

# 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 Tenailon

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, Lluís 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, Changhoon Kim\*

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 Willerslev

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 Hammerschmidt, Giddy Landan, Fernando Domingues Kuemmel Tria, Tal Dagan\*

O-01-AE07

**Evolution of mRNA editing and linear multipartite genome in mitochondria of calcareous 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 reveals 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

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

Eriko Sasaki\*, Magnus Nordborg

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, Steven Maere\*



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, Taylor Mouton, Amanda Larracuent

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 Nevenon, 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, Aoifé 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-Neutalomes 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  $N_e$  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**

Hiroshi 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 *Arabidopsis thaliana***

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, Iliia Kurochkin, Olga Efimova, Aleksandra Mitina, Dmitry Zubkov, Philipp Khaitovich

O-01-OS16

**Mutation dynamics and fitness effects followed in single cells**

Marina ELEZ\*, Lydia ROBERT, Jean OLLION

**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 Hespels, Bernard Hallet

O-03-OS06

**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\*

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-lactamase 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 evolutionary 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 predictions 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

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-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 adrenocorticotrophic 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 Foliault\*, 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 Vågane, 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

**The rise and fall of "cheater" viruses in experimentally evolved MS2 phage populations**

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 (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.

### 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

#### **Detecting 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-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

**Vomer nasal 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*.**

Jeffrey 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 Castillénjos, 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-225

**Early environmental changes and metabolism evolution**

Anne Oudart\*, Celine Brochier-Armanet

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 Baptiste

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. Mogue

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 differentially 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\*, Floyd A. Reed

***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 crocodylians**

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 Muiira

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-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**

Iliia 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 Escrava, 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 Pouillet\*, 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 Patterson's D and fD for Detecting Regions of Introgression**

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

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Yoshihito Niimura\*, Atsushi Matsui, Kazushige Touhara

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

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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

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

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**Unveiling the architecture and evolution of microbial genomes from their homologous sequences**

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Rebecca A Chong\*, Nancy A Moran

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

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

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

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Vera Mukhina\*, Mikhail Gelfand

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

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

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Kerttu Majander\*, Elina Salmela, Kati Salo, Theseas Christos Lamnidis, Stephan Schiffels, Paivi Onkamo, Johannes Krause

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Michal Feldman\*, Eva Fernandez-Dominguez, Luke Reynolds, Raffaella Bianco, Cosimo Posth, Adrian Nigel Goring-Morris, Jessica Pearson, Hila May, Israel Hershkovitz, Douglas Baird, Choongwon Jeong, Johannes Krause

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Jeffrey Chan\*, Yun Song

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**Giant deer (*Megaloceros giganteus*) phylogeography and population dynamics: Insights from Late Pleistocene and Holocene mitochondrial genomes from Eurasia**

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**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

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**Reliable Inference of Genetic Diversity within and between Ancient and Modern Genomes**

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Theseas 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

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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

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

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**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

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

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**Detecting polygenic adaptation in human history**

Fernando Racimo\*

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**Pseudogenization of PON1 in Marine Mammals Implies Sensitivity to Organophosphate Pesticides**

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

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

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

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**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

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**Evolutionary analysis of epitopes and low complexity regions in Plasmodium**

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

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**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

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**Simulation of Intratumor Heterogeneity and its Medical Implication**

Watal M. Iwasaki\*, Hideki Innan

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**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

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

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

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**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

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**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

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

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**Using genotype abundance to improve phylogenetic inference**

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

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**Rapid adaptation of bacteriophage to their host after host-switching**

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

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

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

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Venkatesh Nagarajan-Radha\*, Damian Kimon Dowling

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

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

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

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Kara Boyer\*, Nicole Creanza, Maanasa Raghavan

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Yicheng Zhu\*, Cheng Soon Ong, Gavin Huttley

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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

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Juan Cristobal Opazo\*

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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

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Mariko F. Matsuura\*, Sarah Lucas, Vanessa E. DeLey Cox, Eric A. Gaucher

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Masato Nikaido\*, Hikoyu Suzuki, Takehiko Ito, Junji Hirota

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Joeselle Serrana\*, Sakiko Yaegashi, Shunsuke Kondoh, Bin Li, Christopher Robinson, Kozo Watanabe

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Cheng-Ruei Lee\*, Eric Schranz, Thomas Mitchell-Olds

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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

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Jennifer James, Adam Eyre-Walker\*

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

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Lou Nielly-Thibault\*, Christian R Landry

