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WELCOME

Dear Delegates

We would like to welcome you to the 2018 Annual Meeting of the Society for Molecular Biology and Evolution (SMBE 2018) in Yokohama, Japan. This is a special occasion to celebrate the 50th anniversary of the neutral theory of molecular evolution.

In 1968, Dr. Motoo Kimura said “Calculating the rate of evolution in terms of nucleotide substitutions seems to give a value so high that many of the mutations involved must be neutral ones” in his Nature paper. Since then, we have witnessed the development of theory-based hypothesis testing approaches in evolutionary biology at the molecular level. At the fiftieth anniversary of the neutral theory, we are delighted to be holding this meeting in the home country of Dr. Kimura to enjoy the latest progress of molecular evolutionary studies together with more than a thousand of delegates from over the world. We are grateful that so many people have made long-distance travel to Yokohama for SMBE 2018.

The venue, Pacifico Yokohama, is one of the largest convention complexes in the world, equipped with all the functions required for our meeting as well as any convention. The vertical alignment of the main hall for the plenary sessions on the first floor, conference rooms for the parallel oral sessions on the third floor, and large meeting rooms for poster sessions on the fifth floor in the Conference Center building facilitate your easy access across sessions. We are confident that you will be satisfied with the excellent conference environment. If the weather permits, we recommend eating lunch outside with beautiful ocean scenery, which will refresh you completely. We are hoping that the rainy season is over by the time of SMBE 2018.

Yokohama is Japan's first port of call, opening the door to the world 150 years ago. Yokohama represents a fusion of Japanese tradition and world culture, and

there are plenty of places worth visiting as a tourist. Just ten to fifteen minute walking down the street along the coastline, you will get to see Red Brick Warehouse, one of the famous sightseeing spots, where you can enjoy shopping and gourmet dining. There is Yokohama Museum of Art within ten minutes by walk as well. Moreover, taking a train, you can access downtown Tokyo within an hour.

We would like to thank you for coming to SMBE 2018 and hope you enjoy staying in Yokohama.

On behalf of the local organizing committee
Koichiro Tamura
Tokyo Metropolitan University

Local organizing committee members

Chair

Koichiro Tamura Tokyo Metropolitan University

Vice-chair

Yoko Satta SOKENDAI
(The Graduate University for
Advanced Studies)

Committee members

Hideki Innan SOKENDAI
(The Graduate University for
Advanced Studies)

Tatsuya Ota SOKENDAI
(The Graduate University for
Advanced Studies)

Shoji Kawamura The University of Tokyo

Naruya Saitou National Institute of Genetics

Naoko Takezaki Kagawa University

DELEGATE INFORMATION

1. Registration

SMBE 2018 registration desk will be located in the lobby (2F) and open during the following hours.

Registration Desk Opening Hours	
Sunday, July 8	16:00-19:00
Monday, July 9	8:00-17:00
Tuesday, July 10	8:30-17:00
Wednesday, July 11	9:00-16:00
Thursday, July 12	9:00-13:00

SMBE 2018 registration includes:

- Access to all sessions during the conference
- Program book
- Welcome reception (July 8)
- Morning break, lunch and afternoon break
- Delegate bag
- Access to the conference App

* SMBE Conference Dinner ticket is NOT included in the registration fee.

2. Internet Access

There will be free Wi-Fi access in the meeting rooms and surrounding areas.

SSID: FREE-PACIFICO

3. Photographing and Recording

Photographing / recording sessions is strictly prohibited.

Please note that the organizer will be taking photos in the venue for the purpose to use in conference report / website / other media.

4. SMBE2018 Mobile App

The SMBE2018 Mobile App allows you instant access to all sessions, presentations, posters, abstracts, maps.

- Browse sessions by Day or Presentation Type
- Create your personalized program and take notes of specific presentations
- Find practical information
- Receive the latest news

Download the app by searching for “SMBE2018” in your app store.
Or scan the QR-code below to get easy access to the app.

<for iOS>

App Store

<https://goo.gl/jS9ks7>



<for Android>

Google Play

<https://goo.gl/xZ66FC>



SOCIAL PROGRAM**Welcome Reception**

Date: Sunday, July 8

Time: 18:30-20:00

Venue: 301-304, Pacifico Yokohama (3F)

Free of charge for conference attendees.

Conference Dinner

Date: Thursday, July 12

Time: 18:30-20:30

Venue: Grand Ballroom HOH-SHOH, Yokohama Royal Park Hotel
JPY 8,000 for full delegates – tickets must be pre-booked.

Access: 10 min-walk from the conference venue. There will be guides on the route.

CONFERENCE POLICIES

Policy on harassment, discrimination and liability

SMBE and the Annual Meeting organizers are dedicated to providing a safe, hospitable, and productive environment for all attendees. Accordingly, the SMBE Annual Meeting prohibits all forms of discrimination and harassment. Behaviour that undermines the integrity of intellectual discourse and interactions will not be tolerated. This applies to all conference participants, including staff, volunteers, and attendees. If a participant engages in harassing or discriminatory behaviour, the SMBE Annual Meeting organizers reserve the right to take action ranging from a simple warning to the offender to expulsion from the conference. If you have a question or concern about this policy or would like to report an incident involving yourself or another person, please contact any member of the Local Organizing Committee or email [smbe2018@jtbcom.co.jp]. We take such issues seriously and will maintain your confidentiality (unless legally compelled otherwise). Neither SMBE nor the SMBE Annual Meeting organizers shall be responsible for any defamatory, offensive, or illegal conduct of Meeting participants, and shall not be held liable for personal injury, property damage, theft or damage of any kind suffered by the participants at or in connection with the SMBE Annual Meeting.

Broadcasting policy

The SMBE Annual Meeting supports the communication and discussion of science. Information presented at the Meeting (in oral or poster format) may be reported and discussed by attendees and science writers via blogs, Twitter, or other formats, unless any of the authors requests otherwise. We do request that communications are respectful and do not directly reproduce visual materials (e.g., no posting of photos of slides or posters) unless permission is obtained from the presenter or if they have already made this information freely available in an open-source forum. If a presenter does not want information from his/her presentation to be photographed at all, or broadcast, they should make this clear in their talk/poster and we ask that attendees respect this. If you have questions or concerns about this policy, or would like to report an abuse of it, please contact any member of the Local Organizing Committee or email smbe2018@jtbcom.co.jp.

FOR ORAL PRESENTATION

Presentation Details

Presentation times are allocated as follows:

Invited Speaker: 30 mins including Q&A

Contributed Speaker: 15 mins including Q&A

Note: Symposia have been allocated various durations depending on the number of presenters. Please check the program to see the duration of your symposium.

Please arrive in your presentation room at least 15 minutes before your presentation so you can get acquainted with the layout of the room and meet the session chair.

Technical Specifications

1. All rooms will be fitted with a lectern, laptop, projector and screen. Technicians will be available before and during all sessions to project your presentation.
2. A Windows PC (with Windows 7, PowerPoint 2010, 2013, 2016) is set up. Sound function will not be available. Video files must be produced to be playable with the codec included in the Windows Media Player 11 initial state.
3. The screens in all rooms are in 4:3 ratio. Please check the ratio before starting your presentation. (Please note that PowerPoint 2013 is ratio 16:9 by default.)

Presentation Data Submission

1. Please bring your power point file in a USB memory to the speakers' desk located in front of Room 302. You can make sure how your presentation is displayed in the room there. We recommend you to save the back-up data as a PDF file in case your power point file is not displayed as expected.
2. Please complete the submission at the speaker desk at least 60 minutes before your presentation starts.

Speakers' desk open hours:

Monday, July 9	8:00-17:30
Tuesday, July 10	8:30-18:00
Wednesday, July 11	9:00-16:30
Thursday, July 12	9:00-13:30

FOR POSTER PRESENTATION

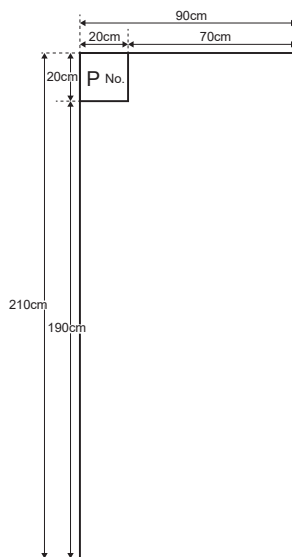
Session Date/Time

If your poster presentation is assigned to Session A (Core time: 18:00-20:00 on Monday, July 9), you should put your poster on your board marked by your poster number from 9:00-12:00 on Monday, July 9 in the catering and exhibition hall. Posters assigned to Session A should be removed by 19:30 on Tuesday, July 10.

