Complete List of Talks and Posters Presented at SMBE 2018

Presenting authors are marked with a *.

Talks

Masatoshi Nei Lecture

9:00-10:00, Monday, July 9

Main Hall

In search of microbe number one
William Martin

Plenary 1

9:00-10:00, Tuesday, July 10

Main Hall

Evolution of sequence-specific anti-silencing systems in Arabidopsis
Tetsuji Kakutani

Plenary 2

16:00-17:00, Thursday, July 12

Main Hall

Tracking a killer: using ancient DNA to understand the evolutionary history of tuberculosis
Anne C. Stone

Walter Fitch Symposium

10:00-12:00, Tuesday, July 10

Main Hall

O-02-WF01
Re-thinking a classic clinal trait: Pleiotropic consequences of thermally adaptive dopamine on pigmentation clines in Drosophila
Ana Marija Jaksic*, Viola Nolte, Neda Barghi, Francois Mallard, Kathrin Anna Otte, Lidija Svecnjak, Kirsten-Andre Senti, Christian Schlotterer

O-02-WF02
Antagonistic pleiotropy is rare among new mutations
Mrudula Sunil Sane*, Deepa Agashe

O-02-WF03
The mechanistic basis of epistatic variety in a metabolic pathway uncovered by high-resolution fitness interaction mapping
Harry Kemble*, Catherine Eisenhauer, Audrey Chapron, Melanie Magnan, Herve Le Nagard, Philippe Nghe, Olivier Tenaillon

O-02-WF04
Long-Term Evolution of Tetrahymena thermopila
Jason Tarkington*, Rebecca Zufall

O-02-WF05
The optimal mating distance resulting from heterosis and genetic incompatibility
Xinzhu Wei*, Jianzhi Zhang

O-02-WF06
KRAB-transposase fusion as a source of new regulatory proteins in evolution
Rachel Leigh Cosby*, Ellen Pritham, Cedric Feschotte

O-02-WF07
The impact of Neanderthal ancestry on human phenotypes
Christopher R Robles*, Andrea Ganna, Alexander Gusev, David Reich, Sriram Sankararaman

O-02-WF08
Archaic introgression and gene regulation: a disproportionate degree of Neanderthal ancestry in T-cells enhancers
Martin Silvert*, Maxime Rotival, Lluis Quintana-Murci

Symposium for the 50th Anniversary of the Neutral Theory of Molecular Evolution

16:00-18:30, Tuesday, July 10

Room 301

O-02-NTS01
Becoming Motoo Kimura
Daniel Hartl

O-02-NTS02
Epigenetics, Chromatin, Gene Activity and Near-Neutrality in Evolution
Tomoko Ohta

O-02-NTS03
My memories of Kimura and the neutral theory.
Warren Ewens

O-02-NTS04
New mathematical insights into the regulation and optimization of translation dynamics
Yun Song

SY01: Asian population genomics

12:30-14:30, Wednesday, July 11

Room 302

O-03-AP01
Northern Asian Genome Project
JEONG-SUN SEO*

O-03-AP02

High-coverage sequencing of diverse human populations in the HGDP-CEPH panel

Anders Bergstrom*, Shane A McCarthy, Ruoyun Hui, Qasim Ayub, Petr Danecek, Mohamed A Almarri, Javier Prado-Martinez, Yuan Chen, John A Kamm, Joshua Randall, Swapan Mallick, Pontus Skoglund, Manjinder S Sandhu, David Reich, Scally Aylwyn, Yali Xue, Richard Durbin, Chris Tyler-Smith

O-03-AP03

Back migrations of Southeast Asian ancestors to South Asia during the Last Glacial Maximum

Namrata Kalsi*, Stephan Schuster, Hie Lim Kim, The Genome Asia 100k consortium

O-03-AP04

Human population history in the southwestern coastal region of Sea of Okhotsk, inferred from ancient genome analysis

Takehiro Sato*, Noboru Adachi, Ryosuke Kimura, Minoru Yoneda, Hiroki Oota, Atsushi Tajima, Atsushi Toyoda, Hiromi Matsumae, Kae Koganebuchi, Kentaro K Shimizu, Tsunehiko Hanihara, Andrzej Weber, Hirofumi Kato, Hajime Ishida

O-03-AP05

Physiological and genetic adaptations to diving in Sea Nomads

Melissa Ilardo*, Ida Moltke, Thorfinn Korneliussen, Jade Cheng, Aaron Stern, Fernando Racimo, Peter de Barros Damgaard, Martin Sikora, Andaine Seguin-Orlando, Simon Rasmussen, Inge van den Munckhof, Rob ter Horst, Rasmus Nielsen, Eske Willerlsev

O-03-AP06

Evolutionary history and adaptation from whole-genome sequences of a pygmy population of Flores Island, Indonesia

Serena Tucci*, Sam H. Vohr, Rajiv C. McCoy, Benjamin Vernot, Matthew R. Robinson, Chiara Barbieri, Wenqing Fu, Gludhug A. Purnomo, Herawati Sudoyo, Guido Barbujani, Peter M. Visscher, Joshua M. Akey, Richard E. Green

O-03-AP07

Allele frequency of pathogenic variants in a Japanese population based on the whole-genome reference panel of ToMMo and inter-population differences

Yumi Yamaguchi-Kabata*, Jun Yasuda, Yoichi Suzuki, Nobuo Fuse, Hiroshi Kawame, Masao Nagasaki, Fumiki Katsuoka, Yosuke Kawai, Kaname Kojima, Takahiro Mimori, Nobuo Yaegashi, Kengo Kinoshita, Shigeo Kure, Masayuki Yamamoto

SY02: Associate Editors Symposium

10:30-12:30, Monday, July 9

Room 301

O-01-AE01

Insights into mutational pathways of biochemical adaptation using ancestral protein resurrection

Jay F Storz*, Xiaojia Zhu, Chandrasekhar Natarajan, Anthony Signore, Federico Hoffmann, Jeremy Tame, Fumin Lei, Angela Fago

O-01-AE02

An animal without aerobic cellular respiration

Dorothee Huchon*, Dayana Yahalomi, Sally Chang, Herve Philippe, Paulyn Cartwright, Jerri Bartholomew, Stephen Atkinson

O-01-AE03
Why panmictic bacterial species are rare
Daniel Falush*, Yujun Cui, Yang Chao

O-01-AE04
Epigenetic conservation of human duplicated genes associated to their transposable element neighborhood
Romain Lannes, Carene Rizzon, Emmanuelle Lerat*

O-01-AE05
Germline and somatic mutation rates in a single cell
Rebecca Zufall*

O-01-AE06
Polarization of ancestor relations reveals the order of traits in the evolution of cyanobacterial multicellularity
Katrin Hammerscmidt, Giddy Landan, Fernando Domingues Kuemmel Tria, Tal Dagan*

O-01-AE07
Evolution of mRNA editing and linear multipartite genome in mitochondria of calcaronean sponges
Dennis Lavrov*

O-01-AE08
Impact of feminizing Wolbachia endosymbionts on the evolution of a male heterogametic system of sex chromosomes (XY-XX)
Thomas Becking, Mohamed Amine Chebbi, Isabelle Giraud, Bouziane Moumen, Jean Peccoud, Clement Gilbert, Richard Cordaux*

SY03: Ecological genomics

Session 1

9:30-11:30, Thursday, July 12
Room 301

O-04-EG01
Biotic and abiotic influences on balancing selection in nature
Thomas Mitchell-Olds*, Julius Mojica, Lauren Carley, Baosheng Wang, Emily Chan, Nadeesha Perera, Carrie Olson-Manning

O-04-EG02
From Population Genomics to Mechanistic understanding: A possible role in adaptation to low calcium serpentine soils by Two Pore Channel 1
Sian M Bray*, Levi J Yant

O-04-EG03
Molecular mechanisms and evolutionary processes underlying genetic assimilation in the digestive tract of medaka
Takafumi Katsumura*, Suguru Sato, Kana Yamashita, Shoji Oda, Takashi Gakuhari, Shodai Tanaka, Tadashi Imai, Yasutoshi Yoshiura, Hirohiko Takeshima, Yasuyuki Hashiguchi, Hiroshi Mitani, Motoyuki Ogawa, Hideaki Takeuchi, Hiroki Oota

O-04-EG04

Whole Genome Sequencing Reveals Metabolic Adaptation to High-Altitude Hypoxia in a Tibetan Locust

Ding Ding, Guang-Jian Liu, Bing Chen*, Le Kang

O-04-EG05

Severe loss of genetic diversity due to cold-temperature adaptation in a progressively warming climate: the Alpine marmot genome

Toni Gossmann*

O-04-EG06

The importance and evolutionary dynamics of chromosomal inversions in sympatric Neotropical cichlid radiations

Alexander Nater*, Andreas F. Kautt, Axel Meyer

O-04-EG07

Evolution of mating systems by a dominant mutation conferred epigenetically by a small RNA in the allopolyploid Arabidopsis

Kentaro K. Shimizu*, Chow Lih Yew, Takashi Tsuchimatsu, Masaomi Hatakeyama, Rie Shimizu-Inatsugi, Shinsuke Yasuda, Seiji Takayama

Session 2

12:30-15:30, Thursday, July 12

Room 301

O-04-EG08

Single generation selection experiments reveal adaptive loci in highly fecund, long-lived species

Melissa H Pespeni*, Reid Brennan, April Garrett, Kaitlin Huber, Heidi Hargarten

O-04-EG09

Genomic footprints of past selection at a local scale associate with present phenotypic variation in teosintes

Natalia Martinez, Margaux-Alison Fustier, Jonas A Aguirre-Liguori, Helene Corti, Venon Antony, Fabrice Dumas, Falque Matthieu, Agnes Rousselet, Hannes Dittberner, Salvador Montes-Hernandez, Luis E Eguiarte, Yves Vigouroux, Domenica Manicacci, Maud Tenaillon*

O-04-EG10

Detecting and interpreting the genomic basis of convergent local adaptation

Sam Yeaman*, Michael Whitlock, Aleeza Gerstein, Kathryn Hodgins

O-04-EG11

Genome-wide RAD-seq revels adaptive divergence among seven stream stoneflies along a nationwide latitudinal gradient in Japan

Maribet Gamboa*, Kozo Watanabe

O-04-EG12

Molecular data support an early shift to an intermediate-light niche in the evolution of mammals

Yang Liu*, Hai Chi, Longfei Li, Stephen J Rossiter, Shuyi Zhang

O-04-EG13
Elucidating the genetic basis of inbreeding depression by contrasting the California Channel Island fox with Isle Royale gray wolf
Jacqueline Robinson, Robert Wayne, Kirk Lohmueller*

O-04-EG14
Genomics of Bwindi mountain gorillas and conservation in eastern gorillas
Javier Prado-Martinez*, Qasim Ayub, Michael Andrew Quail, Steven Leonard, Yong Gu, Ruben Bautista, Irene Lobon, Sojung Han, Tomas Marques-Bonet, Michael Cranfield, Chris Tyler-Smith, Yali Xue

O-04-EG15
Widespread adaptive lateral gene transfer in grasses
Luke Dunning*

O-04-EG16
Harnessing natural variation to study the evolution of social behavior
Sarah Kocher*

O-04-EG17
Early environmental changes and metabolism evolution
Anne Oudart*, Celine Brochier-Armanet

O-04-EG18
The genomics of behavioral adaptation to photoperiodism in an Asian burying beetle
Yuki Haba*, Hsiang-Yu Tsai, Sheng-Feng Shen, Dustin Rubenstein

SY04: Evolution of adaptive immunity and MHC genes

9:30-11:30, Thursday, July 12
Room 303

O-04-EA01
Evolution of adaptive immunity
Masanori Kasahara*

O-04-EA02
Generalists Versus Specialists: A New View Of How MHC Molecules Respond To Infectious Pathogens
Jim Kaufman*

O-04-EA03
Evolutionary trade-offs shape genomic diversity in the MHC
Tobias L Lenz*

O-04-EA04
Differences in peptide-binding affinities among alleles: a key to understand the complex patterns of natural selection on HLA genes
Da Di, Thomas Goeury, Jose Manuel Nunes, Alicia Sanchez-Mazas*

O-04-EA05
Host-parasite evolution and speciation in Neotropical cichlids
Marta Barluenga*

SY05: Evolution of non-coding RNAs and their regulatory networks

10:30-12:30, Monday, July 9
Room 304

O-01-EN01
The PIWI-piRNA Pathway Targets Transposons in Hydra Somatic Stem Cells
Celina Juliano*, Bryan Teefy, Stefan Siebert, Jack Cazet

O-01-EN02
Small RNA Pathways In Arthropods
Eric Miska*

O-01-EN03
microRNAs in the Same Clusters Evolve to Coordinately Regulate Functionally Related Genes
Yirong Wang*, Junjie Luo, Hong Zhang, Jian Lu

O-01-EN04
Noncoding-RNA mediated epigenetics in the ciliate Oxytricha
Laura Landweber*

O-01-EN05
First evidence for HEN1 mediated methylation of miRNAs in animals, and the functional importance of small RNA stabilization in cnidarians
Arie Fridrich*, Vengamanaidu Modepalli, Yehu Moran

O-01-EN06
Prevalent selection against microRNA target sites in human populations
Andrea Hatlen, Antonio Marco*

SY06: Evolutionary epigenomics, progress and prospects

9:30-11:30, Thursday, July 12
Room 302

O-04-EE01
The evolution of gene body methylation in plant species.
Takuno Shohei*

O-04-EE02
Epigenetic variation and regulation of imprinted gene expression
Mary Gehring*

O-04-EE03
Reconstructing Denisovan Anatomy Using DNA Methylation Maps
David Gokhman, Nadav Mishol, Marc de Manuel Montero, David de Juan, Jonathan Shuqrun, Tomas Marques-Bonet, Yoel Rak, Liran Carmel*

O-04-EE04
Molecular evolution of a recombination suppressed avian autosome linked to alternative reproductive phenotype
Dan Sun*, Iksoo Huh, Paramita Chatterjee, Wendy M. Zinzow-Kramer, Donna L. Maney, Soojin V. Yi

O-04-EE05

CTCF in early vertebrate evolution: lessons from jawless and cartilaginous fishes about its phylogeny and establishment of epigenomic functions

Mitsutaka Kadota, Yuichiro Hara, Kazuaki Yamaguchi, Osamu Nishimura, Shigehiro Kuraku*

O-04-EE06

Robustness of Transposable Element regulation but no genomic shock observed in an interspecific Arabidopsis hybrid

Juliette de Meaux*, Ulrike Goebel

SY07: Evolutionary genomics of the human brain

13:30-15:30, Monday, July 9

Room 304

O-01-EG01

Metabolites and lipids of the human brain: evolution and function.

Philipp Khaitovich*

O-01-EG02

Evolution of human-specific gene co-expression networks

Genevieve Konopka*

O-01-EG03

The evolutionary trajectory of spatial transcriptome and epigenome in primate brains

Chuan Xu, Qian Li, Olga Efimova, Liu He, Shoji Tatsumoto, Philipp Khaitovich, Yasuhiro Go*

O-01-EG04

Functional studies in 2D and 3D stem cell systems of candidate genes underlying human-specific features of cerebral cortex development

Alessio Strano*, Tomoki Otani, Jocelyn Tang, Irene Gallego Romero, Rick Livesey

O-01-EG05

Big Brains: What High-Throughput Enhancer Knockouts Reveal about Human Cortical Evolution

Evan Geller*, James Noonan

O-01-EG06

Single-cell transcriptional signatures of the aging nonhuman primate brain

Kenneth L Chiou*, Alex R DeCasien, Michael J Montague, Chet C Sherwood, Michael L Platt, Noah Snyder-Mackler

SY08: 50 years since Ohno's genome duplication: integration across disciplines and time scales

16:00-18:30, Tuesday, July 10

Room 303

O-02-50Y01

The evolutionary significance of polyploidy

Yves Van de Peer*

O-02-50Y02
The evolution of meiosis in autotetraploid Arabidopsis arenosa
Kirsten Bomblies, Clare Henry*

O-02-50Y03
Genomic hotspots of adaptation to whole genome duplication
Levi Yant*

O-02-50Y04
Genome restructuring during early vertebrate evolution
Yoichiro Nakatani*, Aoife McLysaght

O-02-50Y05
Genome stabilization mechanisms in early post-polyploidization evolution
Sira Sriswasdi*, Wataru Iwasaki

O-02-50Y06
Adaptation to the whole genome duplications in Australian burrowing frogs Neobatrachus
Polina Yu. Novikova*, Stephen C. Donnellan, Yves Van de Peer, Levi Yant

O-02-50Y07
Comparative Analysis Between Allopolyploid *Arabidopsis kamchatica* And Its Diploid Progenitors Reveals Effects Of Polyploidy On Genetic Diversity And Selection
Gwyneth Halstead-Nussloch*, Timothy Paape, Kentaro Shimizu

SY09: Gene flow detection and dating methods

13:30-15:30, Monday, July 9
Room 303

O-01-GF01
Methods to characterize geographic structure in genetic variation
John Novembre*, Hussein Al-asadi, Ben Peter

O-01-GF02
Efficient representations of local trees in Coalescent Hidden Markov models for demographic inference
Matthias Steinruecken*, Alexey Miroshnikov, Gautam Upadhya

O-01-GF03
Detecting unknown introgressed archaic haplotypes in modern and ancient human genome sequences
Laurits Skov*, Ruoyun Hui, Asger Hobolth, Aylwyn Scally, Mikkel Heide Schierup, Richard Durbin

O-01-GF04
Assessing population structure through time using ancient DNA
Lindsey Fenderson*, Bastien Llamas, Julien Soubrier, Alan Cooper

O-01-GF05
Native American Genetic History Through Admixed Brazilians
Alex Mas-Sandoval*, Lara R Arauna, Eduardo Tarazona-Santos, Maria Catira Bortolini, David Comas

O-01-GF06
Reconstructing and dating gene flow using efficient haplotype-based techniques
Garrett Hellenthal*

SY10: Genetic conflict and speciation

13:30-15:30, Monday, July 9
Room 302

O-01-GC01
Conflict and speciation: do empirical data support a role for conflict in the isolation of plant species?
Leonie Moyle*

O-01-GC02
Genetic conflict and speciation in Drosophila
Nitin Phadnis*

O-01-GC03
Rapid evolution leads to rapid onset of centromeric histone incompatibility in Drosophila
Emily Coelho, Aida Flor de la Cruz, Benjamin D. Ross, Harmit Singh Malik*

O-01-GC04
Comparative genomics reveals rampant gene duplication and reorganization of the Drosophila melanogaster and the simulans clade Y chromosomes
Ching-Ho Chang*, Colin Meiklejohn, Taylar Mouton, Amanda Larracuente

O-01-GC05
Allorecognition loci act as speciation genes in Podospora anserina
S. Lorena Ament-Velasquez*, Aaron Vogan, Corinne Clave, Eric Bastiaans, Jesper Svedberg, Suzette de Groot, Alfons Debets, Sven J. Saupe, Hanna Johannesson

O-01-GC06
Evolution-guided mutagenesis to understand antiviral protein function
Rossana Colon-Thillet*, Emily Hsieh, Maria Gutierrez , Richard McLaughlin, Harmit Singh Malik, Michael Emerman

SY11: Genomic underpinnings of primate phenotypic evolution and diversity

9:30-11:30, Wednesday, July 11
Room 302

O-03-GU01
Molding the genome with LAVA: Exploring functional roles of a gibbon-specific retrotransposon
Lucia Carbone, Pryce Michener, Kimberly A Nevonen, Brett Davis, Jeff D Wall, Mariam Okhovat*

O-03-GU02
Variant discovery and consequence in the genomes of a bottlenecked vervet population
Vasily Ramensky, Anna J Jasinska, Susan K Service, Richard K Wilson, Mark Cline, Jay R Kaplan, Matthew J Jorgensen, Nelson B Freimer, Wesley C Warren*

O-03-GU03
Population genomics of white faced capuchin monkeys (Cebus capucinus imitator) with unbiased fecal genomes
Joseph Orkin*, Mike Montague, Aoifie Doherty, J. Pedro Magalhaes, Wes Warren, Shoji Kawamura, Tomas Marques-Bonet, Amanda Melin

O-03-GU04
Genomic signatures of high altitude adaptation in gelada monkeys (Theropithecus gelada)
Noah Snyder-Mackler*, Kenneth Chiou

O-03-GU05
Duplication and Convergent Evolution of the Pancreatic Ribonuclease Gene (RNASE1) in a Non-Colobine Primate, the Mantled Howler Monkey (Alouatta palliata)
Mareike Cora Janiak*, Andrew S Burrell, Todd R Disotell

O-03-GU06
Ancient proteins and the thrifty gene hypothesis: Uric acid's contribution to primate evolution
Jennifer E. Farrar*, Lily Tran, Eric A. Gaucher

SY12: Genomics and evolution of symbiotic interactions

10:30-12:30, Monday, July 9
Room 302

O-01-GE01
The genome of *Paulinella* reveals pathways of plastid integration
Debashish Bhattacharya*, Hwan Su Yoon, Udi Zelzion, Dana C Price, Eva Nowack, Duckhyun Lhee

O-01-GE02
Experimental evolution of an insect-bacterium symbiotic association
Takema Fukatsu*

O-01-GE03
Genomic hijacking - how parasitic worms manipulate their hosts
Eddy Dowle*, Robert Poulin, Robert Day, Neil Gemmell

O-01-GE04
Comparative genomics reveals the distinct evolutionary trajectories of the robust and complex coral lineages
Hua Ying, Ira Cooke, Susanne Sprungala, Weiwen Wang, David Charles Hayward, Yurong Tang, Gavin Huttley, Eldon Edward Ball, David John Miller*

O-01-GE05
Rapid evolution of host dependence on environmentally acquired microbes
Aparna Agarwal, Deepa Agashe*

O-01-GE06
The genome study of Apophlaea lyallii (Florideophyceae, Rhodophyta) provides new insights for the algal-fungal symbiotic relationship
Hwan Su Yoon*, Chung Hyun Cho, Wendy Nelson

SY13: Human evolution after out-of-Africa

15:00-17:00, Wednesday, July 11
Room 302

O-03-HE01
ANCESTRAL AND ADMIXTURE HISTORIES IN THE INDIAN SUBCONTINENT
Partha P Majumder*

O-03-HE02
Reconstructing the human population history of Africa
Brenna M Henn*

O-03-HE03
Genome wide analysis of negrito groups in Southeast Asia
Timothy Jinam*, Naruya Saitou

O-03-HE04
Human prehistoric demography revealed by polymorphic pattern of CpG transitions
Xiaoming Liu*

O-03-HE05
'Mother' tongues? A global study of sex-biased genetic and linguistic transmission after Out-of-Africa
Nicole Creanza*, Alexandra Surowiec

