



Scientific Program

SMBE 2017, Austin, July 2–July 6

Sunday 2nd July 2017

Masatoshi Nei Lecture

5:00pm	Laura Landweber, Columbia University Life with 16,000 chromosomes and reflections on 21st century women in science			
	Associate Editor Symposium Session 1	Associate Editor Symposium Session 2	Associate Editor Symposium Session 3	Associate Editor Symposium Session 4
	Howard Ochman, Nancy Moran, Claus Wilke	Howard Ochman, Nancy Moran, Claus Wilke	Howard Ochman, Nancy Moran, Claus Wilke	Howard Ochman, Nancy Moran, Claus Wilke
6:30pm	Kenneth Wolfe, University College Dublin Evolutionary restoration of fertility in an interspecies hybrid yeast, by whole-genome duplication after a failed mating-type switch	Harmitt Malik, Fred Hutchinson Cancer Research Center Combinatorial mutagenesis of positively selected residues reveals negative epistasis and super-restrictor phenotypes in an antiviral protein	Naruya Saitou, National Institute of Genetics, Japan Characteristics of evolutionarily conserved noncoding regions in vertebrate genomes	James McInerney, The University Of Manchester A public goods perspective on evolution
6:45pm	Laura Katz, Smith College Through the Looking Glass: Insights into the biodiversity of eukaryotes through phylogenomic analyses and single-cell 'omics'	Emma Teeling, University College Dublin Comparative genomics of bats: the secret of extended longevity?	Juliette de Meaux, University of Cologne Adaptive remodeling of the transcriptional response to drought stress in Arabidopsis lyrata	Deepa Agashe, National Centre For Biological Sciences, India Bacterial genome evolution: reconciling experiments with phylogeny
7:00pm	Davide Pisani, University of Bristol School of Biological Sciences Compositional heterogeneity, substitutional saturation and the problem of early animal evolution	Brenna Henn, SUNY Stony Brook False negatives are a significant feature of next generation sequencing callsets	Ryan Hernandez, University of California, San Francisco Human evolutionary history has increased the role of rare variants in complex phenotypes	Ruth Hershberg, Technion - Israel Institute Of Technology From boom to bust – bacterial adaptation to prolonged survival following resource exhaustion
7:15pm	Claus Wilke, The University of Texas at Austin Sequence amplification via cell passaging creates spurious signals of positive adaptation in influenza virus H3N2 hemagglutinin.	Tal Pupko, Tel-Aviv University Inferring rates and length-distributions of indels using approximate Bayesian computation	Stephen Blair Hedges, Temple University TimeTree: A resource for timelines, timetrees, and divergence times	Jeffrey Thorne, North Carolina State University Combining disease data and molecular evolution to better understand both

