEYAMA Haruko, Tokyo

Talk time: Wednesday, February 17, 11:00 - 11:25

Talk title: high-resolution analysis of environmental microbes by massively parallel single-cell genome sequencing



Professor, Biomolecular Engineering Laboratory, Department of Life Science and Medical Bioscience, Waseda University, Tokyo

Recent publications

1. Chijiwa R. et al. (2020) Single-cell genomics of uncultured bacteria reveals dietary fiber responders in the mouse gut microbiota. **Microbiome** 8, 5.
2. Yumoto M. et al. (2020) Evaluation of the effects of cell-dispensing using an inkjet-based bioprinter on cell integrity by RNA-seq analysis. **Scientific Reports** 10, 7158.
3. Yamazaki M. et al. (2020) Effective microtissue RNA extraction coupled with Smart-seq2 for reproducible and robust spatial transcriptome analysis. **Scientific Reports** 10, 7083.

Profile of [Invited talk 28](#) Speaker: Dr. FUJIMOTO Akihiro, Tokyo

Talk time: Wednesday, February 17, 11:25 - 11:50

Talk title: Whole genome sequencing with long-reads reveals complex structure and origin of structural variation in human genetic variations and somatic mutations in cancer



Professor, Department of Human Genetics, The University of Tokyo, Graduate School of Medicine, Tokyo

Recent publications

1. Fujimoto A. et al. (2020) Comprehensive analysis of indels in whole-genome microsatellite regions and microsatellite instability across 21 cancer types. **Genome Research** 30: 334-346.
2. Mizuno K. et al. (2019) eVIDENCE: a practical variant filtering for low-frequency variants detection in cell-free DNA. **Scientific Reports** 9, 15017.
3. Ton N. D. et al. (2018) Whole genome sequencing and mutation rate analysis of trios with paternal dioxin exposure. **Human Mutation** 39: 1384–1392.

Profile of [Invited talk 29](#) Speaker: Dr. OOTA Hiroki, Tokyo

Talk time: Wednesday, February 17, 11:50 - 12:15

Talk title: Genome of Jomon people and peopling history of East Eurasians



Professor, Laboratory of Genome Anthropology, Department of Biological Sciences, Graduate School of Science, University of Tokyo, Tokyo

Recent publications

1. Koganebuchi K. and Oota H. (2021) Paleogenomics of human remains in East Asia and Yaponesia focusing on current advances and future directions. **Anthropological Science** 129 (in press).
2. Gakuhari T. et al. (2020) Ancient Jomon genome sequence analysis sheds light on migration patterns of early East Asian populations. **Communications Biology** 3, 437.
- 3 Schmidt R. W. et al. (2020) Analysis of ancient human mitochondrial DNA from Verteba Cave, Ukraine: insights into the Late Neolithic-Chalcolithic Cucuteni–Tripolye culture. **Anthropological Science** 128 (1) : 1-10.

Profile of Invited talk 30 Speaker: Dr. SUZUKI Hitoshi, Sapporo

Talk time: Wednesday, February 17, 13:30 - 13:55

Talk title: Geographic shift of the house mouse *Mus musculus* following humans during the past 15,000 years



Professor, Hokkaido University, Sapporo

Recent publications

1. Suzuki H. (2021) The time-dependent evolutionary rate of mitochondrial DNA in small mammals inferred from biogeographic calibration points with reference to the late Quaternary environmental changes. **Anthropological Science** 129 (in press).
2. Li Y. et al. (2020) House mouse *Mus musculus* dispersal in East Eurasia inferred from 98 newly determined complete mitochondrial genome sequences. **Heredity** 126: 132-147.
3. Thomson V. et al. (2018) A perspective for resolving the systematics of *Rattus*, the vertebrates with the most influence on human welfare. **Zootaxa** 4459 (3): 431–452.

Profile of Invited talk 31 Speaker: Dr. ITOH Takeshi, Tsukuba

Talk time: Wednesday, February 17, 13:55 - 14:20

Talk title: Genomics of plants: the genome concept made real



Leader, Advanced Analysis Center, National Agriculture and Food Research Organization, Tsukuba

Recent publications

1. Itoh T. et al. (2020) Foreign DNA detection by high-throughput sequencing to regulate genome-edited agricultural products. **Scientific Reports** 10(1): 4914 - 4914.
2. Endo M. et al. (2019) Genome editing in plants by engineered CRISPR–Cas9 recognizing NG PAM. **Nature Plants** 5: 14-17.
3. Itoh T., Kawahara Y., and Tanaka T. (2018) Databases for rice omics studies. Pp. 541-554 in In: Sasaki T. and Ashikari M. (eds) **Rice Genomics, Genetics, and Breeding**. Springer, Singapore.