O-03-HE06
Population Genomic Inference from Palaeo-Neutralomes of Mediaeval Germans
Joachim Burger*, Michaela Harbeck, Krishna R. Veeramah

SY14: Improving inference frameworks by accounting for population structure

16:00-18:00, Monday, July 9
Room 303

O-01-II01
Modeling the interaction between population structure and selection
Sohini Ramachandran*, Lauren Alpert Sugden, Michael C Turchin

O-01-II02
Mechanistic models of social processes impacting admixture
Amy Goldberg*

O-01-II03
Whole-genome hierarchical population structure analysis using network-based clustering
Gili Greenbaum*, Amir Rubin, Ellie Armstrong, Alan R. Templeton, Noah Rosenberg

O-01-II04
Introgression of a Y chromosome haplotype into a neo-Y karyotype in Rumex
Felix E.G. Beaudry*, Stephen I. Wright

O-01-II05
Distinction between ancient introgression and incomplete lineage sorting in modern human genomes
Makoto Shimada*

O-01-II06
Genetic risk prediction across diverse populations
Alicia R Martin*, Patrick Turley, Hailiang Huang, Raymond K Walters, Chia-Yen Chen, Max Lam, Duncan Palmer, Christopher R Gignoux, Eimear E Kenny, Benjamin M Neale, Mark J Daly

SY15: Integrating ancient and modern DNA for evolutionary genomics

13:30-15:30, Tuesday, July 10
Room 301

O-02-IA01
Understanding the structure and function of archaic ancestry in present-day humans
Sriram Sankararaman*

O-02-IA02
Using archaic introgression to infer sequence constraints that are shaping human enhancer evolution
Natalie Telis, Kelley Harris*

O-02-IA03
No Evidence for Protracted Selection Against Neandertal Alleles in Humans
Benjamin Vernot*, Martin Petr, Svante Paabo, Janet Kelso

O-02-IA04
Herbarium genomics infers the changes underlying the evolution of C4 photosynthesis in the Andropogoneae grasses
Matheus Bianconi*, Jan Hackel, Alexandre Meunier, Maria Vorontsova, Pascal-Antoine Christin, Guillaume Besnard

O-02-IA05
Tracking plant phenology and genetic diversity during environmental change using contemporary and historical samples
Patricia L.M. Lang*, Franziska M. Willems, Oliver Bossdorf, Hernan A. Burbano

O-02-IA06
Selection trajectories of genetic variants underlying domestic animal traits
Evan K. Irving-Pease*, Laurent A. F. Frantz, Greger Larson, Joshua G. Schraiber

SY16: Intra-host evolutionary dynamics

9:30-11:30, Wednesday, July 11
Room 303

O-03-IH01
The evolutionary dynamics of untreated HIV and the maintenance of the latent reservoir
Fabio Zanini, Jan Albert, Richard Neher*

O-03-IH02
Quantifying the evolutionary dynamics of tumor progression and metastasis
Christina Curtis*

O-03-IH03

The impact of biodiversity on phage immunity and virulence in Pseudomonas aeruginosa

Ellinor Opsal Alseth*, Ellie Pursey, Angus Buckling, Edze Westra

O-03-IH04

Selection and clonal interference in B-cell repertoire response to HIV-1 infection

Armita Nourmohammad*, Marta Luksza, Thierry Mora, Jakub Otwinowski, Aleksandra Walczak

O-03-IH05

Vibrio cholerae genomic diversity within and between patients

Ines Levade*, Yves Terrat, Jean-Baptiste Leducq, Ana A. Weil, Jason Harris B., Regina C. LaRocque, Firdausi Qadri, Jesse B. Shapiro

O-03-IH06

Within-host evolutionary dynamics of dengue virus in its mosquito vector Aedes aegypti

Sebastian Lequime*, Vaea Richard, Albin Fontaine, Meriadeg Ar Gouilh, Isabelle Moltini-Conclois , Van-Mai Cao-Lormeau , Louis Lambrechts

SY17: Linking the mitochondrial genotype to phenotype: a complex endeavour

12:30-14:30, Wednesday, July 11

Room 303

O-03-LM01

The function of genomes in bioenergetic organelles

John Allen*

O-03-LM02

Transmission of mitochondrial heteroplasmy across multigenerational pedigrees

Kateryna Makova*, Arslan Zaidi, Peter Wilton, Kate Anthony, Barbara Arbeithuber, Marcia Su, Anton Nekrutenko, Rasmus Nielsen

O-03-LM03

Role of competition and Ne in the maintenance of heteroplasmic, selfishly acting mitochondrial mutations in Caenorhabditis elegans

Joseph Dubie*, Vaishali Katju, Ulfar Bergthorsson

O-03-LM04

Direct Estimates of Mitochondrial Mutation Rates Across Genotypes and Populations in Daphnia

Fenner Macrae, Leigh Latta IV, Maia Benner, Dieter Ebert, Sarah Schaack*

O-03-LM05

Mitochondrial genomics of exceptional longevity in bats

David Jebb*, Nicole M Foley, Conor V Whelan, Gareth Jones, Roger D Ransome, Gerald Kerth, Sebastien J Puechmaille, Emma C Teeling

O-03-LM06

Climate-related Mitochondrial Lineages Correlate with Functional Differences in Energy Utilisation

Stephanie Falk*, Paul Sunnucks, Alexandra Pavlova, Craig White, Antoine Stier

SY18: Looking beyond the genome: cultural and behavioral drivers of biological evolution

9:30-11:30, Wednesday, July 11
Room 304

O-03-LB01
Cultural traits that shape genetic diversity: a case study in Inner Asia
Evelyne Heyer*, Laure Segurel, Nina Marchi, Tatyana Hegay

O-03-LB02
The evolutionary consequences of sociality and culture: is there gene-culture interaction in non-human animals?
Susanne Shultz*

O-03-LB03
Ancient Genomic Diversity Reveals Differences in Cultural Practices and Cultural Barriers between Prehistoric Farmers and Hunter-gatherers in Europe
Zuzana Hofmanova*, Vivian Link, Ilektra Schulz, Jens Bloecher, Laura Winkelbach, Sofija Stefanovic, Joachim Burger, Daniel Wegmann

O-03-LB04
Complex human histories of Northeast Asia revealed by correlations between genes, language, and music
Hiromi Matsumae*, Patrick E Savage, Balthasar Bickel, Thomas E Currie, Takahiro Sato, Atsushi Tajima, Mark Stoneking, Kentaro K Shimizu, Matt Gillan, Steven Brown, Hiroki Oota

O-03-LB05
The Genomics of Megaliths: An Irish case study into the reconstruction of prehistoric societal landscapes through ancient DNA analysis
Lara M Cassidy*

O-03-LB06
Waves of history in Remote Oceania: language continuity despite population replacement in Vanuatu
Cosimo Posth*, Kathrin Naegele, Heidi Colleran, Frederique Valentin, Stuart Bedford, Kaitip W Kami, Johannes Moser, Julia Gresky, Fiona Petchey, Patrick Roberts, Choongwon Jeong, Russell Gray, Johannes Krause, Adam Powell

SY19: Machine learning approaches in evolutionary genetics

13:30-15:30, Tuesday, July 10
Room 303

O-02-ML01
Supervised learning for analyzing large-scale genome-wide DNA polymorphism data
Ziqian Hao, Haipeng Li*

O-02-ML02
New methods for measuring natural selection and predicting deleterious variants in the human genome.
Adam Siepel*

O-02-ML03

Real-time Phenotype Prediction From Unaligned Whole Genome Sequencing Data Using Deep Learning

Will Landecker, Samuel V Scarpino*

O-02-ML04

A Machine-Learning Approach for Phylogenetic Model Selection

Shiran Abadi*, Dana Azouri, Tal Pupko, Itay Mayrose

O-02-ML05

Statistical inference frameworks for detecting adaptive evolution of variants and genes

Lauren A Sugden*, Elizabeth G Atkinson, Annie P Fischer, Stephen Rong, Brenna M Henn, Sohini Ramachandran

O-02-ML06

A Likelihood-Free Inference Framework for Population Genetic Data using Permutation-Invariant Neural Networks

Sara Sheehan Mathieson*, Jeffrey Chan, Valerio Perrone, Jeffrey P. Spence, Paul A. Jenkins, Yun S. Song

SY20: Mapping genotype and phenotype to fitness

12:30-15:30, Thursday, July 12

Room 303

O-04-MG01

What can we learn from experimental fitness landscapes?

Claudia Bank*

O-04-MG02

An experimental test of the genomic consequences of local adaptation in deer mice

Rowan Barrett*, Stefan Laurent, Riccardo Mallarino, Charles Xu, Susanne Pfeifer, Jean-Marc Lassance, Jeffrey Jensen, Hopi Hoekstra

O-04-MG03

Inference of changes of HIV-1 gp160 protein fitness landscape from sequence data with single-position resolution

Galya V. Klink*, Georgii A. Bazykin

O-04-MG04

Genotype-Fitness Mapping in Cancer Cell Lines using CRISPR-Cas9

Elizabeth Hutton*, Xiaoli Wu, Yuhan Huang, Sofya Polyanskaya, Bin Lu, Timothy Somerville, Yusuke Tarumoto, Yali Xu, Christopher Vakoc, Adam Siepel

O-04-MG05

Uncovering the genotype-phenotype-fitness map of microbes adapting to novel environments

Grant Kinsler*, Kerry Geiler-Samerotte, Dmitri Petrov

O-04-MG06

Population genomic, ecological and physiological roles for the sodium transporter *HKT1* in *Arabidopsis thaliana* populations adapted to fluctuating coastal habitats

Silvia Busoms*, Charlotte Poschenrieder, David Salt, Levi Yant

O-04-MG07
Parallelism of genomic response during rapid seasonal adaptation in Drosophila melanogaster
Sharon Ilana Greenblum*, Alan Bergland, Seth Rudman, Subhash Rajpurohit, Paul Schmidt, Dmitri Petrov

O-04-MG08
Integrating functional genetics and demographic life history modelling: PERPETUAL FLOWERING 1 pleiotropically regulates flowering and seed traits in Arabis alpina
P. William Hughes*, Wim J.J. Soppe, Maria Albani C.

O-04-MG09
Gene Expression Drives the Evolution of Dominance
Christian D. Huber*, Arun Durvasula, Angela M. Hancock, Kirk E. Lohmueller

O-04-MG10
Functional genetic variants revealed by massively parallel precise genome editing
Eilon Sharon, Shi-An Chen, Neil Khosla, Justin Smith, Jonathan Pritchard, Hunter Fraser*

SY21: Microbial evolution: human-microbe interactions and the role of deep sequencing in time series analysis

12:30-14:30, Wednesday, July 11
Room 304

O-03-ME02
Episodic convergent evolution drives dynamic history of passage adaptation and vaccine efficacy in the H3N2 influenza virus
Weiwei Zhai*, Hui Chen, Jacob Alvarez, Sock Hoon Ng, Rasmus Nielsen

O-03-ME03
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
Julio Felix Diaz Caballero*, Shawn T Clark, Pauline W Wang, Sylva L Donaldson, D Elizabeth Tullis, Yvonne CW Yau, Valerie J Waters, David M Hwang, David S Guttman

O-03-ME04
Consequences of European arrival on the microbiota of ancient Native Americans
Laura S Weyrich*, Keith Dobney, Lars Fehren-Schmitz, Wolfgang Haak, Bastien Llamas, Alan Cooper

O-03-ME05
Adaptive landscape and evolutionary history of the multidrug resistant W148 Russian clone
Thierry WIRTH*, Maxime BARBIER, Philip SUPPLY, Matthias MERKER, Stefan NIEMANN

O-03-ME06
MMC-ABC: Inference of population genetic parameters from time-sampled allele frequency data in populations with sweepstakes reproduction
Andrew Sackman*, Jeffrey Jensen

O-03-ME07
Colliding histories and opposing forces: ancient DNA of vaccination and smallpox
Ana Duggan*, Jennifer Klunk, Ashleigh Porter, Anna Dhody, Robert Hicks, Edward Holmes, Hendrik Poinar

O-03-ME08
The evolution of pathobiology in the genus Acinetobacter
Bardya Djahanschiri*, Sachli Zafari, Ruben Iruegas Lopez, Adrian Podolski, Ingo Ebersberger

SY22: Molecular bases of the different forms of flowers on plants of the same species

16:30-18:30, Tuesday, July 10
Room 304

O-02-MB01
Diversification of sexual system: insights from the persimmon genome
Takashi Akagi*

O-02-MB02
Characterisation of the S locus that controls heterostyly in Primula
Philip Gilmartin*, Jinhong Li, Jonathan Cocker, Calum Raine, Yasuko Yoshida, Cock van Oosterhout

O-02-MB03
Identification of genes at the S-locus controlling heteromorphic self-incompatibility in buckwheat through genetic and genomic analyses
Yasuo Yasui*, Nobuyuki Mizuno, Jotaro Aii, Tatsuya Ota

SY23: Open Symposium

Session 1

13:30-15:30, Monday, July 9
Room 301

O-01-OS01
Whole genome integration of giant virus to chlorella and its implication to the evolution of giant virus and the symbiosis of chlorella and ciliates
Atsushi Ogura*, Ryuhei Minei, Yoshino Murase, Ryo Hoshina

O-01-OS02
Estimating a time tree of the Australian radiation of Eugongylus group lizards by applying StarBEAST2 to a genome-scale data set
Huw Ogilvie*, Jason Bragg, Ana Afonso Silva, Mozes Blom, Sally Potter, Craig Moritz

O-01-OS03
Diversity and fitness impacts of extracellular vs. intracellular bacterial associates of butterflies
Kruttika Phalnikar*, Krushnamegh Kunte, Deepa Agashe

O-01-OS04
Drivers of genome reduction in free-living marine bacteria
Haiwei Luo*

O-01-OS05

Implications of population structure for site frequency spectra

Marcy Uyenoyama*, Seiji Kumagai, Naoki Takebayashi

O-01-OS06

Developmental delay caused by mitochondrial replacement reveals co-evolutionary divergence of nuclear and mtDNA

Xu Wang*, Ting Li, Rachel Edwards, John H. Werren

O-01-OS07

Drift robustness and the evolution of genome architecture in small populations

Thomas LaBar*, Christoph Adami

O-01-OS08

Weak selection primes non-coding sequences for de novo evolution

Luke Kosinski*, Joanna Masel

Session 2

16:00-18:00, Monday, July 9

Room 301

O-01-OS09

Retrotransposons spread potential sources of cis-regulatory elements for mammary gland evolution

Hidenori Nishihara*

O-01-OS10

A large fraction of paralogous genes is not free to diverge independently due to molecular interference

Christian Landry*, Axelle Marchant, Lou Nielly-Thibault, Yacine Seffal, Angel Cisneros

O-01-OS11

A reassessment of evolutionary impact of genomic structural variation

Omer Gokcumen*

O-01-OS12

Phylogenomics and comparative genomics of Palaeognathous birds reveal Palaeognath evolutionary history and ZW sex chromosome evolution

Zongji Wang*, Jilin Zhang, Guojie Zhang, Qi Zhou

O-01-OS13

Cavefish Metabolic Adaptation: Hungry, Fat, and Healthy

Nicolas Rohner*

O-01-OS14

Recombination Hotspots and Imprinted Genes in Indigenous African Cattle

Kelsey Caetano-Anolles*, Taehyung Kwon, Heebal Kim

O-01-OS15

A comprehensive lipidome map of human brain

Ekaterina Khrameeva*, Waltraud Mair, Anna Tkachev, Patricia Guijarro, Ilia Kurochkin, Olga Efimova, Aleksandra Mitina, Dmitry Zubkov, Philipp Khaitovich

O-01-OS16
To be determined

Session 3

9:30-11:30, Wednesday, July 11
Room 301

O-03-OS01
A comprehensive map of genetic variation in the world's largest ethnic group - Han Chinese
Charleston W.K. Chiang*, Serghei Mangul, Christopher R. Robles, Warren W. Kretzschmar, Na Cai, Kenneth S. Kendler, Sriram Sankararam, Jonathan Flint

O-03-OS02
Whole genome analysis of the Jomon remain reveals deep lineage of East Eurasian populations
Takashi Gakuhari*, Martin Sikora, Simon Rasmussen, Morten Allentoft, Takehiro Sato, Thorfinn Korneliussen, Minoru Yoneda, Hajime Ishida, Yasuhiro Yamada, Hiroki Shibata, Shigeki Nakagome, Eske Willerslev, Hiroki Oota

O-03-OS03
Divergent mitochondrial phenotypes associated with the Doubly Uniparental Inheritance (DUI) of mitochondria
Stefano Bettinazzi*, Liliana Milani, Enrique Rodriguez, Pierre Blier, Sophie Breton

O-03-OS04
Molecular clocks on Chelicerata suggest an early colonization of land by arachnids and support the monophyly of mites
Davide Pisani*, Alastair R. Tanner, Jakob Vinther, Gregory R. Edgecombe, Jesus Lozano-Fernandez

O-03-OS05
DNA repair in bdelloid rotifers: genome dynamics
Karine Van Doninck*, Matthieu Terwagne, Boris Hespeels, Bernard Hallet

O-03-OS06
Canceled

O-03-OS07
The molecular determinants of pheromone divergence and their role in the evolution of reproductive isolation in orchid bees
Philipp Brand*, Thomas Eltz, Santiago Ramirez

O-03-OS08
Fifty years of Neutral Theory: Past, Present and Future Perspective
Antonio Barbadilla*, Sonia Casillas

Session 4

12:30-14:30, Wednesday, July 11

Room 301

O-03-OS09
The *E. coli* translation machinery evolves towards minimal total mass concentration at the required protein production rate
Xiao-Pan Hu*, Hugo Dourado, Martin J. Lercher

O-03-OS10
Phenotypic and genomic changes involved in cross-species transmission and emergence of a zoonotic virus
Roman Biek*, Nardus Mollentze, Daniel Streicker, Katie Hampson, Pablo Murcia, Denise Marston, Anthony Fooks

O-03-OS11
: A GENOMIC TIMELINE FOR THE EVOLUTION AND DIVERSIFICATION OF SEA SPIDERS (ARTHROPODA: PYCNOGONIDA)
Jesus A Ballesteros*, Claudia P Arango, Georg Brenneis, Prashant P Sharma

O-03-OS12
A Path Integral Method for Analytically Tractable Inference of Evolutionary Dynamics
John P. Barton*, Raymond H. Y. Louie, Matthew R. McKay, Muhammad S. Sohail

O-03-OS13
The thermodynamical roots of pair-wise epistasis in alpha helix of beta-lacatamse TEM-1
Andre Birgy, Harry Kemble, Jimmy Mullaert, Herve Jacquier, Olivier Tenaillon*

O-03-OS14
Using transcriptomics to study hibernation in a natural primate population.
Jose Luis Villanueva-Canas*, Sheena Lee Faherty, Marina Blanco, M. Mar Alba, Anne Diane Yoder

O-03-OS15
Insights into the population history of the "Hidden Ones": From oral history to genome-wide analysis
Hiba Babiker*, Abbie Hantgan, Johann-Mattis List, Jeffrey Heath, Russell Gray

O-03-OS16
Sex Differences in Reference Genome Affect Variant Calling and Differential Expression
Melissa A. Wilson Sayres*

Session 5

15:00-17:00, Wednesday, July 11

Room 301

O-03-OS17
Towards more accurate phylogenomic inference using IQ-TREE
Bui Quang Minh*, Olga Chernomor, Stephen Crotty, Heiko Schmidt, Diep Thi Hoang, Le Sy Vinh, Lars Jermiin, Huai-Chun Wang, Edward Susko, Andrew Roger, Arndt von Haeseler

O-03-OS18
Inadvertent paralog inclusion impacts phylogenomic relationships and timetree estimates in the Lissamphibia
Karen Siu-Ting*, Maria Torres-Sanchez, Diego San Mauro, Mark Wilkinson, Davide Pisani, Mary J OConnell, Christopher J Creevey

O-03-OS19
Incomplete lineage sorting in mammalian phylogenomics
Nicolas Galtier*, Celine Scornavacca

O-03-OS20
Evolution of bacterial communities associated with termites
Thomas Bourguignon*, Nathan Lo, Carsten Dietrich, Jan Sobotnik, Sarah Sidek, Yves Roisin, Theodore Alfred Evans

O-03-OS21
Concordance and divergence of the VLR-based adaptive immune system in jawless vertebrates: Functional and evolutionary implications
Sabyasachi Das*, Jianxu Li, Masayuki Hirano, Yoichi Sutoh, Jonathan Rast, Max D Cooper

O-03-OS22
Intra-individual analysis of the MHC-dependent TCR repertoire diversity
Ana Teles*, Benno Woelfing, Philip LF Johnson, Manfred Milinski, Tobias L Lenz

O-03-OS23
Deciphering The Evolution Of Drought Tolerance In populations Of Silver Fir (Abies alba Mill.) Populations Across Switzerland And Southern France
Katalin Csillery*, Nina Buchmann, Bruno Fady, Felix Gugerli, Otso Ovaskainen, Christoph Sperisen, Alex Widmer

O-03-OS24
Genetics of parallel leaf shape evolution in the Mimulus guttatus species complex
Kathleen Gray Ferris*, Graham Coop, Johanna Schmitt

SY24: Phylogenomics - genome-scale data and the methods and analyses for phylogeny construction and time estimation

12:30-15:30, Thursday, July 12
Room 302

O-04-PG01
Using equivalent information trees to maximize the power of taxon and gene sampling in phylogenetics and phylogenomics
Jeffrey Peter Townssend*, Zheng Wang, Dylan Greaves, Christoph Leuenberger, Alex Dornburg

O-04-PG02
Enhanced phylogenetic resolution of three highly-diverse flowering plant lineages from the Neotropics using Anchored Hybrid Enrichment
Carolina Granados Mendoza*, Gerardo A. Salazar, Susana Magallon, Eric Hagsater, Stefan Wanke, Itzi Fragoso-Martinez, Martha Martinez-Gordillo, Marie-Stephanie Samain, Emily Moriarty Lemmon, Alan R. Lemmon

O-04-PG03
Bayesian species tree estimation under the multispecies coalescent
Ziheng Yang*

O-04-PG04
Genome-wide estimation of the evoutionary history of six baboon species with polymorphism-aware phylogenetic models
Carolin Kosiol*, Dominik Schrempf

O-04-PG05
Phylogenomics of Pancrustacea
Andreas Zwick*, Luisa Teasdale, Diana Hartley, Blanca Prado, Carmen Pozo, Hong Shen

O-04-PG06
Genome-wide sequence information reveals multiple past hybridizations that shaped the ancestors of wheat
Nadine Bernhardt*, Jonathan Brassac, Xue Dong, Eva-Maria Willing, Korbinian Schneeberger, Benjamin Kilian, Frank Blattner R.