Monday 3rd July 2017

	Evolutionary systems biology of cells Session 1	Epigenetics and evolution Session 1	Mechanisms of protein evolution Session 1	Integrating Ancient and Modern DNA Session 1
	Laurence Loewe, Anne-Ruxandra Carvunis	Alexandros Bousios, Soojin Yi, Brandon Gaut	Benjamin Jack, Ashley Teufel	Simon Aeschbacher, Laurent Excoffier, Anna-Sapfo Malaspinas
8:30am	Michael Lynch, Indiana University Mutation, drift, and the origin of cellular features	Damon Lisch, Purdue University A possible link between epigenetic regulation of trans duplicated gene fragments and microRNA function in maize.	Jesse Bloom, Fred Hutchinson Cancer Research Center / University of Washington Quantitative models of protein evolution informed by experimental data	Stephan Schiffels, Max Planck Institute for the Science of Human History Functional implications of Neandertal introgression in modern humans
9:00am	Trey Ideker, University of California, San Diego Active Interaction Mapping reveals the hierarchical organization of autophagy	Isabel Mendizabal, Georgia Institute of Technology Epigenetic regulatory loci of human brain evolution and their role on the susceptibility to neuropsychiatric disorders	Mary O'Connell, University of Leeds Evolution of novel proteins by gene remodeling in animals.	Beth Shapiro, University of California Santa Cruz Passenger pigeon genomes reveal the cost of natural selection for a large population
9:30am	Ingo Ebersberger, Goethe University Frankfurt How universal is the minimal gene set for bacterial life?	Oana Carja, University of Pennsylvania Epigenetic variance as evolutionary strategy for life in an uncertain world	Brandon Xia, McGill University The impact of native state switching on protein sequence evolution at the residue level	Tom Van der Valk, Uppsala University Temporal genetic diversity in eastern gorillas
9:45am	Kerry Geiler-Samerotte, Stanford University Pleiotropic genetic effects on cell morphology are mediated by underlying relationships among single-cell morphological features	Mia Levine, University of Pennsylvania Genetic conflict shapes Drosophila telomere biology	Claudia Weber, Temple University Using structural conservation to evaluate biological realism in models of protein evolution	Joseph Lachance, Georgia Institute of Technology The genomic health of ancient hominins
10:00am	Marco Fumasoni, Harvard University Analysis of the replisome plasticity and its consequences for genome evolution	Grace Lee, Lawrence Berkeley National Laboratory Pervasive epigenetic effects of euchromatic transposable elements that shape their own population dynamics	Joanna Masel, University Of Arizona Progressively more subtle aggregation avoidance strategies form a long-term arrow of protein evolutionary time	Michael Dannemann, Max Planck Institute for Evolutionary Anthropology Functional implications of Neandertal introgression in modern humans
10:15am	Leslie Babonis, University Of Florida Conserved transcription factors are required for patterning cnidocytes (a novel cell type) in the sea anemone Nematostella vectensis	Stevie Anne Bain, University of Edinburgh Epigenetic mechanisms underlying Paternal Genome Elimination in the scale insect, Planococcus citri	Marcin Bogusz, Uppsala University The interaction between selective constraints acting on substitutions and small-scale insertions and deletions in proteins	Pontus Skoglund, Harvard Medical School Reconstructing prehistoric African population structure and adaptation