Profile of [Invited talk 32](#) Speaker: Dr. HANADA Kousuke, Iizuka

Talk time: Wednesday, February 17, 14:20 - 14:45

Talk title: Positive selective sweeps of epigenetic mutations regulating specialized metabolites in plants



Professor, Department of Bioscience and Bioinformatics, Kyushu Institute of Technology

Recent publications

1. Ezoe A., Shirai K., and Hanada K. (2021) Degree of functional divergence in duplicates is associated with distinct roles in plant evolution. **Molecular Biology and Evolution** (in press).
2. Higuchi-Takeuchi M. et al. (2020) Effect of small coding genes on the circadian rhythms under elevated CO₂ conditions in plants. **Plant Molecular Biology** 104(1), 55-65.
3. Nakaminami K. et al. (2018) AtPep3 is a hormone-like peptide that plays a role in the salinity stress tolerance of plants. **Proc. Natl. Acad. Sci. USA** 115 (22): 5810-5815.

Profile of [Invited talk 33](#) Speaker: Dr. IMANISHI Tadashi, Isehara

Talk time: Wednesday, February 17, 15:05 - 15:30

Talk title: Rapid profiling of drug-resistant bacteria using a single-molecule DNA sequencer



Professor, Biomedical Informatics Laboratory, Department of Molecular Life Science, Tokai University School of Medicine

Recent publications

1. Ohno A. et al. (2021) Rapid profiling of drug resistant bacteria using DNA-binding dyes and a nanopore-based DNA sequencer. **Scientific Reports** 11: 3436.
2. Hashimoto S. et al. (2020) Implications of HLA diversity among regions for bone marrow donor searches in Japan. **HLA** 96: 24-42.
3. Asogawa M. et al. (2020) Human short tandem repeat identification using a nanopore-based DNA sequencer: a pilot study. **Journal of Human Genetics** 65 (1): 21-24.

Profile of [Invited talk 34](#) Speaker: Dr. KANZAWA-KIRIYAMA Hideaki, Tsukuba

Talk time: Wednesday, February 17, 15:30 - 15:55

Talk title: Genome from the initial to final Jomon: Genetic history throughout the Jomon period



Associate Curator, Department of Anthropology, National Museum of Nature and Science, Tsukuba

Recent publications

1. Eisenhower R., Kanzawa-Kiriyama H., Shinoda K., and Weyrich L. S. (2020) Investigating the demographic history of Japan using ancient oral microbiota. **Proceedings of the Royal Society B** 287. <https://doi.org/10.1098/rstb.2019.0578>
2. Kanzawa-Kiriyama H. et al. (2019) Late Jomon male and female genome sequences from the Funadomari site in Hokkaido, Japan. **Anthropological Science** 127(2): 83-108.
3. Kanzawa-Kiriyama H. et al. (2017) A partial nuclear genome of the Jomons who lived 3000 years ago in Fukushima, Japan. **Journal of Human Genetics** 62: 213-221.

Profile of [Invited talk 35](#) Speaker: Dr. Timothy A. JINAM, NIG

Talk time: Wednesday, February 17, 15:55 - 16:20

Talk title: Population substructure within mainland Japanese suggests multiple waves of migration



Assistant Professor, Population Genetics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Jinam T. A., Kawai Y., and Saitou N. (2021) Modern human DNA analyses with special reference to the Inner-Dual structure model of Yaponesian. **Anthropological Science** 129 (in press).
2. Jinam T. A. et al. (2021) Genome-wide SNP data of Izumo and Makurazaki populations support inner- dual structure model for origin of Yamato people. **Journal of Human Genetics** online. <https://doi.org/10.1038/s10038-020-00898-3>
3. Jinam T. A. et al. (2017) Discerning the origins of the negritos, First Sundaland People: deep divergence and archaic admixture. **Genome Biology and Evolution** 9 (8): 2013-2022.

Profile of [Invited talk 36](#) Speaker: Dr. SUZUKI Rumiko, NIG

Talk time: Wednesday, February 17, 16:40 - 17:05

Talk title: Genome mapping of F1 hybrid camels



Project Associate Professor, Population Genetics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Ono T. et al. (2020) Discovery of unique African *Helicobacter pylori* CagA-multimerization motif in the Dominican Republic. **World Journal of Gastroenterology** 26 (45): 7118–7130.
2. Suzuki R. et al. (2019) Genome-wide mutation analysis of *Helicobacter pylori* after inoculation to Mongolian gerbils. **Gut Pathogens** 11, 45.
3. Wastito L. A. et al. (2018) Distribution and clinical associations of integrating conjugative elements and *cag* pathogenicity islands of *Helicobacter pylori* in Indonesia. **Scientific Reports** 8, 6073.