O-04-PG07
Systematic error is ubiquitous, and frequently misleads phylogenetic inference
Robert Lanfear*, Suha Naser, Wenqi Zhang

O-04-PG08
Stepwise Bayesian Inference of Phylogeny using RevBayes
Sebastian Hoehna*

O-04-PG09
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
Andre E Moura*, Kypher Shreves, Michael McGowen, Rus Hoelzel

O-04-PG10
A new approach to model amino-acid compositional heterogeneity sheds new insight on the origin of mitochondria
Ding He*, Simon Whelan

SY25: Post-transcriptional modifications: functions, diversity, pathogenesis and evolution

16:00-18:30, Tuesday, July 10

Room 304

O-02-PT01
Antiviral APOBEC Enzymes Drive Tumor Evolution
Reuben s. Harris*

O-02-PT02
Post-transcriptional modifications: Adaptations or cellular errors?
Jianzhi Zhang*

O-02-PT03

The role of innate immune mechanisms in molecular evolution and pathogenesis of flaviviruses

Helen Piontkivska*, Noel-Marie Plonski, Madeline Frederick, Dhani Prakoso, Kelli Lynn Barr, Michael Masao Miyamoto, Marta L. Wayne, Maureen Therese Long

SY26: Predictability of rapid evolutionary processes

15:00-17:00, Wednesday, July 11

Room 303

O-03-PR01

Evolutionary predicions from biophysical models

Michael Lassig*

O-03-PR02

Prediction in optimal immune systems

Thierry Mora*

O-03-PR03

Evolution of the adaptive immune system in response to cancer

Yuval Elhanati*, Zachary Sethna, Curtis Callan

O-03-PR04

High-resolution lineage tracking of laboratory yeast populations over 1000 generations

Ivana Cvijovic*, Alex N Nguyen Ba, Jose I Rojas Echenique, Katherine R Lawrence, Artur Rego-Costa, Sasha F Levy, Michael M Desai

O-03-PR05

Clonal diversity accelerates the evolution of antimicrobial resistance

Ignacio Vazquez-Garcia*, Elisa Alonso-Perez, Jing Li, Johan Hallin, Magda Reis, Gianni Liti, Jonas Warringer, Ville Mustonen

O003-PR06

Historical contingency shapes genome-wide diversity after antibiotic-driven bottlenecks

Alejandro Couce*, Andre Birgy, Coralie Pintard, Olivier Tenaillon

SY27: Quantitative genetics of developmental evolution

15:00-17:00, Wednesday, July 11

Room 304

O-03-QG01

Evolutionary Quantitative Genetics of Zebrafish Development

Katrina McGuigan*

O-03-QG02

Characterising patterns of selection and the distribution of fitness effects using single-cell open chromatin data

David Garfield*, Dermot Harnett

O-03-QG03

Somatic genome rearrangements in Oxytricha trifallax - a single-cell model for nuclear differentiation and development

Rafik Neme*, Jaspreet S Khurana , Laura F Landweber

O-03-QG04

Fishing for genes driving tooth evo-devo exclusive of the vertebrate jaw

Julia C Boughner*, Gareth J Fraser, Nasim Rostampour, Cassy M Appelt, Alexandre Thiery, Aunum Abid

O-03-QG05

Genetic Basis of Natural Variations in Germline RNAi in C. elegans

Han Ting Chou*, Annalise B. Paaby

O-03-QG06

The genetic basis of evolutionary transitions in early development

Christina Zakas*, Matthew Rockman

SY28: Selection on complex traits: reuniting quantitative and population genetics

12:30-15:30, Thursday, July 12

Room 304

O-04-SC01

A population genetic interpretation of complex trait architecture in humans

Guy Sella*

O-04-SC02

Anterior pituitary transcriptome suggests differences in adrenocorticotropic hormone release in tame and aggressive foxes

Anna V Kukekova*, Hekman P Jessica, Jennifer L Johnson, Whitney Edwards, Anastasiya V Vladimirova, Rimma G Gulevich, Anastasiya V Kharlamova, Yury Herbeck, Gregory M Acland, Lori T Raetzman, Lyudmila N Trut

O-04-SC03

New Insights into the Genetic Basis and Evolutionary History of Lactase Persistence in Africa

Alessia Ranciaro*, Michael C. Campbell, Elizabeth Eyerman, Simon Thompson, William Beggs, Sununguko Wata Mpoloka, Gaonyadiwe George Mokone, Thomas Nyambo, Dawit Wolde Meskel, Gurja Belay, Meredith Yeager, Stephen Chanock, Sarah A Tishkoff

O-04-SC04

Paleo-population genetics: Illuminating the role of selection in shaping human diversity

Yassine Souilmi*, Raymond Tobler, Fernando Racimo, Christian Huber, Angad Johar, Iain Mathieson, Murray Cox, Graham Gower, Matthew Williams, Matthew Robinson, Joao Teixeira, Alan Cooper

O-04-SC05

Identifying natural selection by constructing genome-wide genealogies

Leo Speidel*, Simon Myers

O-04-SC06

Polygenic adaptation in response to a sudden change in the environment

Laura Katharine Hayward*, Guy Sella

O-04-SC07

A dual field approach uncovers the complex genomics of local adaptation in Swedish A. thaliana

Daniele Filiault*, Benjamin Brachi, Svante Holm, Caroline Dean, Joy Bergelson, Magnus Nordborg

O-04-SC08

The effects of demography and genetic architecture on the neutral distribution of quantitative traits

Evan Koch*

O-04-SC09

Evidence for stabilizing selection at pleiotropic loci for human complex traits

Emily S Wong*, Steve Chenoweth, Mark Blows, Joseph Powell

O-04-SC10

Demography drives differences in the distribution of gene expression

Arun Durvasula*, Kirk E Lohmueller

SY29: Somatic mutation and the evolution of multicellularity

16:00-18:00, Monday, July 9

Room 304

O-01-SM01

Mutation and Selection Within an Individual

Maria E Orive*

O-01-SM02

Somatic evolution in cancer and healthy tissues

Inigo Martincorena*

O-01-SM03

Somatic mutation in Sitka spruce

Vincent Hanlon*, Sarah P Otto, Sally N Aitken

O-01-SM04

Somatic Mutations, Development, and Phylogenomics

Reed Cartwright*

O-01-SM05

Accumulation of mutations and natural selection in experimental evolution of basidiomycete fungus Schizophyllum commune

Aleksandra Bezmenova*, Alexey Penin, Elena Zvyagina, Artem Kasianov, Tatiana Neretina, Georgii Bazykin, Alexey Kondrashov

O-01-SM06

Multicellular organisms face an inescapable double bind between cell senescence and cancer

Paul G Nelson, Joanna Masel*

SY30: Timing methodologies and applications

13:30-15:30, Tuesday, July 10

Room 304

O-02-TM01
Six impossible things before breakfast: assumptions, models and belief in molecular dating
Lindell Bromham*

O-02-TM02
Undersampling genomes has biased time and rate estimates
Blair Hedges*, Julie Marin

O-02-TM03
Phylogenetic incongruences - opportunities to improve the reconstruction of a dated tree of life
Dominik Schrempf*, Gergely Szollosi

O-02-TM04
Pervasive correlation of molecular evolutionary rates in the tree of life
Qiqing Tao*, Koichiro Tamura, Fabia Battistuzzi, Sudhir Kumar

O-02-TM05
Global rate variation in bony vertebrates
Naoko Takezaki*, Hidenori Nishihara

O-02-TM06
Recalcitrance of avian divergence times and phylogenetic topology may be related to selection for reduced body size across the K-Pg boundary
Jacob Berv*, Daniel Field

SY31: Tracing back bacterial pathogen evolution from ancient and modern genomics

10:30-12:30, Monday, July 9

Room 303

O-01-TB01
The genetic history of plague: From the Stone Age to the 18th century.
Johannes Krause*

O-01-TB02
Adoption of the pathogenic niche
Caitlin Pepperell*

O-01-TB03
A 2,200 year old Mycobacterium leprae genome from an Egyptian mummy
Judith Neukamm*, Saskia Pfrengle, Martyna Molak, Michael Francken, Beatrix Welte, Katerina Harvati, Kay Nieselt, Johannes Krause, Verena J. Schuenemann

O-01-TB04
Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico
Alexander Herbig*, Åshild J Vågene, Michael G Campana, Nelly M Robles García, Christina Warinner, Susanna Sabin, Maria A Spyrou, Aida Andrades Valtueña, Daniel H Huson, Noreen Tuross, Kirsten I Bos, Johannes Krause

O-01-TB05
A Single, >2.2 Ga Old Event of Host Adaptation in the Order Legionellales
Eric Hugoson, Daniel Leenheer, Tea Ammunet, Helena Ishak, Tiscar Graells, Madeleine Larsson, Anaisa Moreno, Lionel Guy*

O-01-TB06
A high-quality 17th century Mycobacterium tuberculosis genome adds resolution to mycobacterial dating and phylogeography
Susanna Sabin*, Alexander Herbig, Ashild J. Vagene, Torbjorn Ahlstrom, Gracijela Bozovic, Elizabeth A. Nelson, Caroline Arcini, Kirsten I. Bos

SY32: Transposable elements in gene regulation and genome evolution

16:00-18:30, Tuesday, July 10
Room 302

O-02-TE01
Transposable elements as catalysts of convergent evolution
Cedric Feschotte*

O-02-TE02
Chromatin sinks and mutational burdens in males
Lauren Gibilisco*, Doris Bachtrog

O-02-TE03
The contribution of transposable elements to regulation of genes underlying symbiosis in _Epichloe_
David Winter*

O-02-TE04
Pervasive epigenetic effects of euchromatic transposable elements impact genome evolution
Grace Yuh Chwen Lee*, Gary H Karpen

O-02-TE05
Poxvirus capture of host genes by retrotransposition in infected cells
Della Fixsen*

O-02-TE06
The birth of new genome defense genes by transposable elements
Richard McLaughlin*, Harmit Malik, Michael Emerman

O-02-TE07
The tuatara genome - a detailed look into early amniote genome evolution and a smorgasbord of recently active transposons
Alexander Suh*, Valentina Peona, Claire Peart, Vera Warmuth, Neil Gemmell

O-02-TE08

The role of transposable-element mediated rewiring of regulatory networks: dosage compensation in Drosophila

Doris Bachtrog

SY33: Trash to treasure and treasure to trash: invasion, persistence, neofunctionalization, and gene decay in evolution

9:30-11:30, Thursday, July 12

Room 304

O-04-TT01

Experimentally evolving molecular Rube Goldberg machines

Anthony Poole*

O-04-TT02

Inteins and Homing Endonucleases: long term survival and constructive neutral evolution

Johann Peter Gogarten*, Shannon M Soucy, Joshua Skydel, Artemis Dyanna Louyakis

O-04-TT03

Can the human genome be 100% functional? An argument based on the concept of mutational load

Dan Graur*

O-04-TT04

Selfish modifiers of recombination and mutation, their response to stress, and implications for evolvability

Lilach Hadany*

O-04-TT05

An evolutionary lock-in event facilitates the persistence of self-splicing introns in S. cerevisiae

Tobias Warnecke*

O-04-TT06

Functional Shifts in Duplicated Genes via Specialization of Interacting Partners

Ashley Irene Teufel*, Claus Wilke

SY34: Virus genome evolution

13:30-15:30, Tuesday, July 10

Room 302

O-02-VG01

Patterns of genomic diversification in natural communities of marine bacteriophages

Marcia F Marston*

O-02-VG02

Uncovering hidden properties of an RNA virus

Adi Stern*

O-02-VG03
Intra-patient evolutionary dynamics of HIV drug resistance evolution
Alison Feder*, Soo-Yon Rhee, Susan Holmes, Robert Shafer, Zandrea Ambrose, Joachim Hermisson, Pleuni Pennings, Dmitri Petrov

O-02-VG04
The origin of Vertebrate RNA Viruses
Mang Shi*, Edward Holmes, Yong-zhen Zhang

O-02-VG05
Host switches and intrahost speciations play a central role in herpesvirus evolution
Anderson Brito*, John Pinney

O-02-VG06
Norovirus pandemics emerge from hidden reservoirs and are not driven by the acquisition of viral genetic changes
Christopher Ruis, Judith Breuer, Richard Allen Goldstein*

SY35: Weak forces in genome evolution

16:00-18:00, Monday, July 9
Room 302

O-01-WF01
The dark side of recombination: biased gene conversion in the tree of life
Laurent Duret*

O-01-WF02
Genomic disintegration in woolly mammoths on Wrangel island
Rebekah L Rogers*, Montgomery Slatkin

O-01-WF03
The role of genetic variation in the evolution of enzyme functions
Nobuhiko Tokuriki*

O-01-WF04
Contrasting the influence of gBGC on adaptive statistics in primates and birds
Marjolaine Rousselle*, Alexandre Laverre, Emeric Figuet, Benoit Nabholz, Nicolas Galtier

O-01-WF05
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
Tomotaka Matsumoto*, Hiroshi Akashi

O-01-WF06
Direct measurement of fitness effects of natural variation through precision genome editing
Shi-An A Chen*, Eilon Sharon, Neil M Khosla, Jonathan K Pritchard, Hunter B Fraser

Posters

Poster session has two groups, and 3-digit of program number (POA) shows sessions.

Core times are divided whether the last 3-digit is even number or odd number.

Session time and core times are below:

- Poster session has two groups (session A and session B), and the first 3 letters of the program number (POA or POB) indicate the group in which the poster is presented.

Core times are divided by whether the last 3 digits represent an even number or an odd number.

The session times and core times are shown below:

Session A

Poster Session: 9:00-18:00 on Monday, July 9 and Tuesday, July 10

Core time: Even number -> 18:00-19:00 on Monday, July 9
Odd number -> 19:00-20:00 on Monday, July 9

Session B

Poster Session: 9:00-18:00 on July 11 / 9:00-18:30 on Thursday, July 12

Core time: Even number -> 18:00-19:00 on Wednesday, July 11
Odd number -> 19:00-20:00 on Wednesday, July 11

SY01: Asian population genomics

POB-111
Population migration and dairy pastoralism on the Bronze Age Mongolian steppe
Christina Warinner*, Choongwon Jeong, Shevan Wilkin, Tsend Amgalantugs, Abigail Bouwman, William Taylor, Sabri Bromage, Soninkhishig Tsolmon, Christian Trachsel, Judith Littleton, Cheryl Makarewicz, Erdene Myagmar, Bruno Frohlich, Jessica Hendy

POB-113
Human demographic history and adaptation in the abode of snow: the Himalayas and the Tibetan Plateau.
Elena Arciero*, Thirsa Kraaijenbrink, Asan -, Marc Haber, Qasim Ayub, Yuan Chen, Shane McCarthy, Huanming Yang, Mark Jobling, George van Driem, Peter de Knijff, Yali Xue, Chris Tyler-Smith

POB-114
The genetic origins and admixed ancestry characterization of Japanese people
Wen-Ya Ko*, Koichiro Higasa, Han-Yu Wang, Maiko Narahara, Kaori Iida, Fumihiko Matsuda, Ryo Yamada

POB-115
Detectng signatures of polygenic selection in East Asians
Kazuhiro Nakayama*

POB-116

Population history of Native Siberians

Elena S. Gusareva*, Hie Lim Kim, Vladimir Kharkov N., Vadim Stepanov A., Stephan Schuster C.

POB-117

Genetic adaptation and ancestry inference of the Taiwanese indigenous and Han people

Yun-Hua Lo*

POB-118

Lipidome Changes in Prefrontal Cortex of African American, Caucasian and Han Chinese Populations

Anna Tkachev*, Ekaterina Khrameeva, Philipp Khaitovich

POB-119

Y-chromosome and mtDNA haplogroup differences between populations in Russia

Anton Logachev*, Dasha Zhernakova, Vladimir Brukhin, Stephen James O'Brien

POB-120

Genetic diversity and admixture history of the Uyghurs in Xinjiang

Shuhua Xu*

POB-121

Population genomics of ancient Beringia

Martin Sikora*, Jose Victor Moreno-Mayar, Vitor C Sousa, Morten E Allentoft, Ben A Potter, Lasse Vinner, Matthias Steinrucken, Simon Rasmussen, Yun S Song, Rasmus Nielsen, Laurent Excoffier, David J Meltzer, Eske Willerslev

POB-122

History of risk allele of diffuse-type gastric cancer in East Asian

Risa Iwasaki*, Takehiro Sato, Ryosuke Kimura, Yoko Satta

POB-123

Genome-wide genetic variation of people in Japan and its implication of demographic history

Yosuke Kawai*, Takahiro Mimori, Yuki Hitomi, Seik-Soon Khor, Olivier Gervais, Masao Nagasaki, Katsushi Tokunaga

SY02: Associate Editors Symposium

POA-407

Molecular evolution and functional diversity of doublesex, a master regulator of polymorphisms in insects

Saurav Baral, A Gandhimathi, Riddhi Deshmukh, Krushnamegh Kunte*

SY03: Ecological genomics

POA-412

Vomeronasal type 2-like receptors showed different evolutionary patterns in basal teleosts such as eels and in other teleosts

Tzi-Yuan Wang*, Wen-Yu Chung, Jinn-Jy Lin, Wen-Hsiung Li, Feng-Yu Wang

POB-187

Transcriptome analysis of the reef-building octocoral, Heliopora coerulea

Christine Guzman*, Chuya Shinzato, Tsai-Ming Lu, Cecilia Conaco

POB-189

Comparative avian genomics: Identifying the genetic basis of beak shape variation.

Leeban Yusuf*, Toni Gossmann, Chris Cooney

POB-190

Is gene transfer a source of ecological adaptation in eukaryotes? The case of nitrate metabolism

Eduard Ocana-Pallares*, Sebastian Najle, Claudio Scazzocchio, Inaki Ruiz-Trillo

POB-191

Photosensitive alternative splicing of the circadian clock gene timeless is population specific in a cold-adapted fly, Drosophila montana

Riikka Tapanainen, Darren Parker J, Maaria Kankare*

POB-194

The genomic basis for convergent evolution of carnivory in shrew rats

Emily J Roycroft*, Anang S Achmadi, Jacob A Esselstyn, Jeffrey M Good, Adnan Moussalli, Kevin C Rowe

POB-195

Evolution of sperm proteins and non-fertilizing sperm in two Lepidoptera with different mating systems

Andrew Joseph Mongue*, James R. Walters

POB-198

Ancient and modern evolution of opsins in *Daphnia*.

Jeffry L. Dudycha*, Matthew J. Greenwold, Christopher S. Brandon

POB-199

Gene expression variation and diapause regulation in wood white (*Leptidea*) butterflies.

Niclas Backstrom*, Luis Leal, Venkat Talla, Thomas Kallman, Magne Friberg, Christer Wiklund, Vlad Dinca, Roger Vila

POB-200

Tissue- and temperature-specific RNAseq differential gene expression and SNP variation by sex, geography, and linkage reveal adaptive potential and population genomic health of marine turtles

Andrew M Shedlock*

POB-201

Transcriptome sequencing reveals genomic adaptations to life at high elevations in Ethiopian frogs

Jacobo Reyes-Velasco*, Yann Bourgeois, Stephane Boissinot

POB-203

Local adaptation under gene flow: Recombination, conditional neutrality and genetic trade-offs shape genomic patterns in Arabidopsis lyrata

Tuomas Hamala*, Outi Savolainen

POB-204

Uncovering the demographic history of endangered Formosan fruit bats (Pteropus dasymallus formosus) in Taiwan

Kung-Ping Lin*, Yun-Hua Lo, Shiang-Fan Chen, Masako Izawa, Wen-Ya Ko

POB-205

The genomics of local adaptation in the alpine Brassicaceae Arabis alpina

Aude Rogivue*, Kevin Leempoel, Rimjhim Roy Choudhury, Stefan Zoller, Stephane Cretegny, Francois Felber, Michel Kasser, Christian Parisod, Stephane Joost, Felix Gugerli

POB-206

THE IMPACT OF INCREASED SANDSTORM ACTIVITIES ON THE RED SEA MICROBIOTA

Hayedeh Behzad*, Hajime Ohyanagi, Badr Alharbi, katsuhiko Mineta, Takashi Gojobori

POB-207

Capybara genome sequencing scrutinizes factors affecting evolutionary rates

Isaac Adeyemi Babarinde*, Naruya Saitou

POB-208

Seasonal dynamics of the microbial communities by time-series metagenomics in the Red Sea

Katsuhiko Mineta*, Yoshimoto Saito, Intikhab Alam, Hayedeh Behzad, Mohamed Alarawi, Hiroshi Shimizu, Siham Fatani, Amani Al-Ma'abadi, Kosuke Goto, Hajime Ohyanagi, Magbubah Essack, John Archer, Vladimir Bajic, Takashi Gojobori

POB-209

Uncovering the genomic determinants of adaptive radiations: Comparative transcriptomics of convergent prey specialization in Dysdera spiders from the Canary Islands

Joel Vizueta*, Nuria Macias-Hernandez, Miquel A. Arnedo, Alejandro Sanchez-Gracia, Julio Rozas

POB-210

Using a combined RNAi/RNA-seq approach to assess the role of heat shock transcription factor (HSF) in the evolution of thermal adaptation

Alice Harada*, Sumaetee Tangwancharoen, Ronald Burton

POB-211

Transcription Termination is a Mutational Target During Extreme Feast/Famine Cycles in Escherichia coli.

Megan G Behringer*, Samuel F Miller, Gwyneth Boyer, Michael Lynch

POB-212

Adaptive divergence and molecular evolution of venom gland transcriptomes of long-jawed orb weavers Tetragnatha versicolor (Araneae: Tetragnathidae)

Michael Brewer*

POB-213

Microbiome analysis of raw fish ceviche through a metagenomic approach

Humberto Martinez Montoya*, Guadalupe Concepcion Rodriguez Castillenjos, Regulo Ruiz Salazar, Maria Cristina Hernandez Jimenez

POB-214

Comparisons of behavioral and TRPA1 heat sensitivities in three Cuban Anolis lizards from distinct thermal microhabitats

Hiroshi Akashi*, Shigeru Saito, Antonio Cadiz Diaz, Takashi Makino, Makoto Tominaga, Masakado Kawata

POB-215

Detection of genes involved in adaptive evolution to hot-open habitat in Cuban Anolis lizards

Shunsuke Kanamori*

POB-216

Genetic architecture of mate preference behaviours and the corresponding warning pattern cue facilitates ecological speciation in sympatric tropical butterflies

Richard Merrill*, Matteo Rossi, Pasi Rastas, John Davey, W Owen McMillan, Chris Jiggins

POB-217

The rises and falls of opsin genes in 59 ray-finned fish genomes and their implications for environmental adaptation

Jinn-Jy Lin*, Feng-Yu Wang, Wen-Hsiung Li, Tzi-Yuan Wang

POB-218

Inferring global population structure and genetic diversity in wild house mice (Mus musculus) using a genome-wide SNP array

Jonathan Hughes*, Andrew Parker Morgan, John Didion, Jeremy Searle, Fernando Pardo-Manuel de Villena

POB-219

Diet and roosting behavior shape the color vision of leaf-nosed bats (Phyllostomidae)

Amanda Dawn Melin*, Kelly Kries, Marilia A. S. Barros, Gwen Duytschaever, Joseph Orkin, Daniel Pessoa

POB-221

Influence of sexual conflict on reproductive mode and fecundity in a facultative parthenogen

Mercedes Burns*, Nobuo Tsurusaki

POB-222

The reconstruction of ecological interactions through eDNA metabarcoding analyses on ice cores extracted from the largest and deepest southern European Alps glacier: Adamello, Italy

Cristiano Vernesi*, Alexis Marchesini, Matteo Montagna, Matteo Girardi, Antonella Cristofori, Valter Maggi, Daniela Festi, Camilla Wellstein, Stefan Zerbe, Klaus Oeggl

POB-223

Why is the dN/dS ratio substantially lower in nature than in long-term laboratory evolution?