	Keynote Lecture			
11:00am	Rasmus Nielsen, University of California Berkeley The genetic basis of human adaptation to local environments			
	Evolutionary systems biology of cells Session 2	Epigenetics and evolution Session 2	Mechanisms of protein evolution Session 2	Open Symposium Session 1
	<i>Laurence Loewe, Anne-Ruxandra Carvunis</i>	<i>Alexandros Bousias, Soojin Yi, Brandon Gaut</i>	<i>Benjamin Jack, Ashley Teufel</i>	<i>Howard Ochman, Nancy Moran, Claus Wilke</i>
1:30pm	Jacob Musser, EMBL Heidelberg Comparative single-cell transcriptomics in sponges sheds light the origins of animal cell type diversity	Z. Jeffrey Chen, The University of Texas at Austin Genetic and epigenetic mechanisms for gene expression and evolutionary novelty in plant polyploids	Tyler Starr, University of Chicago Contingency and evolvability across the sequence space of an ancestral protein	David Rand, Brown University Mitonuclear transcriptomes uncover common features of epistasis (GxG) and genotype x environment (GxE) interactions in Drosophila
1:45pm	Joshua Rest, Stony Brook University Stochastic differences in gene expression levels contribute to the overall metabolism of a clonal cellular population	Tim Stuart, The University of Western Australia Population scale mapping of transposable element variation in Arabidopsis	Hugh Haddox, Fred Hutchinson Cancer Research Center / University of Washington Quantifying the divergence in mutational effects among distant homologs of HIV's envelope protein	Einat Hazkani-Covo, The Open University of Israel The number of independent organelle DNA insertions in genomes
2:00pm	Christian Landry, Université Laval Gene duplication imparts robustness and fragility to protein interaction networks	Nader Aryamanesh, University of Oulu Epigenetics and local adaptation in Arabidopsis lyrata	Colin Brown, University of Texas at Austin Massively-parallel bacteriophage evolution quantifies the adaptive utility of genetic codes expanded with nonstandard amino acids	Amanda Larracuent, University of Rochester Parallel selective sweeps of selfish Segregation Distorter complexes in African and European Drosophila melanogaster populations.
2:15pm	Harry Kemble, INSERM High-resolution fitness mapping of a metabolic pathway	Victoire Baillet, Institut de Biologie de l'Ecole Normale Supérieure (IBENS) Impact of DNA methylation on the rate and spectrum of mutations in Arabidopsis thaliana	Zachary Sailer, University of Oregon High-order epistasis is inevitable in molecular systems	Falk Hildebrand, EMBL Heidelberg Tracking bacterial genetic variation over short time spans with metagenomics
2:30pm	Jolien Van Hoof, Hubrecht Institute Unique distributions of the Ska and Dam1 complexes support functional analogy and point to multiple parallel displacements of Ska by Dam1	Christina Barr, NIH/NIAAA Lab of Comparative Behavioral Genomics Behavioral variation in primates as a function of epigenetic regulation and genetic polymorphism at the oxytocin receptor (OXTR) gene	Adrian Serohijos, University of Montreal Tuning the course of evolution on the biophysical fitness landscape of an RNA virus using droplet microfluidics	Felix M. Key, Max Planck Institute for the Science of Human History High-throughput pathogen detection in ancient metagenomic data
2:45pm	Riddhiman Garge, University of Texas at Austin Humanized yeast as a platform to study gene family expansion and understand genetic variation	Groves Dixon, University of Texas at Austin Role of gene body methylation in coral adaptation and acclimatization	Jessica Siltberg-Liberias, Florida International University Evolution of a conformational ensemble	Adam Eyre-Walker, University Of Sussex Large scale variation in the rate of de novo mutation in humans: quantification, causes and the relationship to divergence and diversity