If your poster presentation is assigned to Session B (Core time: 18:00-20:00 on Wednesday, July 11), you should put your poster on your board marked by your poster number from 9:00-12:00 on Wednesday, July 11. Posters from Session B should be removed by 18:30 on Thursday, July 12.

In Advance and On Arrival

- Posters must be brought to the meeting by the presenter and should not be mailed in advance.
- The size of one poster board is 90cm wide x 210cm high. A label of your poster number (20cm wide x 20cm high) will be put on the board in advance by the Conference Secretariat.
- Presenters should use pushpins to put up posters. Pushpins will be prepared by the Conference Secretariat and provided in the poster area.
- Equipment or electricity for use of projector or computer animation accompanying a poster presentation will not be provided.
- Please note that the set-up, removal and storage of posters are the presenters' responsibility. Any posters remaining on the boards after each poster session time will be disposed of by the Conference Secretariat.
- Poster presenters are requested to stand-by their posters during the manned session core times.
- It is the responsibility of poster presenters to ensure that at least one of the authors is in attendance to make the brief introductory presentation and to take part in the poster discussion.



*Correct at time of print, subject to change.

SUNDAY, JULY 8	
8:30 - 17:00	SMBE Council Meeting @RM313+314
10:00 - 12:00	Workshop for High School Students in Yokohama @RM302
13:00 - 16:00	TMU International Symposium on Evolutionary Biology @RM302
16:00 - 19:00	Registration
18:30 - 20:00	Welcome Reception @ RM301-304

MONDAY, JULY 9				
8:00 - 17:00	Registration			
8:45 - 9:00	Opening Ceremony			
9:00 - 18:00	Poster Session (Group A)			
9:00 - 10:00	Masatoshi Nei Lecture: Prof. William Martin			
10:00 - 10:30	Break			
10:30 - 12:30	Symposium 02	Symposium 12	Symposium 31	Symposium 05
12:30 - 13:30	Lunch			
13:30 - 15:30	Symposium 23 (Session 1)	Symposium 10	Symposium 09	Symposium 07
15:30 - 16:00	Break			
16:00 - 18:00	Symposium 23 (Session 2)	Symposium 35	Symposium 14	Symposium 29
18:00 - 20:00	Poster Session Core time (Group A)			

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TUESDAY, JULY 10				
8:30 - 17:00	Registration			
9:00 - 19:30	Poster Session (Group A)			
9:00 - 10:00	Plenary 1 Prof. Tetsuji Kakutani			
10:00 - 12:00	Walter Fitch symposium			
12:00 - 13:30	SMBE Business Meeting			
12:00 - 13:30	Lunch			
13:30 - 15:30	Symposium 15	Symposium 34	Symposium 19	Symposium 30
15:30 - 16:00	Break			
16:00 - 18:30	Neutral Theory Symposium	Symposium 32	Symposium 08	Symposium 25 Symposium 22

WEDNESDAY, JULY 11				
9:00 - 16:00	Registration			
9:00 - 18:00	Poster Session (Group B)			
9:30 - 11:30	Symposium 23 (Session 3)	Symposium 11	Symposium 16	Symposium 18
11:30 - 12:30	Lunch			
12:30 - 14:30	Symposium 23 (Session 4)	Symposium 01	Symposium 17	Symposium 21
14:30 - 15:00	Break			
15:00 - 17:00	Symposium 23 (Session 5)	Symposium 13	Symposium 26	Symposium 27
18:00 - 20:00	Poster Session Core time (Group B)			

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THURSDAY, JULY 12				
9:00 - 13:00	Registration			
9:00 - 18:30	Poster Session (Group B)			
9:30 - 11:30	Symposium 03 (Session 1)	Symposium 06	Symposium 04	Symposium 33
11:30 - 12:30	Lunch			
12:30 - 15:30	Symposium 03 (Session 2)	Symposium 24	Symposium 20	Symposium 28
15:30 - 16:00	Break			
16:00 - 17:00	Plenary 2 Prof. Anne C. Stone			
17:00 - 17:30	Award Ceremony / Invitation to SBE 2019			
18:30 - 20:30	Conference Dinner @Yokohama Royal Park Hotel			

PLENARY SPEAKERS



William Martin
University of Dusseldorf

William F. (Bill) Martin received his undergraduate degree in biology in 1985 from the University of Hannover, Germany. He received his PhD in 1988 for work on plant transposons and molecular evolution at the Max Planck Institut for Breeding Research in Cologne, Germany. From 1989 -1999 he worked on energy metabolism, endosymbiosis, and gene transfer in microbial evolution at the University of Braunschweig. He has been full professor at the University of Düsseldorf, Germany, since 1999. He has published over 300 scientific papers. He is a member of the American Academy of Microbiology and EMB0. His academic awards include the Heinz Maier-Leibnitz Prize (Germany), a Julius von Haast Fellowship (New Zealand), the Spiridion Brusina Medal (Croatia) and the Kluh Foundation Prize (Germany). He was a founding member of SMBE and has served the society as Editor since 2003. His scientific contributions have impacted our understanding of lateral gene transfer, physiology in evolution, and the chemical basis of cell origins.



Tetsuji Kakutani
The University of Tokyo / National Institute of Genetics

Tetsuji Kakutani has been investigating dynamics and evolutionary impact of epigenetic modifications using *Arabidopsis* as a model organism. After receiving PhD from Faculty of Science, Kyoto University, for cell biology on *Dictyostelium*, he started to work on *Arabidopsis* during post-doctoral stay in Eric Richards lab in Washington University. In 1994, he organized his own group in National Institute of Agrobiological Resources. In 2000, he moved to National Institute of Genetics as an Associate Professor, and was promoted to Professor in 2005. Since 2015, he has also been appointed as a Professor in Department of Biological Sciences, The University of Tokyo.

PLENARY SPEAKERS



Anne C. Stone

School of Human Evolution and Social Change,
Arizona State University

Anne Stone is Regents' Professor in the School of Human Evolution and Social Change at the Arizona State University. Currently, her research focuses on population history and understanding how humans and the great apes have adapted to their environments, including their disease and dietary environments. This includes: (a) Native American population history, (b) the evolutionary history of the Great Apes, and (c) understanding the evolutionary history of mycobacteria (specifically the causative agents of tuberculosis and leprosy). Stone has been a Fulbright Fellow (1992-93), a NIH NRSA postdoctoral fellow (1997-1998), and a Kavli Scholar (2007). She is a fellow of the American Association for the Advancement of Science (2011) and a member of the National Academy of Sciences (2016). Stone currently serves as a senior editor of *Molecular Biology and Evolution*.

SCIENTIFIC PROGRAM

MONDAY, JULY 9

*Correct at time of print, subject to change.

9:00	MASATOSHI NEI LECTURE William Martin, University of Dusseldorf In search of microbe number one				Main Hall
	SY02: Associate Editors Symposium Room 301 Naoko Takezaki, Naruya Saitou	SY12: Genomics and evolution of symbiotic interactions Room 302 Cheong Xin Chan, Rebecca A. Chong, Hao Zheng	SY31: Tracing back bacterial pathogen evolution from ancient and modern genomics Room 303 Verena J. Schuenemann	SY05: Evolution of non-coding RNAs and their regulatory networks Room 304 Yehu Moran, Masafumi Nozawa	
10:30	Jay F Storz University of Nebraska Insights into mutational pathways of biochemical adaptation using ancestral protein resurrection	Debashish Bhattacharya Rutgers University, New Brunswick The genome of <i>Paulinella</i> reveals pathways of plastid integration	Johannes Krause Max Planck Institute for the Science of Human History The genetic history of plague: From the Stone Age to the 18th century	Celina Juliano University of California, Davis The PIWI-piRNA Pathway Targets Transposons in Hydra Somatic Stem Cells	
10:45	Dorothee Huchon Tel-Aviv University An animal without aerobic cellular respiration				
11:00	Daniel Falush University of Bath Why panmictic bacterial species are rare	Takema Fukatsu National Institute of Advanced Industrial Science and Technology (AIST) Experimental evolution of an insect-bacterium symbiotic association	Caitlin Pepperell University of Wisconsin-Madison Adoption of the pathogenic niche	Eric Miska University Of Cambridge/ Wellcome Trust Sanger Institute Small RNA Pathways In Arthropods	
11:15	Emmanuelle Lerat CNRS - Universite Lyon 1 Epigenetic conservation of human duplicated genes associated to their transposable element neighborhood				
11:30	Rebecca Zufall University of Houston Germline and somatic mutation rates in a single cell	Eddy Dowlé University of Otago Genomic hijacking - how parasitic worms manipulate their hosts	Judith Neukamm University of Tuebingen/ University of Zurich A 2,200 year old <i>Mycobacterium leprae</i> genome from an Egyptian mummy	Yirong Wang Peking University microRNAs in the Same Clusters Evolve to Coordinately Regulate Functionally Related Genes	
11:45	Tal Dagan Kiel University Polarization of ancestor relations reveals the order of traits in the evolution of cyanobacterial multicellularity	David John Miller James Cook University Comparative genomics reveals the distinct evolutionary trajectories of the robust and complex coral lineages	Alexander Herbig Max Planck Institute for the Science of Human History, Jena/University of Tuebingen <i>Salmonella enterica</i> genomes from victims of a major sixteenth-century epidemic in Mexico	Laura Landweber Columbia University Noncoding-RNA mediated epigenetics in the ciliate <i>Oxytricha</i>	