Piaopiao Chen*, Jianzhi George Zhang

POB-226

Detecting signatures of convergent adaptation in population genomic data

Kristin M Lee*, Jessica Selby, John Willis, Graham Coop

POB-227

Turning sex into apomixis: Genetic crossing reveals the mode of apomixis transfer into sexual populations of the genus Boechera

Martin Mau*, Tiina Liiving, Liza Fomenko, Richard Goertzen, Laura Boettner, Timothy Francis Sharbel

POB-228

From Genotyping-by-Sequencing to aDNA, a peek into the past and future of the New Zealand Kaka

Denise Martini*, Neil Gemmell, Bruce Robertson, Michael Knapp

POB-229

Genomic analyses of the population structure in *Daphnia pulex*.

Takahiro Maruki*, Zhiqiang Ye, Michael Lynch

POB-230

Speciation and secondary contact between two Sulawesi macaque species, Macaca tonkeana and M. hecki

Yohey Terai*, Sohei Takuno, Hiroo Imai, Laurentia Henrieta Purba, Kanthi Arum Widayati, Bambang Suryobroto

POB-231

Genomes of Hawaiian Canacidae (Beach Flies)

Nina Pak*

POB-233

Population genomics of woodland strawberry reveal strong selection of extensive adaptive introgressions in different climates

Tuomas Toivainen*, Samia Samad, Takeshi Kurokura, Ari Loytynoja, Patrick P Edger, David Pose, Lars Paulin, Petri Auvinen, Timo Hytonen

POB-234

Evolution of RNA polymerase subunits in endosymbionts proteobacteria with extreme genome reduction

CYNTHIA RANGEL*, Edgardo Galan, Agustino Martinez

POB-237

Searching for deep prokaryotic lineages in the ocean.

Romain Lannes*, Philippe Lopez, Eric Bapteste

POB-238

Comparative genomics of bioluminescent fungi

Isheng Jason Tsai*, Huei-Mien Ke, Chan-Yi Lin, Pei Hsuan Wu, Chiung-Chih Chang, Hsiao-Wei Kao

POB-240

Population divergence and thermal selection: Combining reverse ecology with population transcriptomics

Maike Herrmann*

POB-241

Genomic architecture of adaptation to the freshwater in ten independently adapted freshwater populations of G. aculeatus from the White Sea basin.

Nadezhda V. Terekhanova*, Alexey S. Kondrashov, Georgii A. Bazykin, Nikolai S. Mugue

POB-242

Genome re-sequencing of natural isolates reveals patterns of local and continental population structure in the green alga *Chlamydomonas reinhardtii*.

Rory J Craig*, Katharina B Boendel, Rob W Ness, Nick Colegrave, Peter D Keightley

POB-243
Lineage specific deferentially expressed genes in eight endangered amphibians in Ryukyu Archipelago
Takeshi Igawa*, Quintin Lau, Masatoshi Matsunami, Masayuki Sumida

POB-246
Genomic investigation of hybridisation and incipient speciation in Eucalyptus
Kevin D Murray*, Tim Collins, Justin Borevitz, Rose Andrew

POB-248
Molecular Basis of Variable Glyphosate Resistance in Bacterial Gut Symbionts of Honey Bees
Erick Vicente Da Silva Motta*, Kasie Raymann, Nancy Moran

POB-250
Presence-absence polymorphisms of highly expressed FP sequences contribute to fluorescent polymorphisms in the stony coral, Acropora digitifera
Shiho Takahashi-Kariyazono*, Yohey Terai

POB-252
Why fly when you can walk? The convergent evolution of flightlessness in rails.
Gillian Gibb*, Steve Trewick

POB-256
Genetic analysis of diversifying genitalia in ripening-fruit-consuming Drosophila species
Leona Muto, Yoshitaka Kamimura, Kanoko Takahashi, Airi Sato, Kentaro M. Tanaka, Aya Takahashi*

POB-257
Transcriptomic response of the Drosophila melanogaster Minutes
Jai Andrew Denton*, A. Reed Floyd

SY04: Evolution of adaptive immunity and MHC genes

POB-286
Understanding the molecular diversification of self recognition through ray-finned fish innate immune receptor families
Dustin Wcisel, Jeffrey Yoder, Alex Dornburg*

POB-288
Studying selection in 'real-time' by genotyping HLA immune genes from ancient DNA
Federica Pierini*, Marcel Nutsua, Lisa Boehme, Almut Nebel, Ben Krause-Kyora, Tobias L. Lenz

POB-289
Variation of the MHC and other immune receptors in wild zebrafish
Jaanus Suurvaeli*, Thomas Wiehe, Maria Leptin

POB-290
Evolution of type I interferon and receptor genes in crocodilians
Katherine Brittain, Elizabeth A. Jones, David Ray A., Jaime Gongora*

POB-291

Evolution and diversity of MHC class II DQB1 and DRB1 in wild pigs and peccaries

Carol Lee*, Alvaro Perdomo, Claire Rogel-Gaillard, Jaime Gongora

POB-292

Worldwide genetic variation of the IGHV and TRBV immune receptor gene families in humans

Jane A Yu*, Shishi Luo, Yun S Song

POB-294

Understanding how Japanese frogs are resistant to a deadly worldwide fungal disease through in silico analyses of major histocompatibility complex (MHC)

Quintin Lau*, Takeshi Igawa, Tiffany Kosch, Lee Skerratt, Lee Berger, Alex Roberts, Yoko Satta

POB-295

Survival of the Fastest not the Fittest: Modeling the effect of multilevel immune selection on B cell lineages in adaptive immune system population dynamics

Maksim Shestov*, Latifa F Jackson, Jason H Moore

POB-296

Gene expression variability across cells and species shapes the innate immune response

Tzachi Hagai*, Sarah Teichmann

POB-298

Testing Hypotheses on the Evolution of Resistance to Amphibian Chytridiomycosis

Minjie Fu *, Bruce Waldman

SY05: Evolution of non-coding RNAs and their regulatory networks

POA-052

First *in vivo* evidence of the functionality of a sncRNA of mitochondrial origin (smithRNA) targeting a nuclear transcript and affecting histone methylation

Federico Plazzi*, Manuel Delpero, Andrea Pozzi, Marco Passamonti

POA-053

How and why new genes die- de novo microRNAs in the Red Queen race

Guang-An Lu*

POA-054

The impact of translation and RNA-protein interactions in the observed conservation patterns of long non-coding RNAs.

Jorge Ruiz-Orera*, M.Mar Alba

POA-055

Long non-coding RNA ortholog reconstruction from splice sites

Katja Nowick*, Anne Nitsche, Maria Beatriz Walter Costa

POA-056

Caste-specific microRNA expression in termites: insights into social evolution

Masatoshi Matsunami*, Masafumi Nozawa, Yudai Masuoka, Ryutaro Suzuki, Kouhei Toga, Katsushi Yamaguchi, Kiyoto Maekawa, Shuji Shigenobu, Toru Muira

POA-058

Functional sequence constraint on pseudogene 3' UTRs is suggestive of widespread competitive endogenous RNA activity

Cian Glenfield*, Aoife McLysaght

POA-060

Exploring the relationship between vaccination and anti-NMDA receptor encephalitis based on microRNA phylogenetic tree

Hsiuying Wang*

POA-061

Does Lamarckian evolution exist? Direct evidence of small RNA transport from somatic brain tissue to offspring

Elizabeth O'Brien, Kathleen Ensbey, Paul Baldock, Bryan Day, Guy Barry*

SY06: Evolutionary epigenomics, progress and prospects

POB-263

The Methylome of the Lakes : environmental epigenomics in East African cichlids

Gregoire Vernaz*, Eric A. Miska, Richard Durbin, Milan Malinsky, Hannes Svardal, George Turner, Emilia Santos

POB-265

Convergent increase of gene body methylation in mangroves and its role in gene expression homeostasis

Yushuai Wang*, Aimei Dai, Tian Tang

POB-266

Origination of Human Exons through Differential Nucleosome Occupancy

Yumei Li*, Chen Li, Chuan-Yun Li, Aibin He

POB-267

On the track of the evolutionary forces shaping gene-body methylation conservation and variation in *Brassicaceae*

Robert Horvath*, Shohei Takuno, Benjamin Laenen, Tajan Slotte

POB-268

Characterisation of extinct bison methylomes using bisulphite sequencing

Bastien Llamas*, Holly Heiniger, Graham Gower, Paul Gooding, Catherine M Suter, Stefan Hiendleder, Jeremy F Taylor, John R Stephen, Alan Cooper

POB-269

Differences in open chromatin states reveal heterogeneous dosage effects along the Z-chromosome

Ana Catalan*

POB-270

Drought stress-specific DNA methylation differences found in tolerant and susceptible maize varieties.

Ryan R Morrison*, Robin G. Allaby, Logan Kistler

POB-271

Global natural variation of DNA methylation and its genetic architecture in Arabidopsis thaliana

Eriko Sasaki*, Magnus Nordborg

POB-272

Amphioxus functional genomics reveals the evolution of vertebrate regulatory traits

Ignacio Maeso*, Ferdinand Marletaz, Panos N. Firbas, Juan J. Tena, Ozren Bogdanovic , Malcolm Perry, Elisa de la Calle-Mustienes , Stephanie Bertrand, Boris Lenhard, Peter W.H. Holland, Ryan Lister, Hector Escriva, Manuel Irimia, Jose Luis Gomez-Skarmeta

POB-273

Epigenetic mutations contribute to specialized metabolites variation in Arabidopsis thaliana accessions

Kazumasa Shirai*, Fumio Matsuda, Ryo Nakabayashi, Mitsuhiko P Sato, Masanori Okamoto, Maho Tanaka, Akihiro Fujimoto, Minami Shimizu, Kazuo Shinozaki, Motoaki Seki, Kazuki Saito, Kousuke Hanada

POB-274

Epigenome-based Adaptive Evolution in Unicellular Bacteria: Evidence from Genomes, Methylomes, Transcriptomes and Phenotypes

Ichizo Kobayashi*

POB-275

Role of DNA methylation in Paternal Genome Elimination, a peculiar reproductive strategy found in insects

Stevie Anne Bain*, Dominik R Laetsch, Laura Ross

POB-276

Effect of pleiotropy on regulatory sequence evolution different than on gene evolution

Peter Orchard, Zane Kliesmete, Beate Vieth, Ines Hellmann*

POB-277

Genome-wide and single-base resolution DNA methylomes of the Sea Lamprey (Petromyzon marinus) Reveal Gradual Transition of the Genomic Methylation Pattern in Early Vertebrates

Zhixi Su*, Zhao Zhang, Zhan Zhou, Gangbiao Liu, Yangyun Zou, James Lloyd P. B., David W. McCauley, Weiming Li, Xun Gu

POB-278

Regulatory Differences in Natal Down Development between Altricial and Precocial Birds

Chih-Kuan Chen*, Pei-Chi Su, I-Ming Liu, Hao-Fen Chuang, Wen-Hsiung Li, Chen Siang Ng

POB-279

Assessing epigenetic effects of a lifestyle transition in human history

Olaf Thalmann*, Kristian Hanghoej, Karl-Heinz Herzig, Jaroslaw Walkowiak, Ludovic Orlando, Mattias Jakobsson

POB-280

A novel model for the evolution of mammalian epigenomic traits

Noah Ethan Dukler*, Yi-Fei, Huang, Adam Siepel

POB-281

Genomic Landscape of Methylation Islands in Hymenopteran Insects

Hyeonsoo Jeong*, Xin Wu, Brandon Smith, Soojin V. Yi

POB-282

Methylome and Transcriptome Reprogramming associated with Wolbachia in a parasitoid wasp

Xin Wu*, Amelia Lindsey, Dan Sun, Paramita Chatterjee, Jack Werren, Richard Stouthamer, Soojin V Yi

SY07: Evolutionary genomics of the human brain

POA-167

The effects of young duplicated genes to human developmental brain

Taisuke Hori*, Takashi Makino, Daiki Sato, Masakado Kawata

POA-168

Transgenic rhesus monkeys carrying the human MCPH1 gene copies show human-like neoteny of brain development

Bing Su*, Lei Shi, Xin Luo, Yongchang Chen, Cirong Liu, Min Li, Hong Wang, Yanjiao Li, Yuyu Niu, Yundi Shi, Martin Styner, Qiang Lin, Jin Jiang, Weizhi Ji

POA-170

No evidence for recent selection at *FOXP2* among diverse human populations

Elizabeth G Atkinson*, Amanda J Audesse, Julia A Palacios, Dean Bobo M, Ashley E Webb, Sohini Ramachandran, Brenna M Henn

POA-171

The Role of CNTNAP2 in the Evolution of the Human Synapse

Frances St George-Hyslop*, Frederick J. Livesey, Toomas Kivisild

POA-173

Molecular signatures of autism in prefrontal cortex

Ilia Kurochkin*, Ekaterina Khrameeva, Anna Tkachev, Philipp Khaitovich

POA-175

Towards the most comprehensive lncRNA catalogue and in-depth evolutionary analysis of human long non-coding RNAs

Amin Saffari*, Peter Stadler, Katja Nowick

POA-176

Investigation of single cell genome instability in normal and neurodegeneration brains

Raheleh Rahbari*, Sarah Geurs, Marie-Christine Galas, Bart Dermaut, Thierry Voet

SY08: 50 years since Ohno's genome duplication: integration across disciplines and time scales

POA-357

The expansion of a ligand transporter related gene family in cluster specific to teleost fishes

Langyu Gu*, Canwei Xia

POA-359

Revisiting Ohno's hypothesis of dosage compensation by using the neo-sex chromosomes in *Drosophila*

Masafumi Nozawa*

POA-360
Faster evolving primate genes are more likely to duplicate.
Aine Niamh O'Toole*, Laurence D Hurst, Aoife McLysaght

POA-361
Prevalence, Mechanisms and Importance of Duplicate Gene Divergence in Exon-Intron Structure
Xuehao Fu, Hongyan Shan, Peipei Wang, Hongzhi Kong, Guixia Xu*

POA-362
Testing the Ortholog Conjecture for whole genome duplications
Tina Begum, Marc Robinson-Rechavi*

POA-363
Mechanisms of loss and preservation of whole-genome duplicates revealed by population genomics
Parul Johri*, Jean-Francois Gout, Michael Lynch

POA-364
Tissue specific ploidy variation in sexual and apomictic seeds
Dorota Paczesniak*, Marco Pellino, Devan Guenter, Siegfried Jahnke, Andreas Fischbach, John T. Lovell, Timothy F. Sharbel

POA-365
Ancient polyploidy in orchids
Zhen Li*, Rolf Lohaus, Guo-Qiang Zhang, Zhong-Jian Liu, Yves Van de Peer

POA-367
Specialization is the main route of regulatory evolution following whole genome duplication in vertebrates
Ferdinand Marletaz, Panos Firbas, Ignacio Maeso, Juan Tena, Jon Permanyer, Hector Escriva, Jose Luis Gomez-Skarmeta, Manuel Irimia*

POA-368
Subgenome-Enriched Transposable Elements Reveal Allopolyploid Origins Following Whole-Genome Duplications
Adam M Session*, Daniel S Rokhsar

POA-369
Beyond Ohno's gene duplication: evolution of enzyme substrate specificity driven by gene loss and horizontal gene transfer
Francisco Barona-Gomez*

POA-370
Reshaped Patterns of Alternative Splicing after Allopolyploidy in Brassica napus
Keith Adams*, David Tack

POA-371
Are variable constraints on gene function the only cause of asymmetric fates of paralogs?
Yuichiro Hara*, Miki Takeuchi, Kaori Tatsumi, Yuka Kageyama, Masahiko HIbi, Hiroshi Kiyonari, Shigehiro Kuraku

POA-373

Using genetic duplication and machine learning to explore important features of genes associated with both heritable, and somatic disease.

Alexandra Claire Martin-Geary*, Mark Reardon, David Wells Newman, David L Robertson

POA-374

Reciprocally retained genes in the angiosperm lineage show the hallmarks of dosage balance sensitivity

Setareh Tasdighian, Michiel Van Bel, Zhen Li, Yves Van de Peer, Lorenzo Carretero-Paulet, Steven Maere*

POA-375

Dosage-sensitive ohnologs have restricted evolutionary trajectories

Alan M Rice*, Pauric Donnelly, Aoife McLysaght

POA-376

Preferential retention of homeologs from a single parental subgenome after polyploidy is shaped by functional interactions and dosage-based intrinsic selective constraint

Yue Hao*, Marianne Emery, M. Madeline Willis, Jacob D. Washburn, Jacob Rosenthal, Brandon Nielsen, Kerrie Barry, Khouanchy Oakgrove, Yi Peng, Jeremy Schmutz, Patrick P. Edger, Eric Lyons, J. Chris Pires, Gavin C Conant

POA-377

Human Segmental Duplications Revisited

Marina Braso-Vives*, Diego Andres Hartasanchez, David Juan, Arcadi Navarro

POA-379

The dark side of duplications: what to expect, what to look for, and their collapse

Diego A Hartasanchez*, Marina Braso-Vives, Txema Heredia, Marc Pybus, Arcadi Navarro

POA-380

Inferring ancestral state before WGD from enhancers and CTCF/cohesin loops in developmental genes.

Kenta Sumiyama*

POA-381

Genomic Responses to Fungal Allopolyploidy in a Natural Biological Experiment

David Winter, Nikki Charlton, Carolyn Young, Murray Cox, Austen Ganley*

POA-382

Concerted Divergence after Gene Duplication in Polycomb Repressive Complexes

Yichun Qiu*, Shao-Lun Liu, Keith Adams

POA-384

Exploring the genomic structure of the root-knot nematode Meloidogyne enterolobii

Marine Poullet*, Georgios Koutsovoulos, Etienne Danchin

POA-385

Multi-Species Comparison of Potential Enhancers Found Across the Paramecium Aurelia Species Complex

Timothy James Licknack*, Weibo Zheng, Michael Lynch

SY09: Gene flow detection and dating methods

POA-155

Identifying Loci Under Selection Against Gene Flow in IM Models using linked loci

Sadoune Ait Kaci Azzou*, Daniel Wegmann, Anja Westram

POA-156

The genetic affinities of southern Africa hunter-gatherers prior to the arrival of farming and pastoralist populations.

Mario Vicente*, Peter Ebbesen, Carina Schlebusch

POA-157

Fitting an isolation-migration model to MSMC estimates to infer population sizes and migration rates over time

Ke Wang*, Stephan Schiffels

POA-158

Gene flow in space and time: differential patterns among syntopically occurring species of the water flea genus Daphnia

Anne Thielsch*, Klaus Schwenk

POA-159

Analysis of Pattersons D and fD for Detecting Regions of Introgression

Lesly Lopez*, Emily Jane McTavish, Emilia Huerta-Sanchez

POA-160

Dissecting the Pre-Columbian legacy along the Andes-Amazonia divide

Guido Alberto Gnecchi Ruscone*, Stefania Sarno, Sara De Fanti, Cristina Giuliani, Tullia Di Corcia, Chiara Barbieri, Patrizia Di Cosimo, Ricardo Fujita , Antonio Gonzalez Martin , Zelda Alice Franceschi, Olga Rickards, Donata Luiselli , Marco Sazzini, Davide Pettener

POA-162

Estimated Effective Migration Surfaces with Rare Variation and application to Anopheles gambiae

Daniel N. Harris*, Timothy D. O'Connor

POA-163

Maximum Likelihood Implementation of an Isolation-with- Migration Model with Three Species for Testing Speciation with Gene Flow

Tianqi Zhu*, Ziheng Yang, Daniel Dalquen

SY10: Genetic conflict and speciation

POA-131

Speciation Results from Gene Regulatory Evolution

Chia-Hung Yang*, Samuel V. Scarpino

POA-134

Speciation genetics of Pristionchus nematodes

Kohta Yoshida*, Ralf J. Sommer

POA-136

Mitochondrial-Y chromosome interactions and local adaptation to the Mother's Curse

J. Arvid Agren*, Manisha Munasinghe, Andrew G. Clark

POA-137

EVOLUTION IN CERIANTHARIA (CNIDARIA), A HOLISTIC VIEW: ASPECTS ON MITOCHONDRIAL DNA, LIFE CYCLE, SYMBIOSIS AND TOXINS

Sergio N Stampar*, Maximiliano M Maronna, Celine Lopes, Hellen Ceriello, James D Reimer, Adam Reitzel, Jason Macrander, Marymegan Daly, Michael Broe, Mei Lin Neo, Nicholas Wei Liang Yap, Marcelo V Kitahara, Alvaro E Migotto, Andre C Morandini

POA-140

Transcriptomic analyses of sex chromosome meiotic drive in Drosophila

Sung-Ya Lin*, Shu Fang, Chau-Ti Ting, Catherine Montchamp-Moreau

POA-141

Entensive and fine-grained introgressions in hybrid zones suggest genome-wide adaptive differences between mangrove species

Xinfeng Wang*, Ming Yang, Zixiao Guo, Ziwen He, Suhua Shi

POA-142

Oviposition decision-making behavior in the specialist Drosophila sechellia

Rumi Kondo*, Ami Hagihara, Yoshiko Iwamoto, Yukiko Oishi

POA-143

Sequencing a Large Repetitive Reproductive Gene in Abalone

Alberto Marcos Rivera*, Willie J Swanson

POA-144

When sex-specific hybrid incompatibility does not make sense: Parent-of-origin-specific transcriptome analysis of a pseudohaplodiploid male hybrid

Andres De la Filia*, Dominik Laetsch, Laura Ross

POA-146

The population history of the Green Monkeys inferred from the X to autosome diversity ratio

Moises Coll Macia*, Mikkel Heide Schierup

POA-147

High-throughput investigation of the species-specific binding of coevolving abalone reproductive proteins

Jolie A Carlisle*, Willie J Swanson

POA-148

Laboratory evolution reveals distinct genetic and phenotypic adaptation in two parallel lineages originating from nearly identical enzyme progenitors.