3:00pm	Kasey Swilley, Kansas State University Evolution of the extracellular matrix for multicellularity	Clara Pereira, Trinity College Dublin Long interspersed nuclear elements and monoallelic expression	Juraj Bergman, Institut für Populationsgenetik, Vetmeduni Vienna, Austria Does adaptive evolution proceed by small or large steps at the molecular level?	German Plata, Columbia University Long-term patterns of bacterial phenotypic divergence
3:15pm	Richard McCann, Mercer University School of Medicine A cellular systems approach to origins of the Metazoa: Functional constraints and sequence conservation in coevolution of the core adhesome	Chloe Robins, Emory University Using DNA methylation data to test heritability-based predictions of evolutionary models of human aging	Jakub Otwinowski, University of Pennsylvania Structure of global epistasis in protein sequence-function relationships	Camilla Whittington, The University Of Sydney The genetic basis of vertebrate pregnancy and birth
	Polyploidy and hybridization	Systems approaches to behavior	Extracting insights from personal genomics data	Integrating Ancient and Modern DNA Session 2
	<i>Z. Jeffrey Chen, Pamela S. Soltis</i>	<i>Julia Saltz, Joyce Kao</i>	<i>Adam Boyko, Adam Auton</i>	<i>Simon Aeschbacher, Laurent Excoffier, Anna-Sapfo Malaspinas</i>
4:00pm	Keith Adams, University of British Columbia Regulatory and functional divergence of duplicated genes after ancient polyploidy events	Hans Hofmann, The University of Texas at Austin Complex homology and the neuromolecular evolution of social behavior	Andrew Clark, Cornell University Past and future of prediction of medical phenotypes from genome sequence	David Reich, Harvard Medical School Bridging the divide between modern and ancient DNA
4:30pm	Douglas Soltis, University of Florida Polyploidy, paths and pitfalls to a paradigm: insights from Tragopogon	Lauren O'Connell, Harvard University Cognitive ecology of poison frogs	Alicia Martin, Broad Institute Human demographic history impacts genetic risk prediction across diverse populations	Rafal Gutaker, Max Planck Institute for Developmental Biology Targeted re-sequencing of historic and modern samples reveals the complexity of potato introduction to Europe
4:45pm				Natalie Telis, Stanford University Functional characterization of Neanderthal introgression
5:00pm	Jing Chai, Yunnan University Genomic variations in the nascent generations of an allopolyploidy line by goldfish and common carp	Brian Hollis, École polytechnique fédérale de Lausanne The transcriptomic basis of evolving sexual interactions in Drosophila	Yi-Fei Huang, Cold Spring Harbor Estimation of nucleotide- and allele-specific selection coefficients for personal genomics using deep learning and population genetics	Melinda Yang, The Institute of Vertebrate Paleontology and Paleoanthropology (IVPP), Chinese Academy of Sciences 40,000-year-old individual from Asia provides insight into early population structure in Eurasia
5:15pm	Elizabeth McCarthy, University of California, Riverside The genetic and biochemical basis of floral color differences in Nicotiana allopolyploids	Nicole Creanza, Vanderbilt University Signals of evolutionary history in a learned behavior: song reflects phylogeny in Emberizid sparrows	Elena Sorokin, Stanford University Clinical Characterization of over 30,000 clinically relevant variants in 133 global populations	Alissa Mittnik, Max Planck Institute For The Science Of Human History The genetic history of Northern Europe
5:30pm	Yves van de Peer, VIB/Universiteit Gent	Alejandro Berrio, Duke University	Michelle Kim, Georgia Institute of Technology	Logan Kistler, Smithsonian Institution