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12:00	Dennis Lavrov Iowa State University Evolution of mRNA editing and linear multipartite genome in mitochondria of calcaronean sponges	Deepa Agashe National Centre for Biological Sciences (NCBS), Bangalore Rapid evolution of host dependence on environmentally acquired microbes	Lionel Guy Uppsala University A Single, >2.2 Ga Old Event of Host Adaptation in the Order Legionellales	Arie Fridrich The Hebrew University of Jerusalem First evidence for HEN1 mediated methylation of miRNAs in animals, and the functional importance of small RNA stabilization in cnidarians
12:15	Richard Cordaux CNRS / University of Poitiers Impact of feminizing Wolbachia endosymbionts on the evolution of a male heterogametic system of sex chromosomes (XY-XX)	Hwan Su Yoon Sungkyunkwan University The genome study of Apophlaea lyallii (Floriophyceae, Rhodophyta) provides new insights for the algal-fungal symbiotic relationship	Susanna Sabin Max Planck Institute for the Science of Human History A high-quality 17th century Mycobacterium tuberculosis genome adds resolution to mycobacterial dating and phylogeography	Antonio Marco University of Essex Prevalent selection against microRNA target sites in human populations

	SY23: Open Symposium SESSION 1 Room 301 Hideki Innan, Tatsuya Ota	SY10: Genetic conflict and speciation Room 302 Chau-Ti Ting, Aya Takahashi	SY09: Gene flow detection and dating methods Room 303 Francesc Calafell, Simone Biagini, Carla Garcia Fernandez	SY07: Evolutionary genomics of the human brain Room 304 Stefano Berto, Noriyoshi Usui, Kazuya Toriumi
13:30	Atsushi Ogura Nagahama Institute of Bioscience and Technology Whole genome integration of giant virus to chlorella and its implication to the evolution of giant virus and the symbiosis of chlorella and ciliates	Leonie Moyle Indiana University Conflict and speciation: do empirical data support a role for conflict in the isolation of plant species?	John Novembre University of Chicago Methods to characterize geographic structure in genetic variation	Philipp Khaitovich Skolkovo Institute of Science and Technology/ Shanghai Institutes for Biological Sciences Metabolites and lipids of the human brain: evolution and function
13:45	Huw Ogilvie Australian National University Estimating a time tree of the Australian radiation of Eugongylus group lizards by applying StarBEAST2 to a genome-scale data set			

SCIENTIFIC PROGRAM

14:00	Kruttika Phalnikar NCBS-TIFR Diversity and fitness impacts of extracellular vs. intracellular bacterial associates of butterflies	Nitin Phadnis University of Uth Genetic conflict and speciation in <i>Drosophila</i>	Matthias Steinruecken University of Chicago Efficient representations of local trees in Coalescent Hidden Markov models for demographic inference	Genevieve Konopka UT Southwestern Medical Center Evolution of human-specific gene co-expression networks
14:15	Haiwei Luo The Chinese University of Hong Kong Drivers of genome reduction in free-living marine bacteria		Laurits Skov Aarhus University Detecting unknown introgressed archaic haplotypes in modern and ancient human genome sequences	
14:30	Marcy Uyenoyama Duke University Implications of population structure for site frequency spectra	Harmit Singh Malik Fred Hutchinson Cancer Research Center Rapid evolution leads to rapid onset of centromeric histone incompatibility in <i>Drosophila</i>	Lindsey Fenderson University of Adelaide Assessing population structure through time using ancient DNA	Yasuhiro Go National Institutes of Natural Sciences/National Institute for Physiological Sciences The evolutionary trajectory of spatial transcriptome and epigenome in primate brains
14:45	Xu Wang Auburn University/ HudsonAlpha Institute for Biotechnology Developmental delay caused by mitochondrial replacement reveals co-evolutionary divergence of nuclear and mtDNA	Ching-Ho Chang U of Rochester Comparative genomics reveals rampant gene duplication and reorganization of the <i>Drosophila melanogaster</i> and the simulators clade Y chromosomes	Alex Mas-Sandoval Universidade Federal do Rio Grande do Sul/Universitat Pompeu Fabra Native American Genetic History Through Admixed Brazilians	Alessio Strano University of Cambridge Functional studies in 2D and 3D stem cell systems of candidate genes underlying human-specific features of cerebral cortex development
15:00	Thomas LaBar Michigan State University Drift robustness and the evolution of genome architecture in small populations	S. Lorena Ament-Velasquez Uppsala University Allorecognition loci act as speciation genes in <i>Podospira anserina</i>	Garrett Hellenthal University College London Reconstructing and dating gene flow using efficient haplotype-based techniques	Evan Geller Yale University Big Brains: What High-Throughput Enhancer Knockouts Reveal about Human Cortical Evolution
15:15	Luke Kosinski University of Arizona Weak selection primes non-coding sequences for de novo evolution	Rossana Colon-Thillet Fred Hutchison Cancer Research Center /University of Washington, Seattle Evolution-guided mutagenesis to understand antiviral protein function		Kenneth L Chiou University of Washington Single-cell transcriptional signatures of the aging nonhuman primate brain

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	SY23: Open Symposium SESSION 2 Room 301 Yoko Satta, Hideki Innan	SY35: Weak forces in genome evolution Room 302 Hiroshi Akashi, Tomoko Ohta	SY14: Improving inference frameworks by accounting for population structure Room 303 Marcy K. Uyenoyama, Emilia Huerta Sanchez	SY29: Somatic mutation and the evolution of multicellularity Room 304 Reed Cartwright, Rob Lanfear
16:00	<p>Hidegori Nishihara</p> <p>Tokyo Institute of Technology</p> <p>Retrotransposons spread potential sources of cis-regulatory elements for mammary gland evolution</p>	<p>Laurent Duret</p> <p>CNRS, Université de Lyon</p> <p>The dark side of recombination: biased gene conversion in the tree of life</p>	<p>Sohini Ramachandran</p> <p>Brown University</p> <p>Modeling the interaction between population structure and selection</p>	<p>Maria E Orive</p> <p>University of Kansas</p> <p>Mutation and Selection Within an Individual</p>
16:15	<p>Christian Landry</p> <p>Université Laval</p> <p>A large fraction of paralogous genes is not free to diverge independently due to molecular interference</p>			
16:30	<p>Omer Gokcumen</p> <p>University at Buffalo</p> <p>A reassessment of evolutionary impact of genomic structural variation</p>	<p>Rebekah L Rogers</p> <p>UNC Charlotte</p> <p>Genomic disintegration in woolly mammoths on Wrangel island</p>	<p>Amy Goldberg</p> <p>UC Berkeley</p> <p>Mechanistic models of social processes impacting admixture</p>	<p>Inigo Martincorena</p> <p>Wellcome Trust Sanger Institute</p> <p>Somatic evolution in cancer and healthy tissues</p>
16:45	<p>Zongji Wang</p> <p>University of Vienna/ Zhejiang University/BGI-Shenzhen</p> <p>Phylogenomics and comparative genomics of Palaeognathous birds reveal Palaeognath evolutionary history and ZW sex chromosome evolution</p>			
17:00	<p>Nicolas Rohner</p> <p>Stowers Institute for Medical Research/ KU Medical Center</p> <p>Cavefish Metabolic Adaptation: Hungry, Fat, and Healthy</p>	<p>Nobuhiko Tokuriki</p> <p>University of British Columbia</p> <p>The role of genetic variation in the evolution of enzyme functions</p>	<p>Gili Greenbaum</p> <p>Stanford University</p> <p>Whole-genome hierarchical population structure analysis using network-based clustering</p>	<p>Vincent Hanlon</p> <p>University Of British Columbia</p> <p>Somatic mutation in Sitka spruce</p>