Charlotte Miton*, Eleanor Campbell, Colin Jackson, Nobuhiko Tokuriki

POA-149

Do selfish plasmids drive evolution in budding yeast?

Michelle Hays*, Janet Young M, Harmit Singh Malik

POA-150

The role of rapidly evolving fertilization genes in threespine stickleback reproductive isolation

Emily E Killingbeck*, Damien B Wilburn, Gennifer E Merrihew, Michael J MacCoss, Catherine L Peichel, Willie Swanson J

SY11: Genomic underpinnings of primate phenotypic evolution and diversity

POA-399

RNA-Mediated Gene Fusions Driven By Segmental Duplication In Great Apes

Ann McCartney*, Edel Hyland, Chris Creevey, Paul Cormican, Tomas Marques-Bonet, James McInerney, Julie Aspden, Mary O'Connell

POB-063

How human chromosome 19 got its clusters of duplicated genes

Juan Felipe Ortiz*, Antonis Rokas

POB-064

RhesusBase: Understanding Human Biology in the Genomic Framework of Rhesus Macaque

Jiguang Peng*, Shi-Jian Zhang, Chu-Jun Liu, Xiao-Ming Zhong, Qing Sunny Shen, Chen-Qu Wang, Xiu-Qin Zhang, Chuan-Yun Li

POB-065

Loss of Conserved Protein Ubiquitylation Sites during Human Evolution

Dongbin Park, Chul Jun Goh, Ji Seok Lee, Yoonsoo Hahn*

POB-066

Acceleration of Olfactory Receptor Gene Loss in Primate Evolution: Possible Link to Anatomical Change in Sensory Systems and Dietary Transition

Yoshihito Niimura*, Atsushi Matsui, Kazushige Touhara

POB-067

Gain and loss of functions in the taste receptors of primates

HIROO IMAI*, Emiko Nishi, Laurentia Purba, Nami Suzuki-Hashido, Kanthi Widayati, Takashi Hayakawa, Bambang Suryobroto

POB-068

Isoform evolution in primates through independent combination of alternative RNA processing events

Xuke Luan*, Shi-Jian Zhang, Chenqu Wang, Chuan-Yun Li

POB-069

Natural selection on the genetic and functional variations of bitter taste receptors (TAS2Rs) in wild chimpanzees

Takashi Hayakawa*, Yasuka Toda, Eiji Inoue, Hodaka Matsuo, Naruki Morimura, Miho Inoue-Murayama, Chie Hashimoto, Takumi Misaka, Hajime Ohigashi, Tetsuro Matsuzawa, Hiroo Imai

POB-070

Mitochondrial and exome diversity in Pan troglodytes schweinfurthii at Gombe National Park

Andrew T Ozga*, Timothy H Webster, Maria A Nieves-Colon, Kathleen Fowler, Rebecca Siford, Melissa Wilson Sayres, Rebecca Nockerts, Michael L Wilson, Ian Gilby C, Anne E Pusey, YingYing Li, Beatrice H Hahn, Anne C Stone

POB-071

Phenotypic variation in free-ranging rhesus macaques: heritability and selection

James P Higham*, Clare Kimock, Alex DeCasien, Constance Dubuc

POB-072

Interpreting functional genomic data from the Cayo Santiago rhesus macaques

Michael J Montague*, Noah Snyder-Mackler, Lauren JN Brent, Julie E Horvath, Michael L Platt

POB-073

Adaptation of owl monkeys to nocturnal lifestyle driven by rapid expansion of simple repeat sequence to form megasatellite DNA

Akihiko Koga*, Hidenori Nishihara, Roscoe Stanyon, Hirohisa Hirai

POB-074

Bitter taste receptor function in lemurs provides insight into the evolution of beta-glycoside sensing mechanism in primates

Akihiro Itoigawa*, Takashi Hayakawa, Nami Suzuki-Hashido, Hiroo Imai

POB-075

Acquisition of Human-specific Characteristics of Skin through Gene Expression Changes

Nami Arakawa*, Yohey Terai, Hiroo Imai, Yoko Satta

POB-077

Gene Expression Plasticity At RNA And Protein Levels

Yifan Dai*, Xinzhu Wei, Jianzhi Zhang

POB-079

Locating adaptive events in the evolutionary history of the human coding genome

Ravi Patel*, Sudhir Kumar, Maxwell Sanderford, Tamera Lanham, Koichiro Tamura, Alexander Platt, Benjamin Glicksberg, Ke Xu, Joel Dudley, Laura Scheinfeldt

POB-085

Identifying Lineage-specific Targets of Darwin Selection by Bayesian Analysis of Genomic Polymorphism and Divergence from Multiple Species

Shilei Zhao, Tao Zhang, Bing Su, Peng Shi, Hua Chen*

SY12: Genomics and evolution of symbiotic interactions

POA-003

Dicyemid mesozoan genome reveals adaptations to the parasitic lifestyle

Tsai-Ming Lu*, Hidetaka Furuya, Miyuki Kanda, Noriyuki Satoh

POA-004

The cycad coralloid root contains a diverse endophytic bacterial community including cyanobacteria encoding specific biosynthetic gene clusters

Angelica Cibrian-Jaramillo*, Francisco Barona-Gomez, Antonio Corona-Gomez, Karina Gutierrez-Garcia, Pablo Cruz-Morales, Pablo Suarez-Moo, Nelly Selem-Mojica, Miguel A. Perez-Farrera

POA-007

The coming and going of mutualistic symbionts: The ins and outs of co-obligate endosymbiont replacement in Cinara aphids

Alejandro Manzano-Marin*, Armelle Coeur d'acier, Anne-Laure Clamens, Celine Orvain, Corinne Cruaud, Valerie Barbe, Emmanuelle Jousselin

POA-009

Population genomics and co-evolutionary dynamics of Wolbachia-host symbiotic interaction in different host species

Kun D. Huang*, Matthias Scholz, Davide Albanese, Claudio Donati, Nicola Segata, Omar Rota-Stabelli

POA-010
Global shifts in gene expression profiles accompanied with environmental changes in cnidarian-dinoflagellate endosymbiosis
Yuu Ishii*, Shinichiro Maruyama, Yusuke Aihara, Takeshi Yamaguchi, Katsushi Yamaguchi, Shuji Shigenobu, Hiroki Takahashi, Masakado Kawata, Naoto Ueno, Jun Minagawa

POA-015
Identification of fungal and algal genes involved in the symbiosis of lichen Usnea hakonensis
Mieko Kono*, Yoshiaki Kon, Yoshihito Ohmura, Yoko Satta, Yohey Terai

POA-018
Unveiling the architecture and evolution of microbial genomes from their homologous sequences
Kaoru Yoshida*

POA-019
Coevolution of Termites and Their Microbiomes?
Xianfa Xie*, Alonzo Anderson, Latoya Wran, Myrna Serrano, Gregory Buck

POA-020
Coprolites reveal microbial symbionts facilitated the adaptation to environment of the extinct cave goat Myotragus balearicus
Yichen Liu*, Luis Arriola, Jamie Wood, Josep Alcover Antoni , Joan Pons, Bastien Llamas, Alan Cooper, Laura Weyrich, Pere Bover

POA-021
Polarella genomics: understanding cold adaptation and evolutionary transition to symbiosis in dinoflagellates
Timothy Gordon Stephens*, Debashish Bhattacharya, Mark A Ragan, Cheong Xin Chan

POA-022
Comparative functional genomics of the obligate endosymbiont Buchnera aphidicola
Rebecca A Chong*, Nancy A Moran

POA-024
Evolutionary genomics of coral reef symbionts
Raul Augusto Gonzalez-Pech*, Debashish Bhattacharya, Mark A Ragan, Cheong Xin Chan

POA-025
Evolution of exon-intron boundary recognition in coral symbiotic algae
Shinichiro Maruyama*, Yuu Ishii, Konomi Fujimura-Kamada, Natsumaro Kutsuna, Shunichi Takahashi, Takashi Makino, Jun Minagawa, Masakado Kawata

POA-026
The evolutionary footprint of lichenization - Towards the characterization of a eukaryotic pioneering holo-organism
Bastian Greshake Tzovaras, Arpit Jain, Ingo Ebersberger*

POA-027
Eukaryote genes are more likely than prokaryote genes to be composite
Yaqing Ou*, James McInerney

POA-029

Identification of the Paramecium bursaria genes involved in endosymbiosis with Chlorella spp.

Jun-Yi Leu*, Yu-Hsuan Cheng, Yen-Hsin Yu, Chien-Fu Jeff Liu, Trees-Juen Chuang, Isheng Jason Tsai

POA-030

High-resolution metagenomics uncovers microbiota acquisition dynamics in the mussel Bathymodiolus brooksi

Devani Romero-Picazo*, Tal Dagan, Nicole Dubilier, Rebecca Ansorge, Anne Kupczok

POA-032

Rates of Gut Microbiome Divergence in Mammals

Alex Nishida*, Howard Ochman

POA-033

Diversity and horizontal gene transfer of nodule bacteria associated with *Lotus japonicus* in natural environments

Masaru BAMBA*, Seishiro AOKI, Tadashi KAJITA, Yasuyuki WATANO, Hiroaki Setoguchi, Syusei SATO, Takashi Tsuchimatsu

POA-034

Gut metagenomes reveal the evolution of lignocellulolytic abilities across termites

Lucia Zifcakova*, Thomas Bourguignon

POA-035

Large scale comparative genomics reveals the path to genome reduction in the cockroach endosymbiont, Blattabacterium cuenoti.

Yukihiro Kinjo*, Gaku Tokuda, Nathan Lo, Thomas Bourguignon

POA-037

Strong genomewide selection on protein coding sequences of bacterial endosymbionts and obligate pathogens

Saurabh Mahajan*, Deepa Agashe

POA-038

Game of Introns: in search of plastid-derived HGTs in plant and algal nuclear genomes

Vera Mukhina*, Mikhail Gelfand

SY13: Human evolution after out-of-Africa

POA-413

The Prediction of the Externally Visible Characteristics of Medieval Human Remains from Poulton, UK, using Next Generation Sequencing

Amanda June Skinner, Ashley Lynn May, Anders Gotherstrom, Linus Girdland Flink, Kyoko Moores Yamaguchi*

POB-149

Paternal Lineage Bursts in the Western Mediterranean

Francesc Calafell*, Neus Sole-Morata, Carla Garcia-Fernandez, Patricia Villaescusa, Marian M. de Pancorbo, David Comas

POB-150

Adaptive eQTLs in human populations reveal the evolutionary impacts of pleiotropy and tissue-specificity

Joseph Lachance*, Melanie Quiver

POB-151

Blunted nitric oxide regulation and high altitude adaptation in Tibetans

Yaoxi He*, Xuebin Qi, Chaoying Cui, Bing Su

POB-152

High Resolution SNP Genotyping of Y-Chromosomes from Kazak Populations Living in Jetisuu Region, Kazakstan Affirms a Common Paternal Ancestry

Ayken Askapuli*, Miguel G Vilar, Maxat Zhabagin, Sabitov Zhaxylyk, Timothy A Jinam, Schurr G Theodore, Zhaxybay Zhumadilov, Naruya Saitou

POB-154

Modelling human adaptations in mice

Michal Szpak*, Yali Xue, Qasim Ayub, Valerie Vancollie, Yvette Hooks, Neil J Ingham, Morag A Lewis, Mark Campbell, Sergio Rodriguez-Cuenca, Toomas Kivisild, Antonio Vidal-Puig, Karen P Steel, Chris J Lelliott, Chris Tyler-Smith

POB-155

The European heritage of American populations

Francesco Montinaro*, Linda Ongaro, Marilia Scliar, Kristina Tambets, Jose Rodrigo Flores Espinosa, Stefania Sarno, Guido Alberto Gnecchi Ruscone., Donata Luiselli, Marta E. Alarcon-Riquelme, Andres Moreno Estrada, Alessandro Achilli, Ornella Semino, Anna Olivieri,, Antonio Torroni, Cristian Capelli, Eduardo Tarazona Santos, Luca Pagani, Mait Metspalu

POB-156

Characterizing archaic hominid's contribution to genetic variation in modern human populations following migration out of Africa

Kelsey E. Witt*, Jonathan Rice, Emilia Huerta-Sanchez

POB-157

Recent human demographic history confounds population genetic inference of recessive selection

Daniel M. Jordan*, Daniel J. Balick, Shamil R. Sunyaev, Ron Do

POB-159

Inference of time-varying mutation rates in human populations

Jeffrey P. Spence*, Yun S. Song

POB-160

Uniparental Markers Show Sex-biased Admixture in Ancient Pacific Populations

Kathrin Naegele*, Cosimo Posth, Frederique Valentin, Stuart Bedford, Monica Tromp, Jana Zech, Patrick Roberts, Johannes Moser, Julia Gresky, Russell Gray, Adam Powell, Johannes Krause

POB-162

Phenotype and phylogeny of Neolithic Japanese hunter-gatherers, Jomon people, based on whole nuclear genome sequences

Hideaki Kanzawa-Kiriyama*, Timothy Jinam, Yoshuke Kawai, Takehiro Sato, Kazuyoshi Hosomichi, Atsushi Tajima, Kryukov Kirill, Noboru Adachi, Naruya Saitou, Ken-ichi Shinoda

POB-163

Strong selection favoring Neanderthal-free segments on the X chromosome in out-of-Africa populations

Kasper Munch*, Mikkel Heide Schierup, Laurits Skov, Moises Coll Marcia, Elise Lucotte

POB-164

Origins of the Livestock in Madagascar

Takahiro Yonezawa*, Yoshio Yamamoto, Felix Rakotondraparany, Masahide Nishibori

POB-165

Extremely rare variants reveal complex patterns of germline mutation in humans

Jedidiah Carlson, Jun Li, Sebastian Zollner*

POB-166

Regulatory variation and selection in traditional populations of Southeast Asia

Katalina Sara Bobowik*, Irene Gallego Romero, Murray Cox

POB-169

Study of the North African human genetic landscape through the analysis of complete genome sequences

Gerard Serra-Vidal*, David Comas

SY14: Improving inference frameworks by accounting for population structure

POA-199

Realistic evolutionary simulations for population genetic inferences with SLiM 3

Benjamin C. Haller*, Philipp W. Messer

POA-200

Relative Levels of Nonneutral vs. Neutral Polymorphism under Balancing Selection through Storage Effect

Yeongseon Park *, Yuseob Kim

POA-201

Hitchhiking in space, with varying selection intensity and migration rates among demes

Yichen Zheng*, Thomas Wiehe

POA-202

Properties of haplotype-based Fst computed as a function of haplotype length

Rohan S Mehta*, Alison F Feder, Noah A Rosenberg

POA-203

Efficient and exact computational solutions to Wright-Fisher Markov models with varying population sizes

Ivan Krukov*, Bianca de Sanctis, A. P. Jason de Koning

POA-206

Evidencing divergent selection from linked sites while accounting for hierarchical population structure

Marco Galimberti*, Christoph Leuenberger, Simone Fior, Matthieu Foll, Daniel Wegmann

POA-207

Population structure and vulnerability in mangrove species as a result of geographic barriers and climatic changes

Zhengzhen Wang*, Haomin Lyu, Suhua Shi

POA-208

Multi-species genetic structure, demography and adaptation of the mangrove genus *Rhizophora* in the Atlantic East Pacific and South Pacific region, revealed by re-sequencing data.

Yoshiaki Tsuda*, Takashi Yamamoto, Ryosuke Imai, Takaya Iwasaki, Koji Takayama, Tadashi Kajita

POA-210

The population genomics of the mangrove species Sonneratia alba cast light on the genome shaping from isolation and migration

Qipian Chen*, Zixiao Guo, Ziwen He, Suhua Shi

POA-212

Demographic inferences after a range expansion (can be biased): the test case of the blacktip reef shark (Carcharhinus melanopterus)

Pierpaolo Maisano Delser*, Shannon Corrigan, Drew Duckett, Arnaud Suwalski, Michel Veuille, Serge Planes, Gavin Naylor, Stefano Mona

POA-213

Impacts of Recurrent Hitchhiking on Divergence and Demographic Inference in Drosophila

Jeremy D Lange, John E Pool*

POA-214

Population structure of amphioxus *Asymmetron lucayanum* at West and Central Pacific region

Hsiu-Chin Lin*, Shun-Yi Fang

SY15: Integrating ancient and modern DNA for evolutionary genomics

POA-224

Development Of Next-Generation Sequencing (NGS) Techniques For Museum Specimens

Elsa Call*, Victoria Twort, Niklas Wahlberg

POA-225

Historic Treponema pallidum genomes from Colonial Mexico

Verena J Schuenemann*, Aditya Kumar Lankapalli, Rodrigo Barquera, Elizabeth Nelson, Diana Iraiz Hernandez, Victor Acuna Alonzo, Kirsten I Bos, Lourdes Marquez Morfin, Alexander Herbig, Johannes Krause

POA-226

The evidence of cattle domestication in Thailand: Indicated by ancient DNA of cattle specimens in the Bronze and Iron Ages

Sirianong Siripan*

POA-228

Determining Relatedness of Ancient Individuals

Angela Wieber*, Joshua Schraiber

POA-231

The genetic history of Africa based on modern and ancient DNA

Carina Maria Schlebusch*

POA-233

The Transition to Farming in Eneolithic (Copper Age) Ukraine was Largely Driven by Population Replacement

Ryan William Schmidt*, Daniel Fernandes, Jordan Karsten, Thomas Harper, Gwyn Madden, Sarah Ledogar, Mykhailo Sokhatsky, Hiroki Oota, Ron Pinhasi

POA-234

Population Dynamics at Late Chalcolithic and Early Bronze Age Arslantepe, Anatolia

Eirini Skourtanioti*, Choongwon Jeong, Yilmaz Selim Erdal, Marcella Frangipane, Philipp Wolfgang Stockhammer, Johannes Krause, Wolfgang Haak

POA-235

Ancient dental calculus: unlocking a high-resolution proxy of past human movement and interaction

Raphael Eisenhofer*, Atholl Anderson, Keith Dobney, Scott Fitzpatrick, Alan Cooper, Alain Froment, Laura Susan Weyrich

POA-236

Genetic transition in the Swiss Late Neolithic and Early Bronze Age

Anja Furtwaengler*, Ella Reiter, Gunnar U. Neumann, Inga Siebke, Noah Steuri, Joachim Wahl, Juergen Hald, Verena J. Schuenemann, Philipp Stockhammer, Albert Hafner, Sandra Loesch, Johannes Krause

POA-237

Quantifying performance of admixture detection with ancient DNA

Torsten Gunther, Amy Goldberg, Joshua G Schraiber*

POA-238

Efficiently integrating ancient DNA into modern Y chromosome trees

Rui Martiniano*, Lara Cassidy, Daniel Bradley, Richard Durbin

POA-239

People from Ibiza: an unexpected isolate in the Western Mediterranean

Simone Andrea Biagini*, Neus Sole-Morata, Pierre Zalloua, Lisa Matisoo-Smith, David Comas, Francesc Calafell

POA-240

Into the great wide open: the genomic history of the Greater Caucasus region

Wolfgang Haak*, Chuanchao Wang, Sabine Reinhold, Andrej B. Belinskij, Alexey Kalmykov, Natalia Berezina, Alexandra Buzhilova, Thomas Higham, Thomas Stoellner, Lars Fehren-Schmitz, Viktor Trifonov, David Reich, Svend Hansen, Johannes Krause

POA-242

Lipids and the evolution of human diet

Iain Mathieson*, Sara Mathieson

POA-243

Migration and Social Organization in Medieval Europe - a Paleogenomic Approach

Carlos Eduardo Guerra Amorim*, Stefania Vai, Cosimo Posth, Daniel Winger, Tivadar Vida, Dean Bobo, Susanne Hakenbeck, Guido Barbujani, David Caramelli, Walter Pohl, Caterina Giostra, Johannes Krause, Patrick J Geary, Krishna R Veeramah

POA-246
A new targeted-capture method using bacterial artificial chromosome (BAC) as baits exclusively developed for sequencing relatively large loci of ancient DNA
Kae Koganebuchi*, Takashi Gakuhari, Hirohiko Takeshima, Satoshi Kasagi, Takehiro Sato, Atsushi Tajima, Hiroki Shibata, Motoyuki Ogawa, Hiroki Oota

POA-248
Adaptive Evolution and Archaic Introgression of Copy Number Variants in Melanesians
PingHsun Hsieh*, Zev Kronenberg, Stuart Cantsilieris, Kendra Hoekzema, Katherine Munson, Francesca Antonacci, Mario Ventura, Evan Eichler

POA-250
On the duration of Neandertal admixture
Benjamin Peter*

POA-252
Genome-Wide Ancient DNA Portrays the Forming of the Finnish Population Along a 1400-Year Transect
Kerttu Majander*, Elina Salmela, Kati Salo, Thiseas Christos Lamnidis, Stephan Schiffels, Paivi Onkamo, Johannes Krause

POA-253
The first Epipaleolithic Genome from Anatolia suggests a limited role of demic diffusion in the Advent of Farming in Anatolia
Michal Feldman*, Eva Fernandez-Dominguez, Luke Reynolds, Raffaela Bianco, Cosimo Posth, Adrian Nigel Goring-Morris, Jessica Pearson, Hila May, Israel Hershkovitz, Douglas Baird, Choongwon Jeong, Johannes Krause

POA-254
Robust Reference-Free Archaic Admixture Segmentation Using A Structured Permutation-Equivariant Network
Jeffrey Chan*, Yun Song

POA-256
Giant deer (Megaloceros giganteus) phylogeography and population dynamics: Insights from Late Pleistocene and Holocene mitochondrial genomes from Eurasia
Alba Rey-Iglesia*, Adrian M Lister, Paula F Campos, Selina Brace, Ian Barnes, Anders J Hansen

POA-257
A Systematic Investigation of DNA Preservation in Medieval Skeletal Elements
Cody Edward Parker*, Susanne Friederich, Wolfgang Haak, Kirsten Bos, Johannes Krause

POA-258
Historical and modern rabbit populations reveal parallel adaptation to myxoma virus across two continents
Joel M Alves*, Miguel Carneiro, Jade Y Cheng, Ana Lemos de Matos, Masmudur M Rahman, Liisa Loog, Anders Eriksson, Grant McFadden, Rasmus Nielsen, Thomas P Gilbert, Pedro J Esteves, Nuno Ferrand, Francis M Jiggins

POA-259
Reliable Inference of Genetic Diversity within and between Ancient and Modern Genomes
Vivian Link*, Zuzana Hofmanova, Athanasios Kousathanas, Jens Bloechler, Christoph Leuenberger, Thomas Terberger, Detlef Jantzen, Joachim Burger, Daniel Wegmann

POA-260

Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe

Thiseas Christos Lamnidis*, Kerttu Majander, Choongwon Jeong, Elina Salmela, Anna Wessman, Vyacheslav Moiseyev, Valery Khartanovich, Antti Sajantila, Janet Kelso, Svante Paabo, Paivi Onkamo, Wolfgang Haak, Johannes Krause, Stephan Schiffels

POA-261

Late Pleistocene North African genomes show deep genetic relationship with ancient Near East and sub-Saharan Africa

Marieke Sophia van de Loosdrecht*, Abdeljalil Bouzouggar, Louise Humphrey, Cosimo Posth, Nick Barton, Ayinuer Aximu-Petri, Birgit Nickel, Jean-Jacques Hublin, Svante Paabo, Stephan Schiffels, Matthias Meyer, Wolfgang Haak, Choongwon Jeong, Johannes Krause

POA-262

The evolutionary history of human cancer genes

Jose Maria Heredia-Genestar*, David Juan, Tomas Marques-Bonet, Arcadi Navarro

POA-264

Demographic processes in Estonia from Bronze Age through Iron Age to Medieval times.