Profile of [Invited talk 37](#) Speaker: Dr. Kirill KRYUKOV, NIG

Talk time: Wednesday, February 17, 17:05 - 17:30

Talk title: GenomeSync: streamlining access to current genome data



Specially Appointed Associate Professor, Population Genetics Laboratory, National Institute of Genetics, Mishima

Recent publications

1. Kryukov K. et al. (2020) Sequence Compression Benchmark (SCB) database — a comprehensive evaluation of reference-free compressors for FASTA-formatted sequences. **GigaScience** 9 (7), gaaa072.
2. Kryukov K. et al. (2019) Nucleotide Archival Format (NAF) enables efficient lossless reference-free compression of DNA sequences. **Bioinformatics** 35 (19): 3826-3828.
3. Kryukov K. et al. (2019) Systematic survey of non-retroviral virus-like elements in eukaryotic genomes. **Virus Research** 262: 30-36.

Profile of [Invited talk 38](#) Speaker: Dr. SAITOU Naruya, NIG

Talk time: Wednesday, February 17, 17:30 - 17:55

Talk title: AGTC, iDarwin, and Yaponesia Genome Project



Professor, Population Genetics Laboratory, National Institute of Genetics, Mishima

Specially appointed Professor Advanced Medical Research Center, Faculty of Medicine, University of the Ryukyus

Recent publications

1. Saber M. M. et al. (2021) Possible roles for the hominid-specific DSCR4 gene in human cells. **Genes and Genetic Systems** (in press).
2. Saitou N. (2021) “My Thoughts on Biological Evolution” by KIMURA (2020) – translation of KIMURA (1988) – . **iDarwin** 1: 37-53.
4. Babarinde I. A. and Saitou N. (2020) The dynamics, causes, and impacts of mammalian evolutionary rates revealed by the analyses of capybara draft genome sequences. **Genome Biology and Evolution** 12 (8):1444–1458.

"Genome" was proposed in Winkler (1920); see cover of this book at right.
Winkler H. (1920) Verbreitung und Ursache der Parthenogenesis im Pflanzen- und Tierreiche. Verlag von Gustav Fischer, Jena.

At page 165 of this book, "Distribution and cause of parthenogenesis in plants and animals" in English, he wrote:

Ich schlage vor, für den haploiden Chromosomensatz, der im Verein mit dem zugehörigen Protoplasma die materielle Grundlage der systematischen Einheit darstellt, den Ausdruck: das **Genom zu verwenden,**

...

This can be translated into English:

I suggest to use the word 'genome**' for the haploid chromosome set, which is the material basis of the systematic unit in combination with the associated protoplasm, ...**

(translated by Dr. SUZUKI Rumiko, invited speaker of GCCC)

Hans Karl Albert Winkler (1877-1945)

He was professor of botany in Hamburg University when he published this book at age of 53. He also coined "gene conversion".

His photo below is taken from:

https://www.ranker.com/review/hans-winkler/1127023?ref=wiki_1070897



VERBREITUNG UND URSACHE DER PARTHENOGENESIS IM PFLANZEN- UND TIERREICHE

Introduction of KIHARA Hitoshi

KIHARA Hitoshi conducted “genome analysis” of wheats in 1920s. Kihara (1982) wrote at page 69, in section “4.1 The Concept of the Genome” of Chapter 4 “Genome Analysis I”.

At the time when cytological analysis on the intra- and intergroup hybrids among three *Triticum* groups attained a certain stage, the term genome analysis was introduced to give an appropriate name to this kind of study.

The term “genome” was coined by H. Winkler (1920), and was defined by him as follows;

The present writer proposes a term “GENOME” (Genome) for a haploid set of chromosomes. Such a set of chromosomes gives a substantial basis as the taxonomical unit in corporation with cytoplasm to which it belongs. And the cells or the organism, whose nuclei contain two or more identical genomes are called homogenomic, and the ones which contain two or more kinds of genomes are called heterogenomic.

As Winkler did not define the homologous chromosomes, I have defined them as follows:

Homologous chromosomes have their homologous loci in identical sequence as well as in distance. Therefore when two genomes are homologous, an exchange of homologous partners causes no physiological damage to the gametes or to the zygotes.

Non-homologous chromosomes may have different loci or the same loci different in sequence or in distance. When there are no homologous chromosomes between two genomes, these are nonhomologous genomes; if there are some, they are partially homologous.

These principles and definitions were set out in the article entitled “Genome analysis, III” (1932), and the first report in the same series was devoted to a presentation of the principles and actual data of the analysis.

Kihara H. (1982) Wheat Studies – Retrospect and Prospects –. Kodansha, Tokyo and Elsevier Science Publishing Company, Amsterdam.