SCIENTIFIC PROGRAM

17:15	Kelsey Caetano-Anolles Seoul National University Recombination Hotspots and Imprinted Genes in Indigenous African Cattle	Marjolaine Rousselle University of Montpellier Contrasting the influence of gBGC on adaptive statistics in primates and birds	Felix E.G. Beaudry University of Toronto Introgression of a Y chromosome haplotype into a neo-Y karyotype in <i>Rumex</i>	Reed Cartwright Arizona State University Somatic Mutations, Development, and Phylogenomics
17:30	Ekaterina Khrameeva Skolkovo Institute of Science and Technology/ Institute for Information Transmission Problems A comprehensive lipidome map of human brain	Tomotaka Matsumoto National Institute of Genetics Distinguishing among evolutionary forces acting on genome-wide base composition: Computer simulation analysis of approximate methods for inferring site frequency spectra of derived mutation in recombining regions	Makoto Shimada Institute for Comprehensive Medical Science, Fujita Health University Distinction between ancient introgression and incomplete lineage sorting in modern human genomes	Aleksandra Bezmenova Skolkovo Institute of Science and Technology / Lomonosov Moscow State University Accumulation of mutations and natural selection in experimental evolution of basidiomycete fungus <i>Schizophyllum commune</i>
17:45	Marina ELEZ UPMC, Sorbonne University Mutation dynamics and fitness effects followed in single cells	Shi-An A Chen Stanford University Direct measurement of fitness effects of natural variation through precision genome editing	Alicia R Martin Massachusetts General Hospital/Broad Institute of Harvard and MIT/Broad Institute of Harvard and MIT Genetic risk prediction across diverse populations	Joanna Masel University of Arizona Multicellular organisms face an inescapable double bind between cell senescence and cancer

SCIENTIFIC PROGRAM

TUESDAY, JULY 10

9:00	Plenary 1 Tetsuji Kakutani, The University of Tokyo / National Institute of Genetics Evolution of sequence-specific anti-silencing systems in Arabidopsis	Main Hall
	Walter Fitch Symposium Aoife McLysaght	Main Hall
10:00	Ana Marija Jaksic Vetmeduni Vienna Re-thinking a classic clinal trait: Pleiotropic consequences of thermally adaptive dopamine on pigmentation clines in <i>Drosophila</i>	
10:15	Mrudula Sunil Sane National Centre for Biological Sciences, Tata Institute of Fundamental Research Antagonistic pleiotropy is rare among new mutations	
10:30	Harry Kemble INSERM The mechanistic basis of epistatic variety in a metabolic pathway uncovered by high-resolution fitness interaction mapping	
10:45	Jason Tarkington University of Houston Long-Term Evolution of <i>Tetrahymena thermopila</i>	
11:00	Xinzhu Wei University of Michigan The optimal mating distance resulting from heterosis and genetic incompatibility	
11:15	Rachel Leigh Cosby Cornell University KRAB-transposase fusion as a source of new regulatory proteins in evolution	
11:30	Christopher R Robles University of California Los Angeles The impact of Neanderthal ancestry on human phenotypes	
11:45	Martin Silvert Institut Pasteur/Universite Pierre et Marie Curie Archaic introgression and gene regulation: a disproportionate degree of Neanderthal ancestry in T-cells enhancers	

SCIENTIFIC PROGRAM

	SY15: Integrating ancient and modern DNA for evolutionary genomics Room 301 Michael Dannemann, Hernán A. Burbano, Kay Prüfer	SY34: Virus genome evolution Room 302 Anne Kupczok, Marina Escalera Zamudio, Richard Goldstein	SY19: Machine learning approaches in evolutionary genetics Room 303 Andrew D. Kern, Daniel R. Schrider	SY30: Timing methodologies and applications Room 304 Fabia Ursula Battistuzzi, Beatriz Mello
13:30	Sriram Sankararaman UCLA Understanding the structure and function of archaic ancestry in present-day humans	Marcia F Marston Roger Williams University Patterns of genomic diversification in natural communities of marine bacteriophages	Haipeng Li Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences Supervised learning for analyzing large-scale genome-wide DNA polymorphism data	Lindell Bromham Australian National University Six impossible things before breakfast: assumptions, models and belief in molecular dating
14:00	Kelley Harris University of Washington/Stanford University Using archaic introgression to infer sequence constraints that are shaping human enhancer evolution	Adi Stern Tel Aviv University Uncovering hidden properties of an RNA virus	Adam Siepel Cold Spring Harbor Laboratory New methods for measuring natural selection and predicting deleterious variants in the human genome.	Blair Hedges Temple University Undersampling genomes has biased time and rate estimates
14:30	Benjamin Vernot Max-Planck-Institute for Evolutionary Anthropology No Evidence for Protracted Selection Against Neandertal Alleles in Humans	Alison Feder Stanford University Intra-patient evolutionary dynamics of HIV drug resistance evolution	Samuel V Scarpino Northeastern University Real-time Phenotype Prediction From Unaligned Whole Genome Sequencing Data Using Deep Learning	Dominik Schrempf Eotvos Lorand University, Budapest Phylogenetic incongruences - opportunities to improve the reconstruction of a dated tree of life
14:45	Matheus Bianconi University of Sheffield Herbarium genomics infers the changes underlying the evolution of C4 photosynthesis in the Andropogoneae grasses	Mang Shi The University of Sydney/China CDC The origin of Vertebrate RNA Viruses	Shiran Abadi Tel-Aviv University A Machine-Learning Approach for Phylogenetic Model Selection	Qiqing Tao Temple University Pervasive correlation of molecular evolutionary rates in the tree of life
15:00	Patricia L.M. Lang Max Planck Institute for Developmental Biology Tracking plant phenology and genetic diversity during environmental change using contemporary and historical samples	Anderson Brito Imperial College London Host switches and intrahost speciations play a central role in herpesvirus evolution	Lauren A Sugden Brown University Statistical inference frameworks for detecting adaptive evolution of variants and genes	Naoko Takezaki Kagawa University Global rate variation in bony vertebrates

SCIENTIFIC PROGRAM

15:15	Evan K. Irving-Pease University of Oxford Selection trajectories of genetic variants underlying domestic animal traits	Richard Allen Goldstein UCL Norovirus pandemics emerge from hidden reservoirs and are not driven by the acquisition of viral genetic changes	Sara Sheehan Mathieson Swarthmore College A Likelihood-Free Inference Framework for Population Genetic Data using Permutation-Invariant Neural Networks	Jacob Berv Cornell University Recalcitrance of avian divergence times and phylogenetic topology may be related to selection for reduced body size across the K-Pg boundary
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	Symposium for the 50th Anniversary of the Neutral Theory of Molecular Evolution Room 301 Naruya Saitou	SY32: Transposable elements in gene regulation and genome evolution Room 302 Luz Mayela Soto-Jimenez, Robin Burns	SY08: 50 years since Ohno's genome duplication: integration across disciplines and time scales Room 303 Kentaro Shimizu, Takashi Makino, Xinzhu Wei	SY25: Post-transcriptional modifications: functions, diversity, pathogenesis and evolution Room 304 Helen Piontkivska, Sabyasachi Das
16:00	Daniel L. Hartl Harvard University Becoming Motoo Kimura	Cedric Feschotte Cornell University Transposable elements as catalysts of convergent evolution	Yves Van de Peer Ghent University - VIB The evolutionary significance of polyploidy	Reuben s. Harris Masonic Cancer Center/ University of Minnesota Antiviral APOBEC Enzymes Drive Tumor Evolution
16:30		Lauren Gibilisco University of California, Berkeley Chromatin sinks and mutational burdens in males	Clare Henry John Innes Centre The evolution of meiosis in autotetraploid Arabidopsis arenosa	Jianzhi Zhang University of Michigan Post-transcriptional modifications: Adaptations or cellular errors?
16:35	Tomoko Ohta National Institute of Genetics Epigenetics, Chromatin, Gene Activity and Near-Neutrality in Evolution	David Winter Massey University The contribution of transposable elements to regulation of genes underlying symbiosis in <i>Epichloe</i>		
16:45				
17:00		Grace Yuh Chwen Lee Lawrence Berkeley National Laboratory/ University of California, Berkeley Pervasive epigenetic effects of euchromatic transposable elements impact genome evolution	Levi Yant The John Innes Centre Genomic hotspots of adaptation to whole genome duplication	Helen Piontkivska Kent State University The role of innate immune mechanisms in molecular evolution and pathogenesis of flaviviruses
17:10				