	Coordinated gene expression divergence following whole genome duplication in <i>A. thaliana</i>	Complex selection on a regulator of sexual fidelity	Ascertainment bias creates the illusion of genetic health disparities and limits the generalizability of results across populations	The independent legacy of maize diversification in South America: A test case for adaptation in dispersal using archaeogenomics
5:45pm	David Winter, Massey University Fitting two genomes in one nucleus: the structure and function of genomes in <i>Epichloë</i> hybrids	Ryan York, Stanford University Systems genomics of bower behavior in Lake Malawi cichlid fishes	Genevieve Wojcik, Stanford University Testing the generalizability of current GWAS findings within the multi-ethnic PAGE II Study	Jeremy Rio , Geneva University, Biology Department, Anthropology Genetics and Poepling Unit Investigating population continuity with ancient DNA under a spatially explicit simulation framework

Tuesday 4th July 2017

	Evolutionary genomics of structural variation Session 1 <i>Rebekah L Rogers, Russ Corbett-Detig</i>	Molecular Innovation Session 1 <i>Li Zhao, Victor Luria</i>	Evolution of gene regulation Session 1 <i>Dennis Kostka, Tony Capra</i>	Probing Microbiome Dynamics <i>Nandita Garud, Sharon Greenblum</i>
8:30am	Jeffrey Ross-Ibarra, University of California, Davis Evolutionary genetics of structural variation in maize	David Begun, University of California, Davis Investigating young de novo genes in <i>Drosophila melanogaster</i> .	James Noonan, Yale University Genetic models of human evolution	Howard Ochman, The University of Texas at Austin The extraordinary evolution of the human microbiome
9:00am	Aoife Mclysaght, Trinity College Dublin Ancestral genome reconstruction and ancient polyploidy in vertebrates	Alan Saghatelian, Salk Institute Cell biology of micropoteins encoded by smORFs	Saurabh Sinha, University of Illinois at Urbana-Champaign Studying cis-regulatory evolution with quantitative models of sequence function	Isabel Gordo, Instituto Gulbenkian de Ciência Mutation and horizontal gene transfer as drivers of short-term adaptation within the gut microbiota
9:30am	Matthew Webster, Uppsala University Chromosomal inversions govern adaptation to altitude in honeybees	Rafik Neme, Columbia University Medical Center Molecular innovation in ciliates with complex genome rearrangements	David Murphy, Columbia University The effects of background selection in the human genome reveal extensive purifying selection on non-coding regions	Shelbi Russell, University of California, Santa Cruz Dynamics of intra-host symbiont evolution under mixed modes of transmission
9:45am	Jenn Coughlan, Duke University Understanding the role of chromosomal inversions in life history divergence and local adaptation in <i>Mimulus</i>	Yong Zhang, Institute of Zoology, Chinese Academy of Sciences Origination of retrochimera via the LTR-mediated mechanism in metazoans	Andreas Pfennig, Carnegie Mellon University Epigenetic mechanisms underlying the evolution of learned vocal behavior	Margaret Steele, The University of Texas at Austin Type VI secretion systems and associated toxins in the bee gut microbiota
10:00am	Robert Ruggiero, New York University Abu Dhabi Population genomics of <i>Anolis carolinensis</i> transposable elements: insertion polymorphisms are abundant but rarely approach fixation	Jason Huff, University of California, Berkeley How and why are there so many introns in genomes? Mechanism by which transposable elements generate introns on massive scales	Yehu Moran, The Hebrew University of Jerusalem Cnidarian microRNAs shed new light on the evolution of post-transcriptional regulation of gene expression	Benjamin Good, University of California, Berkeley Dynamics of within- and between-host evolution in the gut microbiome
10:15am	Yongfeng Zhou, University of California, Irvine Structural variation of grape domestication	Lisa Kursel, Fred Hutchinson Cancer Research Center Recurrent gene duplication leads to diverse repertoires of centromeric histones in <i>Drosophila</i> species	Ziyue Gao, Stanford University Detecting stabilizing selection on gene expression level from human genetic and expression variation data	Emily Davenport, Cornell University Modeling human gut microbiome community structure across healthy and diseased states in 2,500 twins
Keynote Lecture				
11:00am	Siv Andersson, Uppsala University Molecular Evolution of Small Bacterial Genomes			
	Evolutionary genomics of structural variation Session 2 <i>Rebekah L Rogers, Russ Corbett-Detig</i>	Molecular Innovation Session 2 <i>Li Zhao, Victor Luria</i>	Evolution of gene regulation Session 2 <i>Dennis Kostka, Tony Capra</i>	Open Symposium Session 2 <i>Howard Ochman, Nancy Moran, Claus Wilke</i>
1:30pm	Emerson Khost, University of Rochester Evolution of satellite DNA loci in <i>Drosophila melanogaster</i> and the simulans clade	Luke Kosinski, University of Arizona Stop codon readthrough errors purge deleterious cryptic sequences, facilitating the later co-option of non-coding sequences into coding	Ling Chen, Vanderbilt University Sequence properties of enhancers are conserved across mammals	David Queller, Washington University in St. Louis Family quarrels in seeds result in molecular arms races
1:45pm	Jeffrey Adrion, Indiana University The effect of spatially varying selection on transposable element insertions in <i>Drosophila</i>	Matthew Cordes, University of Arizona Foldability of a de novo evolved protein	Diego Villar, Cambridge Institute - Cancer Research UK and University of Cambridge The gene expression consequences of mammalian regulatory evolution	John Logsdon, University of Iowa A very recent whole genome duplication in <i>Potamopyrgus antipodarum</i> predates multiple origins of asexuality & associated polyploidy
2:00pm	Katharine Korunes, Duke University The pervasiveness of gene conversion facilitates interspecies gene flow	Anne-Ruxandra Carvunis, University of Pittsburgh Proto-genes, fitness, and de novo gene birth	Margarida Cardoso Moreira, Heidelberg University The evolution of mammalian gene expression across multiple dimensions	Genelle Harrison, McGill University The advent of agriculture shaped innate immune responses to pathogens in humans
2:15pm	Miriam Merenciano, Institute of Evolutionary Biology (CSIC-Pompeu Fabra University) Multiple independent retroelement insertions in the promoter of a stress response gene	Emily Killingbeck, University of Washington “Fishing” for vertebrate fertilization genes: genomic and proteomic characterization of rapidly evolving threespine stickleback egg proteins	Raghavendra Partha, University of Pittsburgh Predicting specific biological functions of gene regulatory regions using convergent evolution	Fatimah Jackson, Howard University New World Africans are an amalgamation of African peoples with modest gene flow from non-Africans
2:30pm	Janine Deakin, University of Canberra Chromosome rearrangements in a recently emerged facial tumour in Tasmanian devils	Chen Xie, Max Planck Institute for Evolutionary Biology A mouse-specific de novo gene has important functions in developing brain by affecting transcriptional networks	Cong Liang, Yale University Integrated analysis of open chromatin and gene expression data identifies gene regulation changes in decidal cell evolution	Marcela Sandoval Velasco, University of Copenhagen Tracing the origins of 19th century enslaved Africans