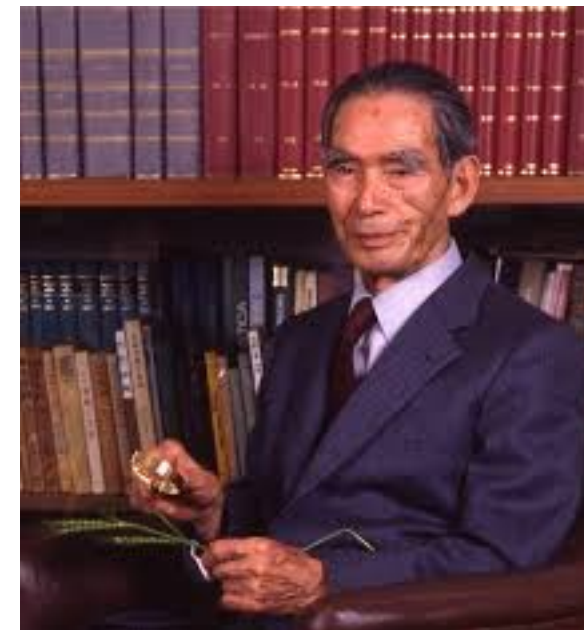
KIHARA Hitoshi (1893-1986)

1927-1956, Professor, Faculty of Agriculture, Kyoto University, Kyoto.

1942-1984, Director, Kihara Institute for Biological Research, Kyoto/Mishima/Yokohama.

1955-1969, Director-General, National Institute of Genetics, Mishima.

His photo shown above is taken from: https://kihara.or.jp/kihara/dr_kihara.html



Introduction of **National Institute of Genetics**, Mishima, Japan
Institute Home Page: <https://www.nig.ac.jp/nig/>

Director-General
Dr. HANAOKA Fumio



There are four Departments in this Institute:

- Department of Informatics (5 laboratories)
- Department of Genomics and Evolutionary Biology (7 laboratories)
- Department of Gene Function and Phenomics (11 laboratories)
- Department of Chromosome Science (5 laboratories)

There are five Centers in this Institute:

- Center for Frontier Research (2 laboratories)
- Bioinformatics and DDBJ Center (3 divisions)
- Advanced Genomics Center (2 divisions)
- Genetic Resource Center (4 divisions)
- Support Center (3 units)



Many researchers are involved in genome and chromosome studies in National Institute of Genetics. Eight GCCC speakers from this Institute belong to Department of Genomics and Evolutionary Biology. KIMURA Motoo (1924-1994), who studied in this institute until he passed away, proposed the neutral theory of evolution in 1968. This neutral theory is now fundamental for evolutionary genomics. Therefore, it is natural for us to celebrate Genome Concept Centennial.



Introduction of Yaponesian Genome Project

Project Home Page: http://www.yaponesian.jp/index_e.php

There was first wave of immigration to Yaponesia (Japanese Archipelago) about 40,000 years ago, followed by several more waves afterwards. In this time frame, we try to understand what kind of ethnic groups the Japanese Archipelago humans were originated from, and how the process of it's establishment and development in Yaponesia took place, by determining and conducting comparative analysis on the genomic sequences of 500 modern humans selected from various area, and 100 ancient humans of Paleolithic - Historic times, to further elucidate the Yaponesian Genome history. Together with the analysis on human, we also elucidate the history of animals and plants immigrated to Yaponesia, by the genomic sequence comparison. We reconstruct the details of history for the past population fluctuations by the existing or newly developed methods estimating by genomic sequences. To investigate the Yaponesian history from various directions, our genome research team collaborates with the Archaeological research team incorporating the age dating method, and the linguistic research team analyzing the Japanese and Ryukyu dialects. From the collaborations we establish the new research filed integrated with social science and science.

This research received the grant from MEXT (Ministry of Education, Culture, Sports, Science and Technology), as a New Academic Field Research, titled as "Elucidating the Origin and Establishment of Yaponesian" (Abbreviated as: Yaponesian Genome).

Following 13 people of this Yaponesian Genome Project give talks in GCCC:

FUJIMOTO Akihiro (B03 group member)

IMANISHI Tadashi (A04 group member)

ITOH Tsuyoshi (A03 group member)

KANZAWA-KIRIYAMA Hideaki (A02 group member)

OTA Hiroki (A04 group member)

SAITOU Naruya (Project P.I. and A01 group leader)

SUZUKI Hitoshi (A03 group leader)

HANADA Kosuke (A04 group member)

INOUE Ituro (A01 group member)

Timothy A. JINAM (A01 group member)

KIMURA Ryosuke (A04 group member)

OSADA Naoki (B03 group leader)

SHINODA Ken-ichi (A02 group leader)