SCIENTIFIC PROGRAM

				SY22: Molecular bases of the different forms of flowers on plants of the same species Room 304 Tatsuya Ota, Yasuo Yasui
17:10	Warren Ewens University of Pennsylvania			
17:15	My memories of Kimura and the neutral theory.	Della Fixsen University Of Utah Poxvirus capture of host genes by retrotransposition in infected cells		Takashi Akagi Kyoto University/JST Diversification of sexual system: insights from the persimmon genome
17:30		Richard McLaughlin Pacific Northwest Research Institute The birth of new genome defense genes by transposable elements	Yoichiro Nakatani Trinity College Dublin, University of Dublin Genome restructuring during early vertebrate evolution	
17:45	Yun S. Song University of California, Berkeley New mathematical insights into the regulation and optimization of translation dynamics	Alexander Suh Uppsala University The tuatara genome - a detailed look into early amniote genome evolution and a smorgasbord of recently active transposons	Sira Sriswasdi The University Of Tokyo/ Chulalongkorn University Genome stabilization mechanisms in early post-polyploidization evolution	Philip Gilmartin University Of East Anglia/ The Earlham Institute Characterisation of the S locus that controls heterostyly in Primula
18:00		Doris Bachtrog University of California Berkeley, Integrative Biology The role of transposable-element mediated rewiring of regulatory networks: dosage compensation in Drosophila	Polina Yu. Novikova VIB/Ghent University Adaptation to the whole genome duplications in Australian burrowing frogs Neobatrachus	
18:15			Gwyneth Halstead-Nussloch University of Zurich Comparative Analysis Between Allopolyploid <i>Arabidopsis kamchatica</i> And Its Diploid Progenitors Reveals Effects Of Polyploidy On Genetic Diversity And Selection	Yasuo Yasui Kyoto University
18:20				Identification of genes at the S-locus controlling heteromorphic self-incompatibility in buckwheat through genetic and genomic analyses

SCIENTIFIC PROGRAM

WEDNESDAY, JULY 11

	SY23: Open Symposium SESSION 3 Room 301 Yoko Satta, Hideki Innan	SY11: Genomic underpinnings of primate phenotypic evolution and diversity Room 302 Amanda Dawn Melin, Shoji Kawamura	SY16: Intra-host evolutionary dynamics Room 303 Alison F. Feder, Katherine S. Xue	SY18: Looking beyond the genome: cultural and behavioral drivers of biological evolution Room 304 Maanasa Raghavan, Nicole Creanza
09:30	Charleston W.K. Chiang University of Southern California/University of California, Los Angeles A comprehensive map of genetic variation in the world's largest ethnic group - Han Chinese	Mariam Okhovat Oregon Health & Science University Molding the genome with LAVA: Exploring functional roles of a gibbon-specific retrotransposon	Richard Neher University of Basel The evolutionary dynamics of untreated HIV and the maintenance of the latent reservoir	Evelyn Heyer National Natural History Museum/CNRS Cultural traits that shape genetic diversity: a case study in Inner Asia
09:45	Takashi Gakuhari Kanazawa University/ Kitasato University Whole genome analysis of the Jomon remain reveals deep lineage of East Eurasian populations			
10:00	Stefano Bettinazzi University of Montreal Divergent mitochondrial phenotypes associated with the Doubly Uniparental Inheritance (DUI) of mitochondria	Wesley C Warren Washington University School of Medicine Variant discovery and consequence in the genomes of a bottlenecked vervet population	Christina Curtis Stanford University School of Medicine/Stanford University Quantifying the evolutionary dynamics of tumor progression and metastasis	Susanne Shultz University of Manchester The evolutionary consequences of sociality and culture: is there gene-culture interaction in non- human animals?
10:15	Davide Pisani University of Bristol Molecular clocks on Chelicerata suggest an early colonization of land by arachnids and support the monophyly of mites			
10:30	Karine Van Doninck University of Namur DNA repair in bdelloid rotifers: genome dynamics.	Joseph Orkin University of Calgary Population genomics of white faced capuchin monkeys (<i>Cebus capucinus imitator</i>) with unbiased fecal genomes	Ellinor Opsal Alseth University of Exeter The impact of biodiversity on phage immunity and virulence in <i>Pseudomonas aeruginosa</i>	Zuzana Hofmanova University of Fribourg/ Fribourg Ancient Genomic Diversity Reveals Differences in Cultural Practices and Cultural Barriers between Prehistoric Farmers and Hunter-gatherers in Europe

SCIENTIFIC PROGRAM

10:45	<p>Jeffrey Chuang The Jackson Laboratory</p> <p>Evolution of an intratumoral ecology susceptible to successive treatment in breast cancer xenografts</p>	<p>Noah Snyder-Mackler University of Washington</p> <p>Genomic signatures of high altitude adaptation in gelada monkeys (<i>Theropithecus gelada</i>)</p>	<p>Armita Nourmohammad Max Planck Institute for Dynamics and Self-organization/University of Washington</p> <p>Selection and clonal interference in B-cell repertoire response to HIV-1 infection</p>	<p>Hiromi Matsumae Yokohama City University/ University of Zurich</p> <p>Complex human histories of Northeast Asia revealed by correlations between genes, language, and music</p>
11:00	<p>Philipp Brand UC Davis</p> <p>The molecular determinants of pheromone divergence and their role in the evolution of reproductive isolation in orchid bees</p>	<p>Mareike Cora Janiak Rutgers University/ University of Calgary</p> <p>Duplication and Convergent Evolution of the Pancreatic Ribonuclease Gene (RNASE1) in a Non-Colobine Primate, the Mantled Howler Monkey (<i>Alouatta palliata</i>)</p>	<p>Ines Levade University of Montreal</p> <p><i>Vibrio cholerae</i> genomic diversity within and between patients</p>	<p>Lara M Cassidy Trinity College Dublin</p> <p>The Genomics of Megaliths: An Irish case study into the reconstruction of prehistoric societal landscapes through ancient DNA analysis</p>
11:15	<p>Antonio Barbadilla Universitat Autònoma de Barcelona</p> <p>Fifty years of Neutral Theory: Past, Present and Future Perspective</p>	<p>Jennifer E. Farrar Georgia Institute of Technology</p> <p>Ancient proteins and the thrifty gene hypothesis: Uric acid's contribution to primate evolution</p>	<p>Sebastian Lequime KU Leuven - University of Leuven /Institut Pasteur</p> <p>Within-host evolutionary dynamics of dengue virus in its mosquito vector <i>Aedes aegypti</i></p>	<p>Cosimo Posth Max Planck Institute for the Science of Human History</p> <p>Waves of history in Remote Oceania: language continuity despite population replacement in Vanuatu</p>

SCIENTIFIC PROGRAM

	SY23: Open Symposium SESSION 4 Room 301 Shoji Kawamura, Naoko Takezaki	SY01: Asian population genomics Room 302 Hie Lim Kim, Atsushi Tajima	SY17: Linking the mitochondrial genotype to phenotype: a complex endeavour Room 303 Liliana Milani, Fabrizio Ghiselli	SY21: Microbial evolution: human- microbe interactions and the role of deep sequencing in time series analysis Room 304 Ana Duggan, Ashleigh Porter, Yuan O. Zhu
12:30	Xiao-Pan Hu Heinrich Heine University Duesseldorf The <i>E. coli</i> translation machinery evolves towards minimal total mass concentration at the required protein production rate	TBA (will be announced on official conference app) Northern Asian Genome Project	John Allen University College London The function of genomes in bioenergetic organelles	Weiwei Zhai Genome Institute of Singapore Episodic convergent evolution drives dynamic history of passage adaptation and vaccine efficacy in the H3N2 influenza virus
12:45	Roman Biek University of Glasgow Phenotypic and genomic changes involved in cross-species transmission and emergence of a zoonotic virus			
13:00	Jesus A Ballesteros University of Wisconsin- Madison : A GENOMIC TIMELINE FOR THE EVOLUTION AND DIVERSIFICATION OF SEA SPIDERS (ARTHROPODA: PYCNOGONIDA)	Anders Bergstrom Wellcome Sanger Institute High-coverage sequencing of diverse human populations in the HGDP-CEPH panel	Kateryna Makova Penn State University Transmission of mitochondrial heteroplasmy across multigenerational pedigrees	Julio Felix Diaz Caballero University of Toronto Population-level, Genome Wide Association Study of Burkholderia multivorans in the Cystic Fibrosis Lung Reveals a Role for Recombination in the Evolution of Antimicrobial Resistance
13:15	John P. Barton University of California, Riverside A Path Integral Method for Analytically Tractable Inference of Evolutionary Dynamics	Namrata Kalsi Nanyang Technological University Back migrations of Southeast Asian ancestors to South Asia during the Last Glacial Maximum		Laura S Weyrich University of Adelaide Consequences of European arrival on the microbiota of ancient Native Americans