2:45pm	Jacob Malte Jensen, Aarhus University Population reference graphs of complex regions	Victor Luria, Harvard Medical School Variation and novelty in evolution: de novo genes arise and enable protein structural innovation	Premal Shah, Rutgers University Evolution of transcriptional and translational regulation during adaptation	Fanny Pouyet, Institute Ecology And Evolution, University of Bern Biased gene conversion drives codon usage in human and precludes selection on translation efficiency
3:00pm	Nicola Barson, Norwegian University of Life Sciences Rainbow trout genome assembly reveals a double inversion harboring a complex multigenic switch for alternative life-history phenotypes	Caroline Weisman, Harvard University Problems and solutions in homology search-based de novo gene identification: toward a computational control for undetected homologs	Rachel Cosby, University of Utah How to build a new transcription factor: a novel bat-specific KRAB-transposase fusion gene acts as a transcriptional repressor	Hiba Babiker, Max Planck Institute for the Science of Human History The genetic identity of the Bangande People “The secret ones”
3:15pm	Josephine Daub, Universitat Pompeu Fabra, Barcelona Detecting and understanding the action of natural selection within segmental duplications in primates	Mar Alba, Pompeu Fabra University – Barcelona De novo gene evolution: How do we transition from non-coding to coding?	Rosina Savisaar, University of Bath How much does RNA-level regulation constrain exonic sequence evolution?	Kaspar Munch, Aarhus University Human X chromosomes show recurring selective sweeps suggestive of meiotic drive

Walter Fitch Symposium

4:00pm	David Carlson, Stony Brook University Does loss of sex lead to increased transposable element accumulation? Evidence from the evening primrose genus <i>Oenothera</i>
4:15pm	Shivani Mahajan, University of California, Berkeley Convergent evolution of Y chromosome gene content in flies
4:30pm	Michal Szpak, Wellcome Trust Sanger Institute Fine-mapping and functional analyses of genetic variants driving local adaptations in humans.
4:45pm	Anna Vickrey, University of Utah Domestic pigeon's checkered past: wing color pattern variation is associated with one gene, two mechanisms, and interspecific introgression
5:00pm	Aaron Wolf, University of Washington Interpreting human genomic regions depleted of archaic Hominin ancestry
5:15pm	Xinzhu 'April' Wei, University of Michigan A new theory on the cause of genetic dominance
5:30pm	Da Yin, University of Maryland Self-fertility triggers rapid genome shrinkage and loss of sperm competition proteins
5:45pm	Katherine Xue, University of Washington Parallel evolution of influenza across multiple spatiotemporal scales

Wednesday 5th July 2017

	Pathogen genomics Session 1 <i>Daniel Jeffares, Tim Anderson, Francois Balloux</i>	Mutational load, Session 1 <i>Stephan Peischl, Isabel Alves</i>	Calibrating the history of life <i>Emma Teeling, Jesus Lozano-Fernandez, Mary O’Connell, Davide Pisani</i>	Evolution of complex traits <i>Camilla Whittington, Michael Thompson</i>
8:30am	Pleuni Pennings, San Francisco State University Evolutionary genetics of HIV drug resistance	Kirk Lohmueller, University of California, Los Angeles The impact of demographic history on genetic load	Fabia Ursula Battistuzzi, Oakland University Calibrating the microbial Tree of Life	Nicola Illing, University of Cape Town Evolution of wing development in the Natal long-fingered bat, <i>Miniopterus natalensis</i>
9:00am	Annette Macleod, University of Glasgow An asexual eukaryote demonstrating the Meselson Effect	Joshua Akey, University of Washington Patterns of deleterious variation within and between geographically diverse populations	Tracy Heath, Iowa State University Hierarchical Bayesian models for integrating paleontological and neontological data	Gunter Wagner, Yale University A gene regulatory network model for the origin of a novel cell type identity