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

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Christiana Scheib\*, Hongjie Li, Vivian Link, Christopher Kendall, 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

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Xiaojun Wang\*, Haiwei Luo

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

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Takashi Kitano\*, Tadashi Minato

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Kazuharu Misawa\*

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

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



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Yosuke Hoshino\*, Eric Gaucher

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Yuka Matsushita\*, Naoko Takezaki, Amanda D. Melin, Shoji Kawamura

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Daniel Schrider\*

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Arunraj Saranya Prakashrao\*, Elisabeth Kaltenecker, Dietrich Ober

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Bernhard Wurzinger\*, Ingo Ebersberger, Katrin Schrader, Markus Teige

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Shivani Mahajan\*, Doris Bachtrog

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Sumita Omer, Bar Lavi, Piotr A Mieczkowski, Shay Covo, Einat Hazkani-Covo\*

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Jia-Hsin Huang\*, Ryan Shun-Yuen Kwan, Zing Tsung-Yeh Tsai, Huai-Kuang Tsai

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Evangelos Antonios Dimopoulos\*, Irina Velsko, Evan Irving-Pease, Laurent Frantz, Greger Larson

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Cheng-Kai Shiau, Jia-Hsin Huang, Huai-Kuang Tsai\*

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Arika Inuyama\*, Yosuke Seto, Yoshitaka Ogawa, Masafumi Nozawa, Koichiro Tamura

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Alon Diamant\*, Anna Feldman, Elisheva Schochet, Martin Kupiec, Yoav Arava, Tamir Tuller

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Rosa Fernandez\*, Toni Gabaldon

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Tommy T.Y. Lam\*

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Beatriz Mello\*

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Matthew Moore\*, David Newman, Martin Rusilowicz, James McInerney

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Anastasia Stolyarova\*, Georgii Bazykin, Tatyana Neretina, Alexey Kondrashov

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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

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**Predicting Disease Causality of Mutations in Human Beta Globin gene**

Sangeetha Udani Ratnayake\*

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Tomohiko Kimura, Yosuke Seto, Yoshitaka Ogawa, Msafumi Nozawa, Koichiro Tamura\*

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David Newman\*, James McInerney, Fiona Whelan, Martin Rusilowicz, Matthew Moore

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Kana Yamada\*, Nicolas Salamin, Iakov Davydov, Romain Studer

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Shir Portugez\*

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Lewis Stevens\*, Mark Blaxter

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Zhengting Zou\*, Jianzhi Zhang

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Chung-Shien Wu\*, Lian-Ming Gao, Chao-Nan Fu, Yu-Wen Chang, Shu-Miaw Chaw

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Michael C Turchin\*, Sohini Ramachandran

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Amanda J Lea\*, Julien F Ayroles

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Luisa F Pallares\*, Anett Schmittfull, Serge Picard, Julien F Ayroles

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Lisa Kursel\*, Harmit Malik

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Michael D. Kessler, Nicholas Bateman, Julie C. Dunning Hotopp, Timothy D. O'Connor\*

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Caroline M. Weisman\*, Andrew W. Murray, Sean R. Eddy

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**Phylogenetically young genes and their function in Anopheles mosquitoes.**

Elzbieta Krzywinska, Jaroslaw Krzywinski\*

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**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

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**Evolution of feeding preferences in Calliphoridae (Diptera)**

Tatiana Teixeira Torres\*, Gisele Antoniazzi Cardoso

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**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

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**Functional co-evolution in metabolic pathways**

Mathias Bockwoldt, Toni I. Gossmann, Mathias Ziegler, Ines Heiland\*

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**Forces shaping the distribution of rice genetic diversity**

Rafal Marek Gutaker\*, Michael Purugganan

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**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***

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**Phylonumerics: A New Mass-Based Molecular Evolution Approach Investigates the Emergence of Antiviral Resistance in the Influenza Virus**

Kevin Downard\*, Elma Akand

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**Orthology assignment of 5 novel Sparidae proteomes and their phylogenetic position among teleosts**

Paschalis Natsidis\*, Pavlos Pavlidis, Costas Tsigenopoulos, Tereza Manousaki

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**Composite Likelihood Estimation of Phylogenies from Genomic Data using Coalescent Theory**

Geno Guerra\*, Rasmus Nielsen

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**c-genie - Assessing the impact of recombination on phylogenomic inference**

Michael Matchiner, Milan Malinsky\*

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**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

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**Inferring cell differentiation processes based on phylogenetic analysis of genome-wide epigenetic information**