SCIENTIFIC PROGRAM

13:30	<p>Olivier Tenaillon University Paris Diderot/ Inserm</p> <p>The thermodynamical roots of pair-wise epistasis in alpha helix of beta-lactamase TEM-1</p>	<p>Takehiro Sato Kanazawa University</p> <p>Human population history in the southwestern coastal region of Sea of Okhotsk, inferred from ancient genome analysis</p>	<p>Joseph Dubie Texas A&M University</p> <p>Role of competition and Ne in the maintenance of heteroplasmic, selfishly acting mitochondrial mutations in <i>Caenorhabditis elegans</i></p>	<p>Thierry WIRTH Natural History Museum - EPHE</p> <p>Adaptive landscape and evolutionary history of the multidrug resistant W148 Russian clone</p>
13:45	<p>Jose Luis Villanueva-Canas Hospital del Mar Research Institute (IMIM), Universitat Pompeu Fabra (UPF)</p> <p>Using transcriptomics to study hibernation in a natural primate population.</p>	<p>Melissa Ilardo University of Copenhagen</p> <p>Physiological and genetic adaptations to diving in Sea Nomads</p>	<p>Sarah Schaack Reed College</p> <p>Direct Estimates of Mitochondrial Mutation Rates Across Genotypes and Populations in <i>Daphnia</i></p>	<p>Andrew Sackman Arizona State University</p> <p>MMC-ABC: Inference of population genetic parameters from time-sampled allele frequency data in populations with sweepstakes reproduction</p>
14:00	<p>Hiba Babiker Max Planck Institute for the Science of Human History</p> <p>Insights into the population history of the "Hidden Ones": From oral history to genome-wide analysis</p>	<p>Serena Tucci Princeton University/ University of Ferrara</p> <p>Evolutionary history and adaptation from whole-genome sequences of a pygmy population of Flores Island, Indonesia</p>	<p>David Jebb University College Dublin</p> <p>Mitochondrial genomics of exceptional longevity in bats</p>	<p>Ana Duggan McMaster University</p> <p>Colliding histories and opposing forces: ancient DNA of vaccination and smallpox</p>
14:15	<p>Melissa A. Wilson Sayres Arizona State University</p> <p>Sex Differences in Reference Genome Affect Variant Calling and Differential Expression</p>	<p>Yumi Yamaguchi-Kabata Tohoku University</p> <p>Allele frequency of pathogenic variants in a Japanese population based on the whole-genome reference panel of ToMMo and inter-population differences</p>	<p>Stephanie Falk Monash University</p> <p>Climate-related Mitochondrial Lineages Correlate with Functional Differences in Energy Utilisation</p>	<p>Bardya Djahanschiri Institute for Cell Biology and Neuroscience, Goethe University Frankfurt, Frankfurt am Main</p> <p>The evolution of Pathobiology in the genus <i>Acinetobacter</i></p>

SCIENTIFIC PROGRAM

	SY23: Open Symposium SESSION 5 Room 301 Naoko Takezaki, Shoji Kawamura	SY13: Human evolution after out-of-Africa Room 302 Naruya Saitou, Partha P. Majumder	SY26: Predictability of rapid evolutionary processes Room 303 Marta Luksza, Armita Nourmohammad	SY27: Quantitative genetics of developmental evolution Room 304 Christina Zakas, Luke Noble
15:00	Bui Quang Minh Australian National University/University of Vienna, Medical University of Vienna Towards more accurate phylogenomic inference using IQ-TREE	Partha P Majumder National Institute of Biomedical Genomics ANCESTRAL AND ADMIXTURE HISTORIES IN THE INDIAN SUBCONTINENT	Michael Lässig University of Cologne, Institute for Biological Physics Evolutionary predictions from biophysical models	Katrina McGuigan The University of Queensland Evolutionary Quantitative Genetics of Zebrafish Development
15:15	Karen Siu-Ting Dublin City University/ Aberystwyth University/ Universidad Nac. Mayor San Marcos Inadvertent paralog inclusion impacts phylogenomic relationships and timetree estimates in the Lissamphibia			
15:30	Nicolas Galtier CNRS - University Montpellier Incomplete lineage sorting in mammalian phylogenomics	Brenna M Henn UC Davis Reconstructing the human population history of Africa	Thierry Mora CNRS and ENS Paris Prediction in optimal immune systems	David Garfield Humboldt University Characterising patterns of selection and the distribution of fitness effects using single-cell open chromatin data
15:45	Thomas Bourguignon Okinawa Institute of Science and Technology Evolution of bacterial communities associated with termites			
16:00	Sabyasachi Das Emory University Concordance and divergence of the VLR- based adaptive immune system in jawless vertebrates: Functional and evolutionary implications	Timothy Jinam National Institute of Genetics Genome wide analysis of negrito groups in Southeast Asia	Yuval Elhanati Princeton Evolution of the adaptive immune system in response to cancer	Rafik Neme Columbia University Somatic genome rearrangements in Oxytricha trifallax - a single-cell model for nuclear differentiation and development

SCIENTIFIC PROGRAM

16:15	<p>Ana Teles</p> <p>Max Planck Institute for Evolutionary Biology</p> <p>Intra-individual analysis of the MHC-dependent TCR repertoire diversity</p>	<p>Xiaoming Liu</p> <p>School of Public Health, The University of Texas Health Science Center at Houston</p> <p>Human prehistoric demography revealed by polymorphic pattern of CpG transitions</p>	<p>Ivana Cvijovic</p> <p>Harvard University</p> <p>High-resolution lineage tracking of laboratory yeast populations over 1000 generations</p>	<p>Julia C Boughner</p> <p>University of Saskatchewan</p> <p>Fishing for genes driving tooth evo-devo exclusive of the vertebrate jaw</p>
16:30	<p>Katalin Csillery</p> <p>University of Zurich/Swiss Federal Research Institute WSL</p> <p>Deciphering The Evolution Of Drought Tolerance In populations Of Silver Fir (<i>Abies alba</i> Mill.) Populations Across Switzerland And Southern France</p>	<p>Nicole Creanza</p> <p>Vanderbilt University</p> <p>'Mother' tongues? A global study of sex-biased genetic and linguistic transmission after Out-of-Africa</p>	<p>Ignacio Vazquez-Garcia</p> <p>Wellcome Trust Sanger Institute/University of Cambridge</p> <p>Clonal diversity accelerates the evolution of antimicrobial resistance</p>	<p>Han Ting Chou</p> <p>Georgia Institute of Technology</p> <p>Genetic Basis of Natural Variations in Germline RNAi in <i>C. elegans</i></p>
16:45	<p>Kathleen Gray Ferris</p> <p>UC Davis</p> <p>Genetics of parallel leaf shape evolution in the <i>Mimulus guttatus</i> species complex</p>	<p>Joachim Burger</p> <p>Institute of Organismic and Molecular Evolution, Mainz University</p> <p>Population Genomic Inference from Palaeo-Neutalomes of Mediaeval Germans</p>	<p>Alejandro Couce</p> <p>Imperial College London/Universite Paris Diderot</p> <p>Historical contingency shapes genome-wide diversity after antibiotic-driven bottlenecks</p>	<p>Christina Zakas</p> <p>New York University</p> <p>The genetic basis of evolutionary transitions in early development</p>

SCIENTIFIC PROGRAM

THURSDAY, JULY 12

	SY03: Ecological genomics SESSION 1 Room 301 Polina Yu. Novikova, Daniele Filiault	SY06: Evolutionary epigenomics, progress and prospects Room 302 Soojin Yi V., Brandon S. Gaut	SY04: Evolution of adaptive immunity and MHC genes Room 303 Sabyasachi Das, Masayuki Hirano, Alicia Sanchez-Mazas	SY33: Trash to treasure and treasure to trash: invasion, persistence, neofunctionalization, and gene decay in evolution Room 304 Peter Gogarten, Dan Graur, Anthony Poole
09:30	Thomas Mitchell-Olds Duke University Biotic and abiotic influences on balancing selection in nature	Takuno Shohei SOKENDAI The evolution of gene body methylation in plant species.	Masanori Kasahara Hokkaido University Faculty of Medicine Evolution of adaptive immunity	Anthony Poole University of Auckland Experimentally evolving molecular Rube Goldberg machines
09:45				Johann Peter Gogarten University of Connecticut Inteins and Homing Endonucleases: long term survival and constructive neutral evolution
10:00	Sian M Bray John Innes Centre From Population Genomics to Mechanistic understanding: A possible role in adaptation to low calcium serpentine soils by Two Pore Channel 1	Mary Gehring Whitehead Institute for Biomedical Research Epigenetic variation and regulation of imprinted gene expression	Jim Kaufman University of Cambridge Generalists Versus Specialists: A New View Of How MHC Molecules Respond To Infectious Pathogens	Dan Graur University of Houston Can the human genome be 100% functional? An argument based on the concept of mutational load
10:15	Takafumi Katsumura Okayama University/ Kitasato University School of Medicine Molecular mechanisms and evolutionary processes underlying genetic assimilation in the digestive tract of medaka			