9:30am	Aida Andrade Valtueña, Max Planck Institute for the Science of Human History The Stone Age plague: 1000 years of Persistence in Eurasia	Jenny James, University of Sussex The influence of selective sweeps on the relationship between the efficiency of natural selection and genetic diversity.	Fernando Tria, University of Kiel Phylogenetic rooting using minimal ancestor deviation	Rebecca Tarvin, University Of Texas At Austin Evolution of alkaloid resistance in poison frogs revealed by comparative phylogenetics
9:45am	Beth Gibson, University of Sussex Investigating variation in the substitution rate across bacteria	Ivana Cvijovic, Harvard University The effect of background selection on mutational dynamics and diversity	Holly Betts, University of Bristol A timescale for life's early evolution: Is it time to leave behind a literal interpretation of the fossil record?	Erica Todd, University of Otago The genomic basis of sex change in fish
10:00am	Liliana Kokusanilwa Rutaihwa, Swiss Tropical and Public Health Institute Origin of the Mycobacterium tuberculosis Beijing family in Africa	Claudia Bank, Instituto Gulbenkian de Ciencia Evolutionary rescue from mutational meltdown	Gergely Szollosi, MTA TKI, The Hungarian Academy of Sciences Reconstructing a dated tree of life using phylogenetic incongruence	Atsushi Ogura, NIBIO, Nagahama Institute of Bio-Science and Technology, Evolution and diversification ef Eye
10:15am	Thomas Hill, University of Kansas Adaptation of Baculoviruses and Nudiviruses in Drosophila and other arthropods	Dan Graur, University of Houston An upper limit on the functional fraction of the human genome	Huw Ogilvie, Australian National University Reconstructing species substitution rates and divergence times from nuclear DNA using StarBEAST2	Nathan Clark, University of Pittsburgh A novel female reproductive organ - the bursa copulatrix - as a dynamic interface for male-female coevolution
Keynote Lecture				
11:00am	Trudy Mackay, North Carolina State University Charting the Genotype-Phenotype Map: Lessons from Drosophila			
	Pathogen genomics Session 2 <i>Daniel Jeffares, Tim Anderson, Francois Balloux</i>	Mutational load, Session 2 <i>Stephan Peischl, Isabel Alves</i>	Open Symposium Session 3 <i>Howard Ochman, Nancy Moran, Claus Wilke</i>	Open Symposium Session 4 <i>Howard Ochman, Nancy Moran, Claus Wilke</i>
1:30pm	Frédéric D. Chevalier, Texas Biomedical Research Institute Parasite invasions: colonization and adaption of schistosomes to the new world during the slave trade	Carlos Eduardo G. Amorim , Columbia University The population genetics of recessive, lethal mutations	Daniel Bolnick , The University of Texas at Austin Genomic and phenotypic repeatability of divergence between 16 pairs of lake and stream stickleback	Javier Blanco, Laboratorio Nacional De Genómica Para La Biodiversidad Genomic Insights into the Ancestry and Human Demography of Remote Polynesia
1:45pm	John Lees, Wellcome Trust Sanger Institute Genome-wide identification of lineage and locus specific variation associated with pneumococcal carriage duration	Donate Weghorn, BWH / Harvard Medical School Estimating the selective effect of heterozygous protein truncating variants from human exome data	Andrew Ellington, The University of Texas at Austin Directed evolution of the genetic code	Judith Wexler, University of California Davis Tracing the evolutionary origins of an insect sexual differentiation pathway based on sex-specific alternative splicing
2:00pm	Ashley Teufel, The University of Texas at Austin Uncovering replication principles from single-cell virology experiments	Olivia Yvellez, Duke University Presence and ecological effect of a raccoon rabies expansion load	Philipp Messer, Cornell University Genetic manipulation of entire populations with CRISPR gene drives	Raquel Assis, Pennsylvania State University Expression evolution of Drosophila nested genes