Kanako O Koyanagi\*

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**Characterization and Molecular Phylogeny of Korean Chrysanthemum Species**

So Youn Won\*, Jae-A Jung, Jung Sun Kim, Sangho Kang

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**Cnidarian phylogenomics to understand the eumetazoan evolution**

Mei-Fang Lin\*, James Reimer, Miyuki Kanda, Nana Arakaki, Hiroshi Watanabe

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**Phylogenomic analysis suggests two independent adaptations to high-salt environments in the Archaea**

Monique Aouad\*

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**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

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**Gene distributions across taxonomic groups reveal recent lateral gene transfers among prokaryotes**

Michael Knopp\*, Jessica Wimmer, William F. Martin

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**Canary: a new approach to identify attraction artifacts in the analysis of single gene families**

James Frederick Fleming\*, Roberto Feuda, Nicholas Roberts, Davide Pisani

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**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

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**Island biogeography of *Candidia temminckii*, a freshwater fish, suggests intraspecific replacements**

Shoji Taniguchi\*, Johanna Bertl, Andreas Futschik, Hirohisa Kishino, Toshio Okazaki

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**Gene fusion as a phylogenetic marker - a study of Metazoan**

Peter Mulhair\*, Mary O'Connell, Raymond Moran, Christopher Creevey, Davide Pisani, Ian Carr

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**Phylogenetic history of ERM proteins in metazoan tree of life**

Victoria Shabardina \*, Yukie Kashima

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**Charting the gene set of the last universal common ancestor**

Madeline C. Weiss\*, William F. Martin

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**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

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**The Likelihood Decay Index: Branch support for the phylogenomics era.**

Chris Creevey\*, Mark Wilkinson, James McInerney

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**Evolutionary metrics**

Satoshi Oota\*

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**Inferring incomplete lineage sorting, duplications, losses and transfers with reconciliations**

Yao-ban Chan\*, Celine Scornavacca, Vincent Ranwez

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**Evolutionary dynamics of Papaveraceae plastid genomes and contrasting patterns of organization and nucleotide substitution rates**

Seongjun Park\*, SeonJoo Park

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**Understanding the effect of calibrations in molecular clock dating**

Alan James Beavan\*, Mark Beaumont, Davide Pisani

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**Computing likelihoods of allele frequencies on phylogenetic trees using diffusion models**

David James Bryant, Stephanus Marnus Stoltz\*

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**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



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**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 CO<sub>2</sub> fixation: unique, ancient and ancestral in biochemistry**

Joana C. Xavier\*, Martina Preiner, William F. Martin

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

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**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

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**Analysis of Plasmid Gene Network**

Ignacio Riquelme Medina\*, James O McInerney

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**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

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**Inferring Prokaryotic Evolution using a Deterministic Model of Speciation**

Ashley Ann Superson\*, Michael Ryan Culver, Anna Maria Spagnuolo, Fabia Ursula Battistuzzi

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**Cis-trans evolution of chloroplast development regulator genes in plants**

Yao-Ming Chang\*, Hsin-Hung Lin, Wen-Hsiung Li

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**Investigating Signals of Local Adaptation on the Human X Chromosome**

Jonathan Rice\*, Emilia Huerta-Sanchez

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**Integration of phylogenomics and 3D protein modeling reveal phylogenetic inertia in ryanodine receptor ligand peptides of scorpion venom**

Carlos Eduardo Santibanez-Lopez\*, Ricardo Kriebel, Jesus Ballesteros, Prashant P Sharma

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**Phylogenomics resolves New World primates phylogeny**

Horacio Schneider\*, Jeferson Carneiro, Iracilda Sampaio

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**PhyCAP: Phylogenomic-noise Cleaning Approach by PCA**

Eisuke Iwamoto\*, Koichiro Tamura

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**Testing the accuracy of mitochondrial genomes reconstruction from transcriptomes: an insight from *Reticulitermes* termites mitogenomics.**

Giobbe Forni\*, Guglielmo Puccio, Barbara Mantovani, Andrea Luchetti

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**Phylogenomic analyses of transcriptome data from individual foraminifera**

Evie Grey Elizabeth Hoffman\*, Alistaire Ruggiero, Naomi Ostriker, Agnes Weiner, Laura Katz

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**Disentangling dietary transitions in termite evolution by transcriptome- and mitochondrial genome-based phylogenies**

Ales Bucek\*, Jan Sobotnik, David Sillam-Dusses, Nathan Lo, Thomas Bourguignon

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**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 abundance 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