Mait Metspalu*, Lehti Saag, Kristiina Tambets, Alena Kushniarevich, Liivi Varul, Jyri Parik, Martin Malve, Heiki Valk, Lauri Saag, Valter Lang, Aivar Kriiska, Richard Villems, Toomas Kivisild, Christiana Lyn Scheib

POA-265

Unravelling the Estonian genome: the whole is greater than the sum of its parts

Davide Marnetto*, Francesco Montinaro, Lauri Saag, Reedik Magi, Mait Metspalu, Luca Pagani

POA-270

Detecting polygenic adaptation in human history

Fernando Racimo*

POA-271

Pseudogenization of PON1 in Marine Mammals Implies Sensitivity to Organophosphate Pesticides

Jerrica Mae Jamison*, Wynn Meyer, Clement Furlong, Rebecca Richter, Nathan Clark

SY16: Intra-host evolutionary dynamics

POB-086

Different types of cell migration during tumor growing process lead to spatial patterns of genetic variation

Yongsen Ruan Ruan*, Ao Lan, Chung-I Wu

POB-087

Genomic Reconstruction of Transmission Networks in Malaria

Seth Redmond*, Bronwyn Maccinnis, Selina Bopp, Amy Bei, Daouda Ndiaye, Daniel Hartl, Dyann Wirth, Sarah Volkmann, Daniel Neafsey

POB-090

Evolutionary analysis of epitopes and low complexity regions in Plasmodium

Sarah Medley*, Alyssa Beaudet, Helen Piontkivska, Fabia Ursula Battistuzzi

POB-092

Recurrent loss of functional repressors in the evolution of *Escherichia coli* in the mice's gut

Mohamed GHALAYINI*, Sara DION, Melanie MAGNAN, Erick DENAMUR, Mathilde LESCAT, Olivier TENAILLON

POB-093

Simulation of Intratumor Heterogeneity and its Medical Implication

Watal M. Iwasaki*, Hideki Innan

POB-094

Evolution of an intratumoral ecology susceptible to successive treatment in breast cancer xenografts

Hyunsoo Kim, Pooja Kumar, Francesca Menghi, Javad Noorbakhsh, Eliza Cerveira, Mallory Ryan, Qihui Zhu, Chengsheng Zhang, James Keck, R Krishna Murthy Karuturi, Carol J Bult, Charles Lee, Edison T Liu, Jeffrey H Chuang*

POB-096

Rapid adaptations to the accidental human host in Legionella pneumophila

Daniel Dennis Leenheer*, Carmen Pelaz, Matilda Morin, Elisabeth Hallin, Daniella Klingenberg, Sophie Jarraud, Christoph Ginevra, Lionel Guy

POB-097

Comparative genomics of *Mycobacterium tuberculosis* samples from patient serial isolates reveals antigenic variation during active TB disease

Roger Vargas*, Luca Freschi, Francis Drobniewski, Inaki Comas, Megan Murray, Maha Farhat

POB-098

Search for the factors related to HCV replication in the HuH-7 cell line lineages

Masaki Kawamoto*, Toshinori Endo, Masayoshi Fukasawa, Kentaro Hanada, Naoki Osada

POB-099

Naturally occurring West Nile virus infections display no evidence for heightened selective constraint in avian hosts over mosquito vectors

Chase W. Nelson*, Tony L. Goldberg, Sergios-Orestis Kolokotronis, Gabriel Hamer L., Christina M. Newman, Samuel D. Sibley, Tavis K. Anderson, Edward D. Walker, Marilyn O. Ruiz, Jeffrey D. Brawn, Uriel D. Kitron

POB-100

The effect of HIV co-infection in the evolution Mycobacterium tuberculosis

Daniela Brites*, Chloe Loiseau, Eddie Wampande , Jan Hattedorf, Henry Boom, Moses Joloba, Sebastien Gagneux

POB-101

Using genotype abundance to improve phylogenetic inference

William S. DeWitt*, Luka Mesin, Gabriel D. Victora, Vladimir N. Minin, Frederick A. Matsen

POB-102

Rapid adaptation of bacteriophage to their host after host-switching

Xuhua Xia*

POB-103

Characterising local epidemiology of *P. falciparum* through the structure of mixed infections

Sha Joe Zhu*, Jason Hendry, Jacob Garcia, Gil McVean

SY17: Linking the mitochondrial genotype to phenotype: a complex endeavour

POB-127

Mitochondrial-encoded genes contribute to thermal divergence between Saccharomyces species

Xueying C. Li*, David Peris, Chris Todd Hittinger, Elaine A. Sia, Justin C. Fay

POB-129

A screen for mitochondrial genetic effects on locomotory performance of fruit flies across a thermal gradient, and implications for climatic adaptation

Venkatesh Nagarajan-Radha*, Damian Kimon Dowling

POB-130

Mitochondrial-Nuclear Interactions and the Thermal Sensitivity of Spermatogenesis

Abhilesh Dhawanjewar*, Kristi Montooth, Colin Meiklejohn

POB-132

Intracellular and intraorganellar co-expression of divergent mitochondrial electron transport chain subunits in the germ line of a naturally heteroplasmic species

Fabrizio Ghiselli, Maria Gabriella Maurizii, Helena Arino, Carmine Cifaldi, Arkadiy Reunov, Yana Alexandrova, Andrea Pecci, Simone Bettini, Marco Passamonti, Valeria Franceschini, Liliana Milani*

POB-133

Molecular evolution of OXPHOS protein subunits in fishes with novel phenotypes

Ahmed A Elbassiouny*, Belinda S.W Chang, Nathan R. Lovejoy

POB-137

Transition transversion ratio in mitochondrial genome is higher in long- versus short-lived mammalian species: effects of ROS and replication timing?

Alina G. Mikhaylova*, Alina A. Mikhaylova, Kristina Ushakova, Evgenii Tretyakov, Andrey Yurchenko, Dmitry Knorre, Ilia Mazunin, Alexandre Reymond, Konstantin Gunbin, Konstantin Popadin

POB-138

Variability in Gibbs energy of tRNA molecules in mitochondrial genomes of Chordates: neutral selection or evolution towards optimization of translation?

Kristina Ushakova*, Alina A. Mikhailova, Alina G. Mikhailova, Dmitry Knorre, Ilia Mazunin, Alexandre Reymond, Konstantin Gunbin, Konstantin Popadin

SY18: Looking beyond the genome: cultural and behavioral drivers of biological evolution

POB-104

Genome-wide variation in the Andes, Amazonia and Pacific coast of western South America

Chiara Barbieri*, Rodrigo Barquera, Leonardo Arias, Jose Raul Sandoval, Oscar Acosta, Ricardo Fujita, Camilo Zurita, Kentaro Shimizu, Paul Heggarty, Russell Gray, Mark Stoneking, Irina Pugach

POB-107

Hybrid type of nuclear and plastid DNAs suggests the hypothesis for ancient propagation of American bottle gourd (Lagenaria siceraria)

dai watabe*, Hiroshi Yuasa, Naoki Osada, Kazuhiro Satomura, Toshinori Endo

POB-108

The founding events in different Roma groups revealed through complete Y chromosome sequences

Carla Garcia Fernandez*, Neus Sole Morata, Neus Font Porterias, Erica Bianco, David Comas, Francesc Calafell

POB-110

Linguistics as a Complementary Metric for Human Migration History and the Peopling of the Americas

Kara Boyer*, Nicole Creanza, Maanasa Raghavan

SY19: Machine learning approaches in evolutionary genetics

POA-299

Neanderthal ancestry in modern-day humans provide clues for the pattern of Neanderthal-human admixture in the past

Fernando A. Villanea*, Joshua G. Schraiber

POA-301

CLADES: A Classification-based Machine Learning Method for Species Delimitation from Population Genetic Data

Jingwen Pei, Chong Chu, Xin Li, Bin Lu, Yufeng Wu*

POA-302

SeleDiff: A fast and scalable tool for testing and estimating selection differences between populations

Xin Huang*

POA-304

Rates of molecular evolution suggest life history and a post-K-Pg nocturnal bottleneck of Placentals

Jiaqi Wu*, Takahiro Yonezawa, Hirohisa Kishino

POA-306

Fast Approximate Inference for Phylogenetic Reconstruction via Stochastic Variational Inference in Large Data Sets

Tung Thanh Dang *

POA-307

Probabilistic modeling of genetic variation reveals protein-protein interactions and the effects of mutations on interactions

Anna Gustafson Green*, Debora Marks

POA-309

Prediction model to infer degree of functionalization based on protein and expression divergence rate in Arabidopsis

Akihiro Ezoe*, Kazumasa Shirai, Kousuke Hanada

POA-310

Learning and interpreting the evolution of the gene regulatory grammar in a deep neural network framework

Ling Chen*

POA-311

Machine reasoning with phenotypes: enhancing expert knowledge about the genetics of an ancient evolutionary transition

Todd Vision*, Dahdul Wasila, James Balhoff, Alex Dececchi, Pasan Fernando, Hilmar Lapp, Paula Mabee, Prashanti Manda, Kellen Mastick, Monte Westerfield, Erliang Zeng

POA-312

Proteome-wide evidence for evolutionary signatures of function in highly diverged disordered regions

Taraneh Zarin*, Alan Michael Moses

POA-313

Machine learning identifies signatures of host adaptation in the bacterial pathogen Salmonella enterica

Nicole E Wheeler*, Paul P Gardner, Lars Barquist

POA-314

Associating the microbiome with experimental treatment groups, using a random forest, in a model of inflammatory bowel disease

Gurdeep Singh*, Sheena Cruickshank, Andrew Brass, Christopher Knight

POA-401

Classifying ENU induced mutations from spontaneous germline mutations in mouse with machine learning techniques

Yicheng Zhu*, Cheng Soon Ong, Gavin Huttley

SY20: Mapping genotype and phenotype to fitness

POA-414

Experimental Determination of the Rate of Muller's Ratchet in Escherichia coli

Joshua John Miranda*, Mrudula Sane, Deepa Agashe

POB-358

Adaptive evolution after losing an essential gene in yeast

Shang-Lin Chang*, Hsuan-Kai Wang, Luh Tung, Tien-Hsien Chang

POB-359

An experimental phylogeny to benchmark ancestral sequence reconstruction

Ryan N. Randall*, Caelan E. Radford, Kelsey A. Roof, Divya K. Natarajan, Eric A. Gaucher

POB-360

Mapping resistance to eight different viruses in the genetic model organism Drosophila melanogaster

Rodrigo Cogni*, Francis Jiggins

POB-361

Mistranslation influences the bacterial stress response

Laasya Samhita*, Parth K Raval, Deepa Agashe

POB-363

A population genetics perspective on measures of intolerance to mutation

Zachary L Fuller*, Jeremy J Berg, Hakhamanesh Mostafavi, Guy Sella, Molly Przeworski

POB-364

Fitness effects of new mutations in Chlamydomonas

Peter Keightley*, Katharina Boendel, Toby Samuels, Susanne Kraemer, Rob Ness, Colegrave Nick

POB-366

Exploring the mutational landscape of TEM-1 beta-lactamase reveals mechanism of bacterial death

Andre Birgy*, Herve Jacquier, Melanie Magnan, Sebastien Fleurier, Karine Panigoni, Julie Lasvergnas, Audrey Chapron, Ivan Matic, Olivier Tenaillon

POB-367

Protein stability potentially governing protein evolution

Ryo Kurahashi*, Shunichi Tanaka, Satoshi Sano, Hiroyoshi Matsumura, Kazufumi Takano

POB-368

Detection and charaterization of deleterious variants in traditional chicken breeds

Chiara Bortoluzzi*, Martijn Derks, Steffen Weigend, Martien AM Groenen, Hendrik-Jan Megens

POB-369

Exploring the biochemical changes driven by protein evolution among phosphoenolpyruvate carboxylases (PEPC), the key carbon fixation enzymes of a C4 grass family.

Chatchawal Phansopa*, Jim Reid, Pascal-Antoine Christin

POB-370

The Genomics of Adaptive Divergence with Gene Flow by Means of Experimental Evolution

Sergio Tusso*, Bart P.S. Nieuwenhuis, Simone Immler, Jochen B.W. Wolf

POB-371

Genomic evidence for mitonuclear incompatibilities in interpopulation hybrids of the copepod Tigriopus californicus

Ronald S Burton*, Thiago G Lima, Ricardo J Pereira

POB-372

Signature of positive selection in Langshan chicken comparison with the Indonesian breed and red jungle-fowl

Tatsuhiko Goto*, Raman A Lawal, John E Pool, Dong-Dong Wu, Ya-Ping Zhang, Paul M Hocking, David W Burt, Olivier Hanotte

POB-373

Adaptation to new environment: the pH challenge

Rita Di Martino*, Sara Mitri

POB-374

Evolution and maintenance of non-male producing phenotypes in Daphnia

Christoph Haag*, Yan Galimov, Celine Reisser, Cecile Molinier, Peter Fields

POB-376

Mutation dynamics and fitness effects followed in single cells

Marina ELEZ*, Lydia ROBERT, Jean OLLION

POB-377

The architecture of adaptation: a master mutation or a mass of mutations?

Sophie Archambeault*, Luis Baertschi, Catherine Peichel

POB-378

Adaptations for dim light vision in cichlids: evidence from opsin gene family evolution and protein function

Frances E Hauser*, Katriina L Ilves, Ryan K Schott, Gianni M Castiglione, Hernan Lopez-Fernandez, Belinda SW Chang

POB-379

Revealing SNPs of 0.1% effect in a diverse yeast cross through Barcoded Bulk QTL mapping

Katherine R Lawrence*, Artur Rego-Costa, Michael M Desai, Alex N Nguyen Ba

POB-381

The joint fitness landscape of two genetically interacting genes

Xukang Shen*, Jianzhi Zhang

POB-382

From DNA to ecosystems: using a model microbial community to study adaptation

Sandeep Venkataram*, Jacob Robertson, Sergey Kryazhimskiy

POB-383

Molecular and phenotypic characterization of *roo* elements inserted in the promoter of a *Drosophila* stress-response gene

Miriam Merenciano*, Josefa Gonzalez

POB-384

The impact of protein architecture on adaptive evolution

Ana Filipa Moutinho*, Julien Yann Dutheil

POB-386

Positive selection and red-shifting substitutions in the rhodopsin gene of a globally distributed family of fishes making evolutionary transitions into freshwater.

Alexander Van Nynatten*, Gianni M Castiglione, Nathan Lovejoy R, Belinda Chang SW

POB-387

Applying phylogenetic tree-based approach to genome-wide association studies in Mycobacterium tuberculosis

Valentina Burskaia*, Gennady Fedonin, Georgii Bazykin, Alexey Neverov

POB-389

Selective landscapes of gene expression and other quantitative molecular traits in mammals

Marco Mariotti*, Siming Ma, Toni Gabaldon, Vadim N Gladyshev

POB-390

Modelling adaptive bet-hedging: the challenges ahead

Omri Tal*

POB-392

Transcriptional and translational effects of adaptive synonymous mutations in *Pseudomonas fluorescens*

Nicholas McCloskey*, Rees Kassen, Aaron Hinz

POB-394

Systematic screening of compensatory mutations across a protein binding interface.

David Ding*, Debora Marks, Mike Laub

POB-396

Deep Mutational Scanning to Probe the Sequence-Function Relationships of Metallo-Beta-Lactamases

John Chen*, Ray Socha, Nobuhiko Tokuriki

POB-397

Gene, environment and cellular interactions underlying behavioral variance and their relation to fitness during experimental evolution

Luke Noble*, Thiago Guzella, Matthew Rockman, Henrique Teotonio

POB-399

Directed evolution of ion-selectivity in bacterial and archaeal flagellar motors

Jessica Clark*, Gonzalo Peralta, Josh M Machet, Mark M Tanaka, Matthew A B Baker

POB-401

The birth and the death of premature start codons in human genome is limited by selection

Vitaly Segodin, Svetlana Iarovenko, Stepan Denisov*, Ruslan Soldatov

POB-403

Quantifying the effects of pleiotropic mutations on the robustness of signaling pathways

Purnima S. Kompella*, Sergio G. Peisajovich, Alan M. Moses

SY21: Microbial evolution: human-microbe interactions and the role of deep sequencing in time series analysis

POA-410

High resolution analysis of emerging mutations at very short timescale

Han Mai, Anton Nekrutenko*

POB-141

Co-evolution within a synthetic microbial community

Philippe Piccardi*, Sara Mitri

POB-142

Reconstruction of Oral Microbiomes from Extinct and Extant Anthropoids through ancient DNA

James A Fellows Yates*, Oral Microbiome Evolution Consortium -, Matthew C Curtis, J. Carlos Diez, Victoria E Gibbon, Mario Menedez, Marco Peresani, Mirjana Roksandic, Michael J Walker, Robert C Power, Domingo C Salazar-Garcia, Johannes Krause, Alexander Herbig, Christina Warinner

POB-145

The co-occurrence and co-exclusion of evolving objects in prokaryotes

Fiona Jane Whelan*, Martin Rusilowicz, James McInerney

SY23: Open Symposium

POA-064
M1CR0B1AL1Z3R - A user-friendly software tool for the analysis of microbial genomics data
Oren Avram*, Tal Pupko

POA-067
A journey from an ancient finger print of Rossmann fold enzymes to cofactor engineering
Paola Laurino*

POA-068
Relaxed evolutionary constraint of gene expression in the snake venom arsenal leads to diversification and parallelism.
Agneesh Barua*, Alexander Mikheyev

POA-069
Evolutionary evidence for independent origins of genes essential for the proper establishment of left-right asymmetry in amphibians and mammals
Juan Cristobal Opazo*

POA-070
Genomic signatures of a Mannheimia haemolytica lineage associated with bovine respiratory disease
Michael Clawson*, Gennie Schuller, Aaron Dickey, Robert Murray, Michael Sweeney, Michael Apley, Keith DeDonder, Sarah Capik, Robert Larson, Brian Lubbers, Brad White, Jochen Blom, Dayna Brichta-Harhay, Timothy Smith

POA-071
Age-dependent patterns of adaptation to diet in Drosophila melanogaster
Grant Allen Rutledge*, Kevin H Phung, Laurence D Mueller, Michael R Rose

POA-072
Evolutionary biology meets synthetic biology: designing a translational machinery that enhances incorporation of non-proteinogenic amino acids into proteins by evolutionary analysis
Mariko F. Matsuura*, Sarah Lucas, Vanessa E. DeLey Cox, Eric A. Gaucher

POA-074
A single pheromone receptor gene shared among most bony vertebrates
Masato Nikaido*, Hikoyu Suzuki, Takehiko Ito, Junji Hirota

POA-075
Ecological influence of sediment bypass tunnels on macroinvertebrates in dam-fragmented rivers using DNA metabarcoding
Joeselle Serrana*, Sakiko Yaegashi, Shunsuke Kondoh, Bin Li, Christopher Robinson, Kozo Watanabe

POA-076
Evolution of rapid life cycle through deletion of a genetic hotspot after recent gene duplication in Boechera stricta
Cheng-Ruei Lee*, Eric Schranz, Thomas Mitchell-Olds

POA-077

Whole genome sequencing of a Japanese endemic pit viper, habu, *Protobothrops flavoviridis* reveals accelerated evolution of venom protein genes enriched in microchromosomal regions.

Hiroki Shibata*, Takahito Chijiwa, Naoko Oda-Ueda, Kazuaki Yamaguchi, Shosaku Hattori, Kazumi Matsubara, Yoichi Matsuda, Ryo Koyanagi, Kanako Hisata, Yasuyuki Fukumaki, Motonori Ohno, Eiichi Shoguchi, Noriyuki Satoh, Tomohisa Ogawa

POA-078

The effective population size is correlated to census population size in mammals.

Jennifer James, Adam Eyre-Walker*

POA-079

Closing the Lipid Divide: Phylogenetic analysis of phospholipid biosynthetic pathways in Archaea and Bacteria

Gareth A. Coleman*, Richard D. Pancost, Tom A. Williams

POA-080

Differences between de novo genes and their non-functional precursors can result from neutral constraints on their birth process, not necessarily from natural selection alone

Lou Nielly-Thibault*, Christian R Landry

POA-081

An initiative for genetic data collection from underrepresented countries and populations

Kimberly F McManus*, Meghan Moreno, Joanne Kim, Kasia Bryc, Joanna Mountain

POA-082

Population structure in pre-contact North America: a whole-genome ancient DNA study

Christiana Scheib*, Hongjie Li, Vivian Link, Christopher Kendell, Genevieve Dewar, Peter William Griffith, Alexander Moerseburg, John R. Johnson, Amiee Potter, Susan L. Kerr, Phillip Endicott, John Lindo, Marc Haber, Yali Xue, Chris Tyler Smith, Manj Sandhu, Richard Durbin, Joseph G. Lorenz, Tori D. Randall, Zuzana Faltyskova, Luca Pagani, Petr Danecek, Tamsin C. O'Connell, Patricia Martz, Alan S. Boraas, Alexandra Sasha Lindgren, Brian F. Byrd, Alan Leventhal, Rosemary Cambra, Ronald Williamson, Louis Lesage, JohnTommy Rosas, Ernestine Ygnacio-De Soto, Mait Metspalu, Jay T. Stock, Andrea Manica, Daniel Wegmann, Ripan S. Malhi, Toomas Kivisild

POA-083

Genetic features of the Korean short-necked clam, Ruditapes philippinarum, via next-generation sequencing and comparative genomic analyses and their gene flow among Asian-Pacific Countries

Hye Suck An*, Seyoung Mun, Jiyoung Woo, Young Se Hyun, Ha Yeun Song, Jongsu Yoo, Kyudong Han

POA-084

Comparative genome analysis of *Ralstonia solanacearum* causing potato bacterial wilt in Korea

Heejung Cho*, Young Kee Lee, Seungdon Lee, Dong Suk Park, Jeong-Gu Kim

POA-085

Phylogenetic incongruence of microdiversity in a marine bacterial population

Xiaojun Wang*, Haiwei Luo

POA-087

The crossover landscape is more conserved than the double-strand-break landscape in yeast evolution

Haoxuan Liu*, Jianzhi Zhang

POA-088

Population Genetic Models for Complex Disease Evolution

Jeremy J Berg*, Guy Sella

POA-090

RNA-seq of single spermatogenic cysts shows gradual loss of dosage compensation but little evidence for meiotic X chromosome inactivation in Drosophila

Yumei Huang*, Aimei Dai, Yixin Zhao, Xu Shen, Tian Tang

POA-091

What drives the chromosomal clustering of functionally related genes?