SCIENTIFIC PROGRAM

10:30	<p>Bing Chen Institute of Zoology, Chinese Academy of Sciences</p> <p>Whole Genome Sequencing Reveals Metabolic Adaptation to High-Altitude Hypoxia in a Tibetan Locust</p>	<p>Liran Carmel The Hebrew University of Jerusalem</p> <p>Reconstructing Denisovan Anatomy Using DNA Methylation Maps</p>	<p>Tobias L Lenz Max Planck Institute for Evolutionary Biology</p> <p>Evolutionary trade-offs shape genomic diversity in the MHC</p>	<p>Lilach Hadany Tel Aviv University</p> <p>Selfish modifiers of recombination and mutation, their response to stress, and implications for evolvability</p>
10:45	<p>Toni Gossmann University of Sheffield</p> <p>Severe loss of genetic diversity due to cold-temperature adaptation in a progressively warming climate: the Alpine marmot genome</p>	<p>Dan Sun Georgia Institute of Technology</p> <p>Molecular evolution of a recombination suppressed avian autosome linked to alternative reproductive phenotype</p>		
11:00	<p>Alexander Nater University of Konstanz</p> <p>The importance and evolutionary dynamics of chromosomal inversions in sympatric Neotropical cichlid radiations</p>	<p>Shigehiro Kuraku RIKEN</p> <p>CTCF in early vertebrate evolution: lessons from jawless and cartilaginous fishes about its phylogeny and establishment of epigenomic functions</p>	<p>Alicia Sanchez-Mazas University of Geneva</p> <p>Differences in peptide-binding affinities among alleles: a key to understand the complex patterns of natural selection on HLA genes</p>	<p>Tobias Warnecke London Institute of Medical Sciences/Imperial College London</p> <p>An evolutionary lock-in event facilitates the persistence of self-splicing introns in <i>S. cerevisiae</i></p>
11:15	<p>Kentaro K. Shimizu University of Zurich</p> <p>Evolution of mating systems by a dominant mutation conferred epigenetically by a small RNA in the allopolyploid <i>Arabidopsis</i></p>	<p>Juliette de Meaux University of Cologne</p> <p>Robustness of Transposable Element regulation but no genomic shock observed in an interspecific <i>Arabidopsis</i> hybrid</p>	<p>Marta Barluenga Museo Nacional de Ciencias Naturales</p> <p>Host-parasite evolution and speciation in Neotropical cichlids</p>	<p>Ashley Irene Teufel The University of Texas at Austin</p> <p>Functional Shifts in Duplicated Genes via Specialization of Interacting Partners</p>

SCIENTIFIC PROGRAM

	SY03: Ecological genomics SESSION 2 Room 301 Polina Yu. Novikova, Daniele Filiault	SY24: Phylogenomics - genome-scale data and the methods and analyses for phylogeny construction and time estimation Room 302 Naoko Takezaki, Koichiro Tamura	SY20: Mapping genotype and phenotype to fitness Room 303 Sandeep Venkataram, Georg Rieckh	SY28: Selection on complex traits: reuniting quantitative and population genetics Room 304 Fernando Racimo, Jeremy Jackson Berg
12:30	Melissa H Pespeni University of Vermont Single generation selection experiments reveal adaptive loci in highly fecund, long-lived species	Jeffrey Peter Townsend Yale University Using equivalent information trees to maximize the power of taxon and gene sampling in phylogenetics and phylogenomics	Claudia Bank Instituto Gulbenkian de Ciencia What can we learn from experimental fitness landscapes?	Guy Sella Columbia University A population genetic interpretation of complex trait architecture in humans
13:00	Maud Tenaillon INRA - Université Paris-Sud - CNRS - AgroParisTech Genomic footprints of past selection at a local scale associate with present phenotypic variation in teosintes	Carolina Granados Mendoza Biology Institute, National Autonomous University of Mexico Enhanced phylogenetic resolution of three highly-diverse flowering plant lineages from the Neotropics using Anchored Hybrid Enrichment	Rowan Barrett McGill University An experimental test of the genomic consequences of local adaptation in deer mice	Anna V Kukekova University of Illinois in Urbana-Champaign Anterior pituitary transcriptome suggests differences in adrenocorticotrophic hormone release in tame and aggressive foxes
13:15	Sam Yeaman University of Calgary Detecting and interpreting the genomic basis of convergent local adaptation			
13:30	Maribet Gamboa Ehime University Genome-wide RAD-seq reveals adaptive divergence among seven stream stoneflies along a nationwide latitudinal gradient in Japan	Ziheng Yang University College London Bayesian species tree estimation under the multispecies coalescent	Galya V. Klink Institute for Information Transmission Problems (Kharkevich Institute) of the Russian Academy of Sciences Inference of changes of HIV-1 gp160 protein fitness landscape from sequence data with single-position resolution	Alessia Ranciaro University of Pennsylvania New Insights into the Genetic Basis and Evolutionary History of Lactase Persistence in Africa

SCIENTIFIC PROGRAM

13:45	<p>Yang Liu Shenyang Agricultural University</p> <p>Molecular data support an early shift to an intermediate-light niche in the evolution of mammals</p>	<p>Carolín Kosiol University of St Andrews/ Vetmeduni Vienna</p> <p>Genome-wide estimation of the evolutionary history of six baboon species with polymorphism-aware phylogenetic models</p>	<p>Elizabeth Hutton Cold Spring Harbor Laboratory</p> <p>Genotype-Fitness Mapping in Cancer Cell Lines using CRISPR-Cas9</p>	<p>Yassine Souilmi University of Adelaide</p> <p>Paleo-population genetics: Illuminating the role of selection in shaping human diversity</p>
14:00	<p>Kirk Lohmueller UCLA</p> <p>Elucidating the genetic basis of inbreeding depression by contrasting the California Channel Island fox with Isle Royale gray wolf</p>	<p>Andreas Zwick CSIRO</p> <p>Phylogenomics of Pancrustacea</p>	<p>Grant Kinsler Stanford University</p> <p>Uncovering the genotype-phenotype-fitness map of microbes adapting to novel environments</p>	<p>Leo Speidel University of Oxford</p> <p>Identifying natural selection by constructing genome-wide genealogies</p>
14:15	<p>Javier Prado-Martinez Wellcome Trust Sanger Institute</p> <p>Genomics of Bwindi mountain gorillas and conservation in eastern gorillas</p>	<p>Nadine Bernhardt Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)</p> <p>Genome-wide sequence information reveals multiple past hybridizations that shaped the ancestors of wheat</p>	<p>Silvia Busoms John Innes Centre, Norwich/Universitat Autònoma de Barcelona</p> <p>Population genomic, ecological and physiological roles for the sodium transporter <i>HKT1</i> in <i>Arabidopsis thaliana</i> populations adapted to fluctuating coastal habitats</p>	<p>Laura Katharine Hayward Columbia University</p> <p>Polygenic adaptation in response to a sudden change in the environment</p>
14:30	<p>Luke Dunning University of Sheffield</p> <p>Widespread adaptive lateral gene transfer in grasses</p>	<p>Robert Lanfear Australian National University</p> <p>Systematic error is ubiquitous, and frequently misleads phylogenetic inference</p>	<p>Sharon Ilana Greenblum Stanford University</p> <p>Parallelism of genomic response during rapid seasonal adaptation in <i>Drosophila melanogaster</i></p>	<p>Daniele Filiault Gregor Mendel Institute</p> <p>A dual field approach uncovers the complex genomics of local adaptation in Swedish <i>A. thaliana</i></p>
14:45	<p>Sarah Kocher Princeton University</p> <p>Harnessing natural variation to study the evolution of social behavior</p>	<p>Sebastian Hoehna LMU Munich</p> <p>Stepwise Bayesian Inference of Phylogeny using RevBayes</p>	<p>P. William Hughes Max Planck Institute for Plant Breeding Research/ University of Cologne</p> <p>Integrating functional genetics and demographic life history modelling: PERPETUAL FLOWERING 1 pleiotropically regulates flowering and seed traits in <i>Arabidopsis alpestris</i></p>	<p>Evan Koch University of Chicago</p> <p>The effects of demography and genetic architecture on the neutral distribution of quantitative traits</p>