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**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

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**Statistical tests for genomic time series data**

Andreas Futschik\*

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**Effect of binding interference on the divergence of paralogous genes that encode homodimers**

Angel Fernando Cisneros\*, Christian Landry

***SY27: Quantitative genetics of developmental evolution***

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**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\*

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**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

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**Differentiation in the facial morphology between Ryukyuan and mainland Japanese**

Ryosuke Kimura\*, Chiaki Watanabe, Eri Miyazato, Kyoko Yamaguchi, Takehiro Sato, Tsuyoshi Ito, Akira Kawaguchi, Ken Yamamoto, Hajime Ishida

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**Genome-wide allele-specific expression of the transcriptional landscape associated to *Capsicum domestication***

Erik Diaz-Valenzuela\*, Angelica Cibrian-Jaramillo, Ruairidh Sawers

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**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***

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**The Physiological and Genomic Impact Intense Selection for Starvation Resistance in *Drosophila melanogaster***

Mark A Phillips\*, James Kezos N, Michael R Rose

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**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

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**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

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**Founder-specific inbreeding depression affects racing performance in Thoroughbred horses**

Evelyn Todd\*, Natasha Hamilton, Simon Ho, Peter Thomson, Brandon Velie, Rachel Ang

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**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

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**Signatures of local adaptation in human zinc transporters genes**

Ana Roca-Umbert, Rocio Caro-Consuegra, Gabriel Felipe Rodriguez-Lozano, Nino Spataro, Elena Bosch\*

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**Evolution of alpha satellites in the human genome**

Manatsu Hamazaki\*, Hideki Innan

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**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

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**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

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**Evolution and Molecular Mechanisms of Photoreceptor Transmutation**

Ryan K Schott\*, Belinda SW Chang

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**Identifying host factors that modulate the outcome of influenza infection in humans**

Mary O'Neill\*, Maxime Rotival, Helene Quach, Lluís Quintana-Murci

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**Cross-species phylogenetic genome-phenome approach to understand the evolution of ageing in mammals**

Xavier Farre\*, Gerard Muntane, Arcadi Navarro

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**Detecting the signature of epistatic selection in subdivided populations**

Champak Beeravolu Reddy\*, Frederic Guillaume, Katalin Csillery

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**A new inference method for ongoing selective sweep**

Naoko T Fujito\*, Yoko Satta, Toshiyuki Hayakawa, Naoyuki Takahata

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**Addiction, Immunity, and Infectious Disease in a Global Population**

Latifa Jackson\*, Maksim Shestov

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**Inference of Microevolutionary Dynamics for Quantitative Molecular Phenotypes**

Shadi Zabad\*, Alan Moses

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**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***

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**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

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**Rules of neutral molecular evolution are only -half right Influences of positive vs. negative selection**

Qingjian Chen\*

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**Low somatic mutational robustness of the human genome**

Sofya Garushyants\*, Georgii Bazykin

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**Considering somatic mutation rate as a measure of genome maintenance capacity in colonial cnidarians**

Elora Hayter Lopez\*, Stephen R Palumbi

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**The missing link of cancer evolution - early remnants of tumorigenesis**

Bingjie Chen\*, Chung-I Wu

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**Measuring DNA mutation rates with Circle-sequencing**

Stephan Baehr\*, Lauren Reyes, Jean-Francois Gout, Michael Lynch

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**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

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**Rates of mutation and recombination in Siphoviridae phage genome evolution over three decades**

Anne Kupczok\*, Horst Neve, Kun D. Huang, Marc P. Hoepfner, 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

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**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

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**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***

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**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***

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**RepetDB: a resource for unified transposable element references with classification**

Joelle Amselem\*, Guillaume Cornut, Nathalie Choisne, Michael Alaux, Françoise Alfama-Depauw, Veronique Jamilloux, Florian Maumus, Thomas Letellier, Isabelle Luyten, Cyril Pommier, Anne-Françoise Adam-Blondon, Hadi Quesneville

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**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

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**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

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**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

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**Detecting structural variations in human genome using nanopore sequencer**

Satomi Mitsuhashi\*, Martin C Frith, Naomichi Matsumoto

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**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

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**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

**Phylogenetic 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

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**Genomic and phylogenetic study of feline paramyxovirus**

Shoichi Sakaguchi\*, Satomi Mitsuhashi, Makoto Ogawa, Takayuki Miyazawa, Tadashi Imanishi, So Nakagawa, Tetsuya Mizutani

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**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\*

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**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***

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