Haiqing Xu*, Jianzhi Zhang

POA-092

Evolution of S100A3 and PADI3 genes during the mammalian lineage

Takashi Kitano*, Tadashi Minato

POA-094

Short tandem repeats in the human, cow, mouse, chicken, and lizard genomes are concentrated in the terminal regions of chromosomes

Kazuharu Misawa*

POA-095

Plastid genome mutational hotspots across gymnosperms with application for phylogenetic and barcoding studies

Edi Sudianto*, Chung-Shien Wu, Shu-Miaw Chaw

POA-096

Evolutionary changes in the thermosensory system contributed to the acquisition of heat tolerance in Buergeria japonica tadpoles inhabiting hot springs

Shigeru Saito*, Claire T. Saito, Takeshi Igawa, Shohei Komaki, Makoto Tominaga

POA-097

Rapid Evolution of Vision in Sea Snakes

Bruno F Simoes*, Filipa L Sampaio, Julian C Partridge, David M Hunt, Nathan S Hart, Davide Pisani, Belinda SW Chang, David J Gower, Kate L Sanders

POA-100

The recombination landscape in species and subspecies of wild murid rodents

Ben Jackson*, Tom Booker, Peter Keightley

POA-101

Comparative study of lactate-mediated neural plasticity genes and its implication to long-term memory formation

Amal Abdulrhman Bajaffer*

POA-103

Helicobacter pylori suggests early human migration in Asia

Rumiko Suzuki*, Osamu Matsunari, Naruya Saitou, Yoshio Yamaoka

POA-104

A developmental switch generating phenotypic plasticity is part of a conserved supergene in Pristionchus nematodes

Bogdan Sieriebriennikov*, Neel Prabh, Mohannad Dardiry, Hanh Witte, Waltraud Roeseler, Manuela R Kieninger, Christian Roedelsperger, Ralf J Sommer

POA-105

Universally High Transcript Error Rates in Bacteria

Weiyi Li*, Michael Lynch

POA-106

Evolution of isoprenoid biosynthesis from bacteria to eukaryotes

Yosuke Hoshino*, Eric Gaucher

POA-107

Native Metals And CO2 Reduction In Early Biochemical Evolution

Martina Preiner*, Mingquan Yu, Sreejith J Varma, Kamila B Muchowska, Filipa L Sousa, Joana C Xavier, Harun Tueysuez, Joseph Moran, William F Martin

POA-108

Origins of novel protein sequences de novo and by sequence divergence

Nikolaos Vakirlis*, Anne-Ruxandra Carvunis, Aoife McLysaght

POA-110

Evolution with recombination using state-of-the-art computational methods

Felipe Medina Aguayo*, Richard Everitt

POA-111

Systematic testing of a unified protocol for extracting DNA and proteins from ancient dental calculus

Zandra Fagernas*, Maite Iris Garcia-Collado, Jessica Hendy, Courtney Hofman, Camilla Speller, Christina Warinner

POA-112

The evolution of the ribosome and its impact on translation dynamics

Khanh Dao Duc*, Sanjit Batra, Nicholas Bhattacharya, Yun S Song

POA-115

Evolution and genetic control of gene expression variability and noise in humans

James J Cai*

POA-117

Chromosome-wide stochastic co-fluctuations of gene expression in mammalian cells

mengyi Sun*, jianzhi zhang

POA-118

Differential movement of song, morphology, and genes across the black-capped/ Carolina chickadee hybrid zone in Missouri

Alana Alexander*, Mark Robbins, Jesse Holmes, Robert Moyle, A. Townsend Peterson

POA-119

Structural phylogenetics with confidence

Ashar Malik, Anthony Poole, Jane Allison*

POA-120
High-throughput sequencing using combinatorial profiling
Luisa Teasdale*, Andreas Zwick

POA-121
Bacterial K-strategies on evolution experiments under various resource limitation
Takahiro Komori*, Saburo Tsuru

POA-122
Evolution of male courtship songs in the Drosophila nasuta species cluster
Matthew James Nalley*, Wynn Meyer, Doris Bachtrog

POA-123
Next-Generation Transcriptome Assembly: Strategies and Performance Analysis
Adam Voshall, Sairam Behera, Xiangjun Li, Edgar B Cahoon, Etsuko N Moriyama*

POA-124
On the multiple ways of calculating F_{ST} from DNA sequence polymorphism
Songeun Lee*, Yuseob Kim

POA-125
Cyclostomes' Hox genes provide insights into the evolutionary origin of temporal colinearity in vertebrates
Juan Pascual-Anaya*, Iori Sato, Fumiaki Sugahara, Shinnosuke Higuchi, Jordi Paps, Ren Yandong, Wataru Takagi, Adrian Ruiz-Villalba, Kinya G. Ota, Wen Wang, Shigeru Kuratani

POA-126
The Genetic mechanism underlying the ERV abundance in vertebrates
Wanjing Zheng*, Yoko Satta

POA-127
Divergent evolution of olfactory receptor repertoire in New and Old World primates revealed by target capture and massive-parallel sequencing
Ryuichi Ashino*, Yoshihito Niimura, Kazushige Touhara, Amanda D. Melin, Shoji Kawamura

POA-128
Nucleotide divergence between L and M opsin genes in New and Old World primates
Yuka Matsushita*, Naoko Takezaki, Amanda D. Melin, Shoji Kawamura

POA-129
Unequal allele frequencies of the L/M opsin gene in New World monkeys
Shoji Kawamura*, Yuka Matsushita, Anthony Di Fiore, Filippo Aureli, Amanda D. Melin

POA-398
The unreasonable effectiveness of population genetic inference via image recognition
Daniel Schrider*

POA-405
Excess of movement out of the X chromosome across 250 million years of Dipteran evolution
Melissa Toups*, Beatriz Vicoso

POA-409
Repeated adaptive evolution of an enzyme in plant specialized metabolism
Arunraj Saranya Prakashrao*, Elisabeth Kaltenegger, Dietrich Ober

POB-001

Evolutionary Dynamics of the CDPK Signalling Network in Plants

Bernhard Wurzinger*, Ingo Ebersberger, Katrin Schrader, Markus Teige

POB-002

Deciphering evolutionary history with multifaceted evidence: an example from one drosophila group in East Asia

Jinming Lu, Huiluo Cao*, Yuan Zhang, Hongwei Chen

POB-004

Massive gene amplification on a recently formed Drosophila Y chromosome

Shivani Mahajan*, Doris Bachtrog

POB-005

Template switching in genome instability and evolution

Sumita Omer, Bar Lavi, Piotr A Mieczkowski, Shay Covo, Einat Hazkani-Covo*

POB-007

Dynamics of cis-regulatory regions for introducing the divergent transcription factor motifs in the human genome

Jia-Hsin Huang*, Ryan Shun-Yuen Kwan, Zing Tsung-Yeh Tsai, Huai-Kuang Tsai

POB-008

From higher-order organisms to microbes: a novel quantitative species identification method based on ancient DNA

Evangelos Antonios Dimopoulos*, Irina Velsko, Evan Irving-Pease, Laurent Frantz, Greger Larson

POB-009

CATANA: Comprehensive Alternative Transcript Atlas based oN Annotation

Cheng-Kai Shiau, Jia-Hsin Huang, Huai-Kuang Tsai*

POB-010

The mayfly Cloeon dipterum as a platform to study evolutionary innovations: novel sexually dimorphic organs and the origin of insect wings

Isabel Almudi*, Isabel Garcia, Carlos Martin-Blanco, Kristofer Davie, Ferdinand Marletaz, Fernando Cruz, Tyler Alioto, Stein Aerts, Fernando Casares

POB-011

Genetic mechanism of achiasmy in *Drosophila albomicans*

Arika Inuyama*, Yosuke Seto, Yoshitaka Ogawa, Masafumi Nozawa, Koichiro Tamura

POB-012

Novel experimental Ribo-seq measurements demonstrate genomic adaptation to decrease ribosome queuing

Alon Diament*, Anna Feldman, Elisheva Schochet, Martin Kupiec, Yoav Arava, Tamir Tuller

POB-013

Experimental evolution of Escherichia coli mutators in a complex environment

Wei-Chin Ho*, Megan G. Behringer, Samuel F. Miller, Michael Lynch

POB-014

Understanding the genomic basis of convergent evolution and evolutionary innovation across the Metazoa Tree of Life: an all-phyla approach.

Rosa Fernandez*, Toni Gabaldon

POB-015

Visual adaptation of sea snake

Takashi Seiko*, Takushi Kishida, Mamoru Toda, Mina Toyama, Takahiko Hariyama, Takashi Okitsu, Akimori Wada

POB-016

Recalibrating Quality Scores for Low-Depth Data of Ancient Genetic Material

Ilektra Schulz*, Vivian Link, Zuzana Hofmanova, Athanasios Kousathanas, Christoph Leuenberger, Daniel Wegmann

POB-017

Multi-stage disease expression profiles revealed dynamics in connectivity of biological networks

Wen-Yu Chung*, Ru-Feng Peng

POB-018

TIPars: Taxa Insertion Using Parsimony and Ancestral Reconstructed Sequences

Tommy T.Y. Lam*

POB-019

Conservation phylogenetics and computational species delimitation of Neotropical primates

Beatriz Mello*

POB-020

Metabolic Capabilities of the Early Eukaryotes

Matthew Moore*, David Newman, Martin Rusilowicz, James McInerney

POB-022

Bursts of amino acid replacements in protein evolution

Anastasia Stolyarova*, Georgii Bazykin, Tatyana Neretina, Alexey Kondrashov

POB-024

Using comparative transcriptomics and ribosome profiling to identify de novo genes in yeast

William Robert Blevins*, Xavier Messaguer, Jorge Ruiz-Orera, Jose Luis Villanueva Canas, Bernat Blasco-Moreno, Laura Avino-Esteban, Guillem Lopez-Grado Salinas, Lorena Espinar, Juana Diez, Lucas Carey, M. Mar Alba

POB-027

Predicting Disease Causality of Mutations in Human Beta Globin gene

Sangeetha Udani Ratnayake*

POB-028

Comparative transcriptome analyses for cold acclimation response in *Drosophila albomicans*

Tomohiko Kimura, Yosuke Seto, Yoshitaka Ogawa, Msafumi Nozawa, Koichiro Tamura*

POB-029

From FECA to LECA; gauging complexity in the First, to the Last, Eukaryote Common Ancestor.

David Newman*, James McInerney, Fiona Whelan, Martin Rusilowicz, Matthew Moore

POB-030

Molecular evolution of RuBisCO subunits in angiosperms

Kana Yamada*, Nicolas Salamin, Iakov Davydov, Romain Studer

POB-031
Extent Mitochondrial plastid combined insertions into the nuclear genome
Shir Portugez*

POB-032
The Caenorhabditis Genomes Project
Lewis Stevens*, Mark Blaxter

POB-033
Amino acid exchangeabilities vary across the tree of life
Zhengting Zou*, Jianzhi Zhang

POB-034
Comparative plastomics of yews reveals a genome structural polymorphism and effective super-barcode
Chung-Shien Wu*, Lian-Ming Gao, Chao-Nan Fu, Yu-Wen Chang, Shu-Miaw Chaw

POB-036
Determining the genomic architecture of complex traits in multiple ethnic human populations
Michael C Turchin*, Sohini Ramachandran

POB-038
Exploring the genetic basis of environmental sensitivity
Amanda J Lea*, Julien F Ayroles

POB-039
Patterns of robustness and deregulation in gene expression networks under dietary stress
Luisa F Pallares*, Anett Schmittfull, Serge Picard, Julien F Ayroles

POB-040
Spatio-temporal biases in the dynamics of horizontal gene transfer
Alexander Esin*, Tobias Warnecke

POB-041
Gene duplication and subfunctionalization of the centromeric histone gene in Drosophila virilis
Lisa Kursel*, Harmit Malik

POB-043
Genetic ancestry in cancer cell lines
Michael D. Kessler, Nicholas Bateman, Julie C. Dunning Hotopp, Timothy D. O'Connor*

POB-044
Using Homology Search to Identify De Novo Genes
Caroline M. Weisman*, Andrew W. Murray, Sean R. Eddy

POB-048
Phylogenetically young genes and their function in Anopheles mosquitoes.
Elzbieta Krzywinska, Jaroslaw Krzywinski*

POB-049
Layout of coexpressed gene modules mirrors ontogeny and organ system classification of animal tissues
Ben-Yang Liao*, Ting-Yan Chang

POB-051
Testing the Expensive Germline Hypothesis
Hwei-yen Chen*, Cecile Jolly, Simone Immler

POB-053
Evolution of feeding preferences in Calliphoridae (Diptera)
Tatiana Teixeira Torres*, Gisele Antoniazzi Cardoso

POB-054
Evolutionary and Structural Analysis of Galectin Genes Involved in Human Immunity and Pregnancy
Zackery A Ely*, Antonis Rokas, John Capra, Amandeep Sangha, Michelle Moon, Xingxing Shen, Jens Meiler

POB-056
Functional co-evolution in metabolic pathways
Mathias Bockwoldt, Toni I. Gossmann, Mathias Ziegler, Ines Heiland*

POB-060
Forces shaping the distribution of rice genetic diversity
Rafal Marek Gutaker*, Michael Purugganan

POB-061
The impact of DNA repair status on germline mutation rate and spectra in mice
Mizuki Ohno*, Noriko Takano, Kunihiko Sakumi, Teruhisa Tuzuki

SY24: Phylogenomics - genome-scale data and the methods and analyses for phylogeny construction and time estimation

POA-400
Phylonumerics: A New Mass-Based Molecular Evolution Approach Investigates the Emergence of Antiviral Resistance in the Influenza Virus
Kevin Downard*, Elma Akand

POA-402
Orthology assignment of 5 novel Sparidae proteomes and their phylogenetic position among teleosts
Paschalis Natsidis*, Pavlos Pavlidis, Costas Tsigenopoulos, Tereza Manousaki

POA-408
Composite Likelihood Estimation of Phylogenies from Genomic Data using Coalescent Theory
Geno Guerra*, Rasmus Nielsen

POA-411
c-genie - Assessing the impact of recombination on phylogenomic inference
Michael Matchiner, Milan Malinsky*

POB-307
Phylogenomic Analyses of Brachyura Illuminates Ancient Origin of Freshwater Crabs and Recent Origins of Hydrothermal Vent Crabs
Ling Ming Tsang*, Ka Yan Ma, Jing Qin, Tin-Yam Chan, Peter Kee Lin Ng, Ka Hou Chu

POB-309

Inferring cell differentiation processes based on phylogenetic analysis of genome-wide epigenetic information

Kanako O Koyanagi*

POB-310

Characterization and Molecular Phylogeny of Korean Chrysanthemum Species

So Youn Won*, Jae-A Jung, Jung Sun Kim, Sangho Kang

POB-311

Cnidarian phylogenomics to understand the eumetazoan evolution

Mei-Fang Lin*, James Reimer, Miyuki Kanda, Nana Arakaki, Hiroshi Watanabe

POB-312

Phylogenomic analysis suggests two independent adaptations to high-salt environments in the Archaea

Monique Aouad*

POB-313

Next generation sequencing for analyzing genetic diversity in cultivars of seven countries rice

Namkuk Kim*, Sujeong Shin, Hyemin Park, Moonok Lee, Myungsil Jung, Heykyoung Kim

POB-314

Gene distributions across taxonomic groups reveal recent lateral gene transfers among prokaryotes

Michael Knopp*, Jessica Wimmer, William F. Martin

POB-315

Canary: a new approach to identify attraction artifacts in the analysis of single gene families

James Frederick Fleming*, Roberto Feuda, Nicholas Roberts, Davide Pisani

POB-317

Swift Neighbor-Joining method for massive sequence data

Naruya Saitou*

POB-318

Searching for binding pockets of FeS clusters in 5,655 prokaryotes

Giacomo Moggioli*, Nathalie Brenner, Joana Xavier, Maurizio Casiraghi, William F. Martin

POB-319

Island biogeography of Candidia temminckii, a freshwater fish, suggests intraspecific replacements

Shoji Taniguchi*, Johanna Bertl, Andreas Futschik, Hirohisa Kishino, Toshio Okazaki

POB-320

Gene fusion as a phylogenetic marker - a study of Metazoan

Peter Mulhair*, Mary O'Connell, Raymond Moran, Christopher Creeevey, Davide Pisani, Ian Carr

POB-321

Phylogenetic history of ERM proteins in metazoan tree of life

Victoria Shabardina *, Yukie Kashima

POB-322
Charting the gene set of the last universal common ancestor
Madeline C. Weiss*, William F. Martin

POB-324
Phylogenomic analyses of testate (shell-building) amoebae in New England bogs and fens
Alistaire D. Ruggiero*, Angela O'Donnell, Agnes Weiner, Naomi Ostriker, Evie Hoffman, Laura A. Katz

POB-325
The Likelihood Decay Index: Branch support for the phylogenomics era.
Chris Creevey*, Mark Wilkinson, James McInerney

POB-327
Evolutionary metrics
Satoshi Oota*

POB-328
Inferring incomplete lineage sorting, duplications, losses and transfers with reconciliations
Yao-ban Chan*, Celine Scornavacca, Vincent Ranwez

POB-329
Evolutionary dynamics of Papaveraceae plastid genomes and contrasting patterns of organization and nucleotide substitution rates
Seongjun Park*, SeonJoo Park

POB-330
Understanding the effect of calibrations in molecular clock dating
Alan James Beavan*, Mark Beaumont, Davide Pisani

POB-331
Computing likelihoods of allele frequencues on phylogenetic trees using diffusion models
David James Bryant, Stephanus Marnus Stoltz*

POB-332
Local demographic patterns buried in the present-day mtDNA pool: A study of Finns
Sanni Oversti*, Paivi Onkamo, Monika Stoljarova, Bruce Budowle, Antti Sajantila, Jukka Palo

POB-333
A novel method for detection of syntenic regions between genomes reveals the extent of DNA transfer between plasmids and chromosomes in prokaryotes
Ahmad Samer Kadib Alban*, Tal Dagan, Giddy Landan

POB-334
Evolutionary history of short specific sequences in the three domains of life
Nicole Gruenheit*, Michael Knopp, Nils Kapust, Peter Lockhart, William Martin

POB-335
CO-dependent CO2 fixation: unique, ancient and ancestral in biochemistry
Joana C. Xavier*, Martina Preiner, William F. Martin

POB-336

Spectral signature of gene family trees

Leonardo de Oliveira Martins*, Christophe Dessimoz

POB-337

Population-level processes impact the inference of macroevolutionary regimes from molecular phylogenies when concatenation is employed

Carlos Schrago*, Anieli Pereira

POB-338

An appraisal of the relationships of Sigmodontinae (Cricetidae): a phylogenomic approach resolve tribal relationships.

Guillermo D'Elia*, Andres Parada

POB-339

Expansion and evolution of Terpene synthase gene families in stout camphor tree

Han-Yu Wang*, Chih-Yao Hsu, Chung-Shien Wu, Ling-Ni Wang, Isheng Tsai, Shu-Miaw Chaw

POB-341

Analysis of Plasmid Gene Network

Ignacio Riquelme Medina*, James O McInerney

POB-342

Hybrids of Paradise: A genomic perspective on intergeneric gene flow among Birds-of-Paradise

Mozes Pil Kyu Blom*, Stefan Prost, Les Christidis, Brett Benz, Valentina Peona, Alexander Suh, Martin Irestedt

POB-344

Inferring Prokaryotic Evolution using a Deterministic Model of Speciation

Ashley Ann Superson*, Michael Ryan Culver, Anna Maria Spagnuolo, Fabia Ursula Battistuzzi

POB-345

Cis-trans evolution of chloroplast development regulator genes in plants

Yao-Ming Chang*, Hsin-Hung Lin, Wen-Hsiung Li

POB-346

Investigating Signals of Local Adaptation on the Human X Chromosome

Jonathan Rice*, Emilia Huerta-Sanchez

POB-347

Integration of phylogenomics and 3D protein modeling reveal phylogenetic inertia in ryanodine receptor ligan peptides of scorpion venom

Carlos Eduardo Santibanez-Lopez*, Ricardo Kriebel, Jesus Ballesteros, Prashant P Sharma

POB-350

Phylogenomics resolves New World primates phylogeny

Horacio Schneider*, Jeferson Carneiro, Iracilda Sampaio

POB-351

PhyCAP: Phylogenomic-noise Cleaning Approach by PCA

Eisuke Iwamoto*, Koichiro Tamura

POB-352

Testing the accuracy of mitochondrial genomes reconstruction from transcriptomes: an insight from Reticulitermes termites mitogenomics.

Giobbe Forni*, Guglielmo Puccio, Barbara Mantovani, Andrea Luchetti

POB-353

Phylogenomic analyses of transcriptome data from individual foramifera

Evie Grey Elizabeth Hoffman*, Alistaire Ruggiero, Naomi Ostriker, Agnes Weiner, Laura Katz

POB-354

Disentangling dietary transitions in termite evolution by transcriptome- and mitochondrial genome-based phylogenies

Ales Bucek*, Jan Sobotnik, David Sillam-Dusses, Nathan Lo, Thomas Bourguignon

POB-356

Using Alignment Uncertainty to improve Phylogenetic Bootstrap Reliability

Evan W. Floden, Kuei Yuan Lan, Javier Herrero, Olivier Gascuel, Cedric Notredame, Jia-Ming Chang*

SY25: Post-transcriptional modifications: functions, diversity, pathogenesis and evolution

POA-387

Adaptation of A-to-I RNA editing in Drosophila

Jian Lu*

POA-388

Newly-originated A-to-I RNA Editing Events Rapidly Evolve as Functional Regulator of RNA Subcellular Localization in Primates

Ni A. An*, Jiguang Peng, Xin-Zhuang Yang, Jia-Yu Chen, Chuan-Yun Li

POA-389

Evolution of structural and abundancy profiles in vertebrate mitochondrial mRNAs

Yao Sun, Masaki Kurisaki, Yasuyuki Hashiguchi, Yoshinori Kumazawa*

POA-390

What is the selective advantage of the widespread nonsynonymous A-to-I RNA editing in coleoids?