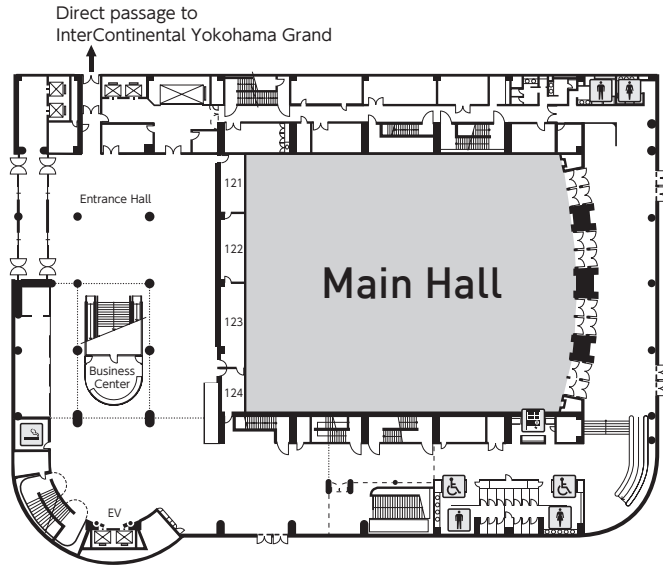
SCIENTIFIC PROGRAM

15:00	<p>Eriko Sasaki</p> <p>Gregor Mendel Institute of Molecular Plant Biology</p> <p>Global natural variation of DNA methylation and its genetic architecture in <i>Arabidopsis thaliana</i></p>	<p>Andre E Moura</p> <p>University of Lincoln</p> <p>Effects of site selection and data partitioning schemes in the phylogenomic inference of the sub-family Delphininae (Cetacea), a recent radiation with an elusive topology and inter-lineage reticulation</p>	<p>Christian D. Huber</p> <p>University of California, Los Angeles</p> <p>Gene Expression Drives the Evolution of Dominance</p>	<p>Emily S Wong</p> <p>The University of Queensland</p> <p>Evidence for stabilizing selection at pleiotropic loci for human complex traits</p>
15:15	<p>Yuki Haba</p> <p>Princeton University/ Columbia University</p> <p>The genomics of behavioral adaptation to photoperiodism in an Asian burying beetle</p>	<p>Ding He</p> <p>Uppsala University</p> <p>A new approach to model amino-acid compositional heterogeneity sheds new insight on the origin of mitochondria</p>	<p>Hunter Fraser</p> <p>Stanford</p> <p>Functional genetic variants revealed by massively parallel precise genome editing</p>	<p>Arun Durvasula</p> <p>University of California, Los Angeles</p> <p>Demography drives differences in the distribution of gene expression</p>

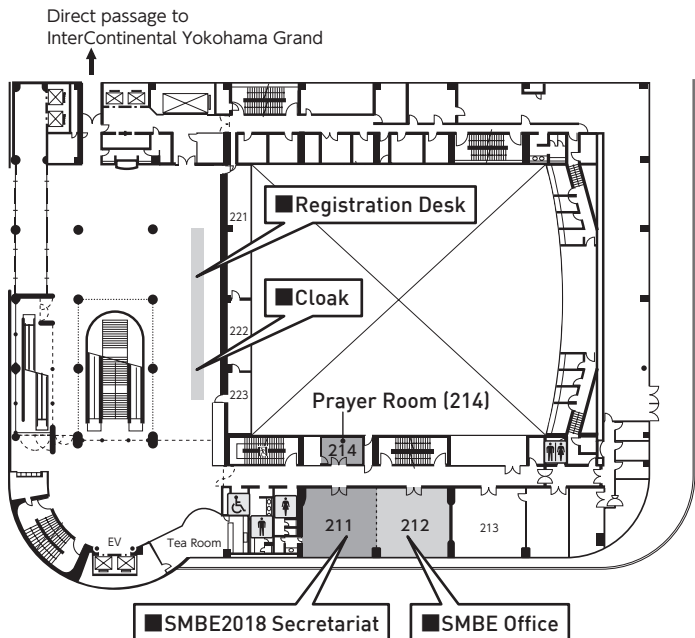
16:00	<p>Plenary 2 Anne C. Stone, Arizona State University</p> <p>Tracking a killer: using ancient DNA to understand the evolutionary history of tuberculosis</p>	Main Hall
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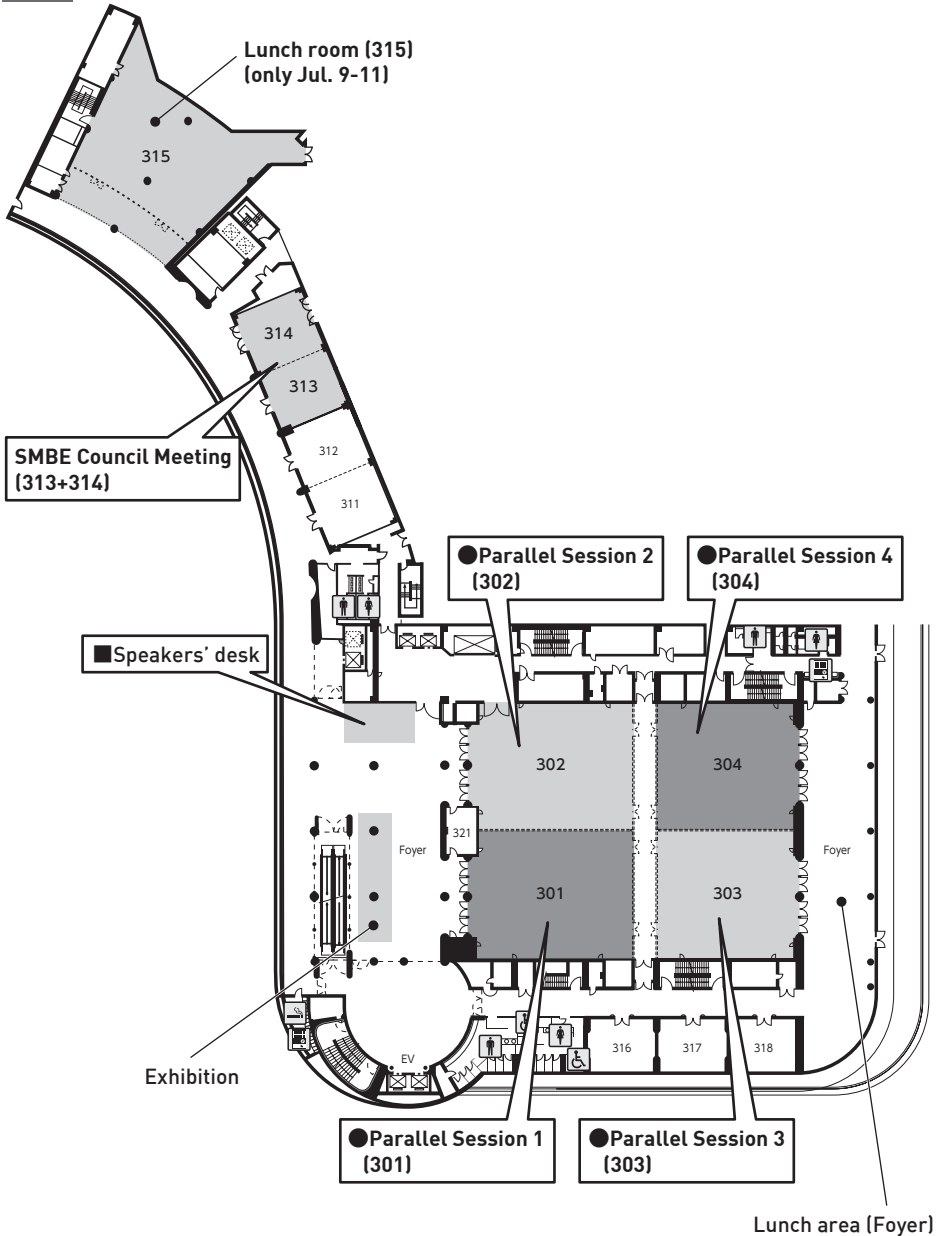


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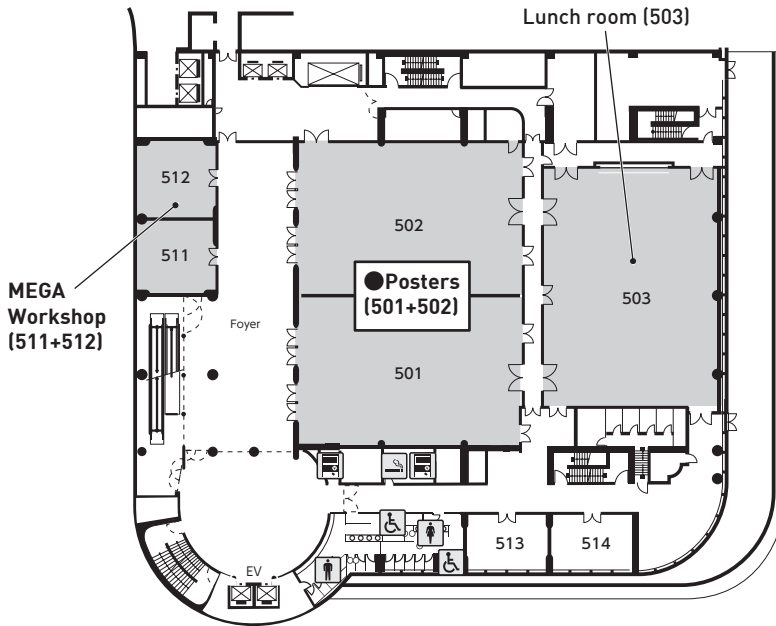
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3970 G T T C T T A T T A -

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