Daohan Jiang*, Jianzhi Zhang

POA-393

Evolutionary landscape and spatiotemporal dynamics of A-to-I RNA editing across metazoan species

Li-Yuan Hung, Yen-Ju Chen, Te-Lun Mai, Chia-Ying Chen, Min-Yu Yang, Tai-Wei Chiang, Yi-Da Wang, Trees-Juen Chuang*

POA-395

Diversification of transcription factor pulsing dynamics is driven by phosphorylation site evolution in intrinsically disordered regions

Ian Shen Hsu*, Alan Moses

SY26: Predictability of rapid evolutionary processes

POB-170

Predicting pathways to multiple drug resistance

Pamela Yeh*

POB-172

H3N2 influenza virus fitness prediction

Ksenia Safina*, Pavel Dvurechensky, Alexey Neverov, Alexander Gasnikov, Alexander Favorov, Georgii Bazykin

POB-173

A "molecular tango" of sperm-egg recognition proteins in Pacific abalone

Damien B Wilburn*, Joshua G Schraiber, Willie J Swanson

POB-174

Origin and evolution of ORFan genes in Lactobacillus kunkeei

Karl David Dyrhage*, Andrea Garcia Montaner, Christian Seeger, Siv Andersson

POB-177

Statistical tests for genomic time series data

Andreas Futschik*

POB-179

Effect of binding interference on the divergence of paralogous genes that encode homodimers

Angel Fernando Cisneros*, Christian Landry

SY27: Quantitative genetics of developmental evolution

POA-406

Feathered Feet Are Just Winging It: Shifts in Pigeon Limb Identity Reveal Conserved Regulatory Networks

Elena F Boer, Hannah F Van Hollebeke, Carlos R Infante, Douglas B Menke, Michael D Shapiro*

POB-180

Genetic framework for brain and cranium development at the transcriptional level

Derek Caetano-Anolles*

POB-181

RNA-seq sex-specific mapping protocol increases expression value on the sex chromosomes in both genetic male and female samples

Sarah Brotman, Kimberly Olney*, Valeria Valverde-Vesling, Jocelyn Andrews, Melissa Wilson Sayres

POB-182

Deciphering genetic basis and copulatory effect underlying the rapid diversification of male genitalia between sibling species of Drosophila melanogaster

Kentaro M. Tanaka*, Yoshitaka Kamimura, Aya Takahashi

POB-183

Differentiation in the facial morphology between Ryukyuans and mainland Japanese

Ryosuke Kimura*, Chiaki Watanabe, Eri Miyazato, Kyoko Yamaguchi, Takehiro Sato, Tsuyoshi Ito, Akira Kawaguchi, Ken Yamamoto, Hajime Ishida

POB-185

Genome-wide allele-specific expression of the transcriptional landscape associated to Capsicum domestication

Erik Diaz-Valenzuela*, Angelica Cibrian-Jaramillo, Ruairidh Sawers

POB-186

The genetic architecture of the divergent ecotypes of Littorina saxatilis

Pragya Chaube*, Anja Westram, Roger Butlin

SY28: Selection on complex traits: reuniting quantitative and population genetics

POB-405

The Physiological and Genomic Impact Intense Selection for Starvation Resistance in Drosophila melanogaster

Mark A Phillips*, James Kezos N, Michael R Rose

POB-406

The transcriptomic landscape of yaks reveals molecular pathways for high altitude adaptation

Xuebin Qi*, Qu Zhang, Yaoxi He, Lixin Yang, Linping Yang, Zhengheng Liu, Shiming Liu, Tianyi Wu, Chaoying Cui, Ouzhuluobu NA, Jianlin Han, Shengguo Zhao, Chunnian Liang, Bing Su

POB-407

Signals of selection in immune response genes of an admixed southern African population

Caitlin Uren*, Eileen G Hoal, Gerard Tromp, Paul D van Helden, Brenna M Henn, Marlo Moller

POB-408

Founder-specific inbreeding depression affects racing performance in Thoroughbred horses

Evelyn Todd*, Natasha Hamilton, Simon Ho, Peter Thomson, Brandon Velie, Rachel Ang

POB-409

The genomic basis of athletic performance and navigation in racing pigeons.

Malgorzata Anna Gazda*, Pedro Andrade, Sandra Afonso, Jolita Dilyte, John Archer, Ricardo Lopes, Rui Faria, Miguel Carneiro

POB-410

Signatures of local adaptation in human zinc transporters genes

Ana Roca-Umbert, Rocio Caro-Consuegra, Gabriel Felipe Rodriguez-Lozano, Nino Spataro, Elena Bosch*

POB-411

Evolution of alpha satellites in the human genome

Manatsu Hamazaki*, Hideki Innan

POB-413

The polygenic basis of an ancient divergence in yeast thermotolerance

Carly Weiss*, Jeremy Roop, Rylee Hackley, Julie Chuong, Igor Grigoriev, Adam Arkin, Jeffrey Skerker, Rachel Brem

POB-415

The spectrum of loss of function tolerance in the human genome

Konrad Karczewski*, Laurent Francioli, Kaitlin Samocha, Beryl Cummings, Daniel Birnbaum, Mark Daly, Daniel MacArthur

POB-418

Evolution and Molecular Mechanisms of Photoreceptor Transmutation

Ryan K Schott*, Belinda SW Chang

POB-419

Identifying host factors that modulate the outcome of influenza infection in humans

Mary O'Neill*, Maxime Rotival, Helene Quach, Lluis Quintana-Murci

POB-420

Cross-species phylogenetic genome-phenome approach to understand the evolution of ageing in mammals

Xavier Farre*, Gerard Muntane, Arcadi Navarro

POB-422

Detecting the signature of epistatic selection in subdivided populations

Champak Beeravolu Reddy*, Frederic Guillaume, Katalin Csillery

POB-423

A new inference method for ongoing selective sweep

Naoko T Fujito*, Yoko Satta, Toshiyuki Hayakawa, Naoyuki Takahata

POB-424

Addiction, Immunity, and Infectious Disease in a Global Population

Latifa Jackson*, Maksim Shestov

POB-426

Inference of Microevolutionary Dynamics for Quantitative Molecular Phenotypes

Shadi Zabad*, Alan Moses

POB-429

A genetic handicap approach: how to estimate the genome-wide burden of slightly-deleterious variants

Konstantin Popadin*, Alexandre Reymond

SY29: Somatic mutation and the evolution of multicellularity

POA-216

Predicting Cancer Driver Sites and Cancer-specific Selection Pressures under Two-Component Evolutionary Models

Zhan Zhou*, Jingcheng Wu, Wenyi Zhao, Zhixi Su, Yangyun Zou, Xun Gu

POA-217

Rules of neutral molecular evolution are only -half right Influences of positive vs. negative selection

Qingjian Chen*

POA-218

Low somatic mutational robustness of the human genome

Sofya Garushyants*, Georgii Bazykin

POA-219

Considering somatic mutation rate as a measure of genome maintenance capacity in colonial cnidarians

Elora Hayter Lopez*, Stephen R Palumbi

POA-221

The missing link of cancer evolution - early remnants of tumorigenesis

Bingjie Chen*, Chung-I Wu

POA-222

Measuring DNA mutation rates with Circle-sequencing

Stephan Baehr*, Lauren Reyes, Jean-Francois Gout, Michael Lynch

POA-404

Convergent somatic mutations in asexual pathogen *Phytophthora ramorum* NA1 contributes to population genetic diversity

Jennifer D. Yuzon*, Renaud Travadon, Madhu Malar C., Sucheta Tripathy, Nathan Rank, Heather Mehl, Richard Cobb, Tedmund Swiecki, Elizabeth Bernhardt, Corinn Small, Tiffany Tang, David Rizzo, Matteo Garbelotto, Takao Kasuga

SY30: Timing methodologies and applications

POA-316

Rates of mutation and recombination in Siphoviridae phage genome evolution over three decades

Anne Kupczok*, Horst Neve, Kun D. Huang, Marc P. Hoeppner, Knut J. Heller, Charles M.A.P. Franz, Tal Dagan

POA-317

Resolving ultrametric phylogeny of prokaryotic strains with frequent homologous recombination from the variation of local SNP density on their genomes

Tin Yau Pang*, Martin Lercher

POA-318

Experimentally informed site-specific substitution models deepen phylogenetic estimates of the divergence of viral lineages.

Sarah K. Hilton*, Jesse D. Bloom

POA-319

The Molecular Clock Winder: Assessing the Effects of Life-history Traits and Reproductive Biology on Substitution Rates in Primates

Lucas Henriques Viscardi*, Vanessa Rodrigues Paixao-Cortes, Guillermo Reales, Maria Catira Bortolini, Carlos Eduardo Guerra Amorim

POA-324

Dating the emergence of DNA by dating the origin of the ribonucleotide reductase protein family

Adrien Jules Boniface*, Timothy M. Vogel, Catherine Larose

SY31: Tracing back bacterial pathogen evolution from ancient and modern genomics

POA-039

Rapid evolution of distinct Helicobacter pylori subpopulations in the Americas

Koji Yahara*, Kaisa Thorell, Elvire Berthenet, Daniel Lawson, Jane Mikhail, Ikuko Kato, Alfonso Mendez, Cosmeri Rizzato, Maria Bravo, Rumiko Suzuki, Yoshio Yamaoka, Javier Torres, Samuel Sheppard, Daniel Falush

POA-041

Recombination signal in Mycobacterium tuberculosis stems from reference-guided assemblies and alignment artefacts

Maxime Godfroid*, Tal Dagan, Anne Kupczok

POA-042

Quantifying population structure of malaria parasites using epidemiological and genomic data

Hsiao-Han Chang*, Amy Wesolowski, Ipsita Sinha, Md Amir Hossain, M Abul Faiz, Olivo Miotto, Dominic Kwiatkowski, Richard Maude, Caroline Buckee

POA-044

Reconstruction of bacterial cell division history to identify new potential antibiotic targets

Pierre Simon Garcia*, Christophe Grangeasse, Celine Brochier-Armanet

POA-045

Historical *Y. pestis* genomes provide insights into the initiation and progression of the second plague pandemic

Maria A. Spyrou*, Marcel Keller, Rezeda I. Tukhbatova, Elisabeth Nelson, Don Walker, Sacha Kacki, Dominique Castex, Sandra Loesch, Michaela Harbeck , Alexander Herbig, Kirsten I Bos, Johannes Krause

POA-046

Evolution pathway of the antimicrobial resistance genes

Marcus Shum*, Tommy Lam

POA-047

Reconstruction of the Killer Whale Oral Microbiome

Courtney A Hofman*, Rita Austin, Michael A. Etnier, Krithivasan Sankaranarayanan

POA-049

The Impact of Acquired Copper Resistance Loci on Epidemic Methicillin Resistant Staphylococcus aureus Pathogenesis and Spread

Paul J Planet*, Ahmed M Moustafa, Chanelle Ryan, Alejandra Londono, Cesar Arias, Jeffrey Boyd, David Heinrichs

SY32: Transposable elements in gene regulation and genome evolution

POA-329

RepetDB: a resource for unified transposable element references with classification

Joelle Amselem*, Guillaume Cornut, Nathalie Choisne, Michael Alaux, Francoise Alfama-Depauw, Veronique Jamilloux, Florian Maumus, Thomas Letellier, Isabelle Luyten, Cyril Pommier, Anne-Francoise Adam-Blondon, Hadi Quesneville

POA-330

Transposable elements lineage-specific activity and genome content during the evolution of branchiopod crustaceans.

Andrea Luchetti*, Barbara Mantovani

POA-331

Multiplatform assembly of a bird-of-paradise genome reveals rapid turnover of repetitive sequences on W chromosomes and near centromeres of birds

Valentina Peona*, Mozes Blom, Luohao Xu, Ignas Bunikis, Qi Zhou, Knud Jonsson, Martin Irestedt, Alexander Suh

POA-332

Transposable elements affect the transcriptional regulation of stress response genes in Drosophila and humans

Josefa Gonzalez*, Vivien Horvath, Jose Villanueva

POA-333

The impact of repetitive DNA on speciation rates in teleost fish

William Reinar*, Ole Toerresen, Michael Matschiner, Jostein Starrfelt, Alexander Nederbragt, Kjetill Jakobsen, Sissel Jentoft

POA-334
REPET: a tool for revealing the secrets of transposable elements
Veronique Jamilloux*, Hadi Quesneville

POA-337
Comparative analysis of genomic repeat content in acridid grasshoppers reveals phylogenetic similarities as well as unexpected differences
Abhijeet Shah*, Holger Schielzeth, Joe Hoffman

POA-338
Detecting structural variations in human genome using nanopore sequencer
Satomi Mitsuhashi*, Martin C Frith, Naomichi Matsumoto

POA-339
Accumulation of repeated elements during dog domestication: insight from grey wolf and dhole genomes
Guo-Dong Wang*, Xiu-Juan Shao, Bing Bai, Jue Ruan, Ya-Ping Zhang

POA-340
Horizontal transfer of transposable elements between parasitic nematodes and their hosts
Sonja Maria Dunemann*, James Wasmuth

POA-341
Network analysis of bacterial genes to predict horizontal co-transfer and mobile genetic elements
Yu Wan*, Ryan R. Wick, Danielle J. Ingle, Michael Inouye, Justin Zobel, Kathryn E. Holt

POA-342
Selection against LTR retrotransposons is balanced by locally adapted transposable element alleles in Arabidopsis thaliana
Michelle C Stitzer*, Jeffrey Ross-Ibarra

POA-343
Transposon activity in the Arabidopsis thaliana 1001 genomes
Luz Mayela Soto Jimenez*, Magnus Nordborg

POA-344
Genome size change and transposon dynamics in the allotetraploid *Arabidopsis suecica*
Robin Burns*, Polina Yu. Novikova, Magnus Nordborg

POA-345
Transcriptome analysis to identify genes derived from endogenous retrovirus that mediate cell-cell fusion during myoblast differentiation
Mahoko Takahashi Ueda*, Satomi Mitsuhashi, Hiroaki Mitsuhashi, Tadashi Imanishi, So Nakagawa

POA-347
Evaluating genome and transcriptome variation across the Antarctic Notothenioid fish radiation to explore causes and consequences of adaptive speciation.
Iliana Bista*, Shane McCarthy, Eric Miska, Thomas Desvignes, Melody Susan Clark, John Postlethwait, C.-H. Christina Cheng, Walter Salzburger, H. William Detrich III, Karen Oliver, Jason Skelton , Michelle Smith, Petr Danecek , Richard Durbin

POA-349

Pilot studies of transposable elements in Bronze Age skeletal human DNA

Oliver Piskurek*

POA-351

The PIWI/piRNA response is relaxed in a rodent that lacks mobilizing transposable elements

Michael W Vandewege, Roy N. Platt, Aliceanne Szeliga, Dana Merriman, David A Ray, Federico G. Hoffmann*

POA-352

Analysis of the red seaweed Gracilariopsis chorda genome provides insights into genome size evolution in Rhodophyta

JunMo Lee*, Debashish Bhattacharya, Hwan Su Yoon

POA-353

Transposable elements and resistome analysis of Staphylococcus lugdunensis isolates from diverse hospital and community sources in Hong Kong

Melissa Chunjiao LIU*, Huiluo CAO

POA-354

Reconstructing the evolutionary history of endogenous retroelements

Laura F. Campitelli*, Mathieu Blanchette, Timothy R. Hughes

POA-397

Coupling between sequence and function in evolution of the binding sites of the male-specific lethal complex in Drosophila

Aimei Dai*, Yushuai Wang, Tian Tang

POA-403

Excision-reintegration at a pneumococcal phase-variable restriction-modification locus drives within- and between-strain epigenetic differentiation and inhibits gene acquisition

Min Jung Kwun*, Marco R Oggioni, Stephen D Bentley, Nicholas J Croucher

SY33: Trash to treasure and treasure to trash: invasion, persistence, neofunctionalization, and gene decay in evolution

POB-299

The majority of novel protein coding genes identified through phylostratigraphy alone are either old genes or recent duplicates

Claudio Casola*

POB-300

Count does not recover major events of gene flux in real biological data

Nils Kapust*, Shijulal Nelson-Sathi, Barbara Schonfeld, Einat Hazkani-Covo, David Bryant, Peter J. Lockhart, Mayo Roettger, Joana C. Xavier, William F. Martin

POB-302

A new method for identifying and splitting fusion proteins in prokaryotes

Constantin Eiteneuer*, Julius Kliss, Mayo Roettger, Madeline C. Weiss, Michael Knopp, William F. Martin

POB-303

Comparative analysis of fusion and non-fusion proteins in prokaryotes based on functional annotation

Julius Kliss*, Constantin Eiteneuer, Mayo Roettger, Joana Xavier, Madeline C. Weiss, William F. Martin

POB-304

Understanding de novo gene evolution from random sequences expressed in E. coli

Johana Fajardo C.*, Diethard Tautz

SY34: Virus genome evolution

POA-273

Phylodynamic assessment of intervention strategies for the West African Ebola virus outbreak

Simon Dellicour*, Guy Baele, Gytis Fudas, Nuno R. Faria, Oliver G. Pybus, Marc A. Suchard, Andrew Rambaut, Philippe Lemey

POA-274

Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-sense RNA viruses

Ci-Xiu Li*

POA-275

Single-virion Sequencing of Lamivudine Treated HBV Populations Reveal Population Evolution Dynamics and Demographic History

Yuan Zhu*, Pauline Aw, Paola de Sessions, Shuzhen Hong, Xian See Lee, Lewis Hong, Andreas Wilm, Chen Hao Li, Stephane Hue, Seng Gee Lim, Niranjan Nagarajan, William Burkholder, Martin Hibberd

POA-277

A brief history of papillomaviruses: on the origin and evolution of (onco)genes and genomes

Anouk Willemsen*, Ignacio G. Bravo

POA-278

The natural evolution of influenza virus hemagglutinin becomes entrenched by a complex epistatic network

Nicholas C. Wu*, Andrew J. Thompson, Jia Xie, Chih-Wei Lin, Corwin M. Nycholat, Xueyong Zhu, Richard A. Lerner, James C. Paulson, Ian A. Wilson

POA-280

Identifying novel viruses associated with Antarctic pinnipeds

Adele Crane*, Mike Goebel, Simona Kraberger, Anne Stone, Arvind Varsani

POA-281

Domain-based evolutionary analysis of HIV-1 Pol proteins using sequence similarity networks

Shohei Nagata*, Junnosuke Imai, Gakuto Makino, Masaru Tomita, Akio Kanai

POA-282

Genomic and phylogenetic study of feline paramyxovirus

Shoichi Sakaguchi*, Satomi Mitsuhashi, Makoto Ogawa, Takayuki Miyazawa, Tadashi Imanishi, So Nakagawa, Tetsuya Mizutani

POA-283

Evolution of influenza virus matrix 2 protein

Hideaki Moriyama*

POA-284

Comparing influenza's evolution across within- and between-host scales

Katherine S Xue*, Jesse Bloom

POA-285

Molecular evolutionary analysis of Ebola virus glycoprotein identified two amino acid mutations that affect viral infectivity

So Nakagawa*, Mahoko Takahashi Ueda, Yohei Kurosaki, Yusuke Nakano, Taisuke Izumi, Olamide K Oloniniyi, Jiro Yasuda, Yoshio Koyanagi, Kei Sato

POA-286

Non-retroviral virus-like elements in eukaryotic genomes

Kirill Kryukov*, Mahoko Takahashi Ueda, Tadashi Imanishi, So Nakagawa

POA-287

Whole genome diversity of inherited chromosomally integrated HHV-6 derived from healthy individuals of diverse geographic origin

Marco Telford*, Arcadi Navarro, Gabriel Santpere

POA-291

Host network structure and fitness effects shape the emergence and spreading of new mutations in viruses

Kent Kawashima*, Hiroshi Akashi

POA-293

Mapping the drivers of within-host pathogen evolution using massive data sets

Duncan Palmer*, Isaac Turner, Sarah Fidler, John Frater, Dominique Goedhals, Philip Goulder, Kuan-Hsiang Gary Huang, Annette Oxenius, Rodney Phillips, Roger Shapiro, Cloete van Vuuren, Angela McLean, Gil McVean

POA-294

Non-stationary evolution of Influenza A surface proteins

Anfisa Popova, Alexey Neverov, Georgii Bazykin*

POA-295

FAVITES: A framework for the simulation of compatible viral transmission networks, phylogenetic trees, and sequences

Niema Moshiri*, Siavash Mirarab

SY35: Weak forces in genome evolution

POA-179

Weak purifying selection in genomic regions with high diversity in great apes

David Castellano*, Adam Eyre-Walker, Kasper Munch

POA-180

Evidence that the motility organelle of Mycoplasma pneumoniae is under translational selection and insights on its pathogenic lifestyle

Hassan Sibroe Abdulla Daanaa*, Ali Mostafa Anwar

POA-181

Population genomics of three North American conifer species: sugar pine, loblolly pine, and douglas-fir

Lida Anita To*, Kristian A. Stevens, Marc W. Crepeau, David B. Neale, Charles H. Langley

POA-182

GC-biased gene conversion and structural variation in highly recombining social insects

Takeshi Kawakami*, Andreas Wallberg, Matthew T Webster

POA-183

Cytosine Methylation affects the Mutational Spectrum Beyond the Base Itself

Vassili Feodorovich Kusmartsev*, Tobias Warnecke

POA-184

Resolving the evolutionary impact of polymorphic gene duplications in humans at the haplotype level

Marie Saitou*, Omer Gokcumen

POA-185

Fine-scale characterization of genomic structural variation hotspots in the human genome reveals adaptive and biomedical roles

Yen-Lung Lin*, Omer Gokcumen

POA-189

The impact of gremlin mutations on cancer risk

Kazuki K Takahashi*, Hideki Innan

POA-190

Evolution of codon bias and gene expression in the highly AT-biased genome of Dictyostelium discoideum

Janaina Lima De Oliveira, Atahualpa Castillo Morales*, Jason Wolf, Chris Thompson

POA-192

Evolutionary origins of taxonomically restricted genes in Drosophila genus

Karina Zile*, Christophe Dessimoz

POA-193

The Red-Queen evolutionary dynamics of recombination hotspots

Thibault Latrille*, Laurent Duret, Nicolas Lartillot

POA-194

Compensatory back mutation in mitochondrial genome of primates

Kazuhiro Satomura*, Naoki Osada, Toshinori Endo

POA-195

The effect of genetic connectivity on the strength of natural selection in Chlamydomonas reinhardtii

Sara El-Shawa*, Rob Ness

POA-196

Translational Efficiency and The Evolution of Position-Dependent Codon Bias

Nelson Morrow*, Ashley Teufel, alon Diament, Claus Wilke