2:15pm	Brian Arnold, Harvard T.H. Chan School of Public Health Stronger together: recombining bacteria can harness weak epistasis to drive adaptation	Kimberly Gilbert, University of Toronto Mutation load across mating systems: how does load change and how do we best estimate it?	Shoji Kawamura, The University of Tokyo Divergent evolution of olfactory and taste receptor repertoire in New World monkeys with diverse color vision types and feeding habits	Chris Clarkson, Wellcome Trust Sanger Institute The Anopheles gambiae 1000 Genomes Project: population genomics and malaria vector control
2:30pm	Chandler Roe, Northern Arizona University Divergence dating of the dispersal of Cryptococcus gattii to the North American Pacific Northwest using BEAST and RelTime.	Martin Lascoux, Uppsala University Genetic diversity and the efficacy of purifying selection across plant and animal species	Gaurav Diwan, National Centre for Biological Sciences, India Changes in genome GC and tRNA content influence the evolution of tRNA modifying enzymes in bacteria	Arbel Harpak, Stanford University How brown rats adapted to life in NYC's concrete jungle
2:45pm	Alison Feder, Stanford University Tracking evolutionary dynamics over time to uncover hidden population structure in within-host Simian-HIV populations	Olivier Tenaillon, Infection Antimicrobial Modelling Evolution, INSERM Draft masks the genomic signature of selection despite thousands of generations of adaptation in mutator bacteria	Greg Wray, Duke University Rewiring key gene interactions during embryonic development alters larval morphology in the sea urchin genus Heliocidaris	Josep Comeron, University of Iowa Predictions of linked (and unlinked) purifying selection as null hypothesis to study diversity across genomes
3:00pm	Angela Early, Broad Institute Haplotype analysis of complex Plasmodium falciparum infections identifies loci under selection	Daniel Balick, Harvard Medical School/Brigham & Women's Hospital Prevalence of recessive selection confounds estimates of the mutation load in humans	Laurent Frantz, University Of Oxford Ancient genomics of pre-Columbian North American dogs	Cian Glenfield, Trinity College, University of Dublin Signatures of constraint on mammalian pseudogenes functioning as competitive endogenous RNAs
3:15pm	Florent Lassalle, Imperial College London Modeling the co-evolution of genes in bacterial genomes to understand the emergence of antibiotic resistance-conferring mobile elements	Mashaal Sohail, Harvard University Negative selection in humans and fruit flies involves synergistic epistasis	Sudhir Kumar, Temple University Ancient Adaptive landscape of the human coding genome	George Zhang, University of Michigan The fitness landscapes of a yeast tRNA gene in multiple environments: GxE is pervasive yet simple

	Infection and immune systems <i>Lluís Quintana-Murci, Luis B. Barreiro</i>	Mutational mechanisms <i>Arbel Harpak, Ziyue Gao, Kelley Harris</i>	Population genomics of ancient DNA <i>Benjamin Peter, Joshua Schraiber</i>	Convergent evolution <i>Nathan Clark, Tim Sackton</i>
4:00pm	Jenny Tung, Duke University How social status changes the immune system: experimental evidence from rhesus macaques	Serena Nik-Zainal, Sanger Institute Advancing the field of mutational signatures: Insights into mutational mechanisms and clinical applications	Montgomery Slatkin, UC Berkeley Methods for combining ancient and modern genomic data sets	Matthew Hahn, Indiana University Convergence and reversion in the presence of gene tree discordance
4:30pm	Iain Mathieson, University of Pennsylvania The immune system was a major target of natural selection during the European Neolithic	Shamil Sunyaev, Harvard University Generating hypotheses about mutational mechanisms from large-scale data	Maanasa Raghavan, University of Cambridge Empirical perspectives on ancient DNA	Jay Storz, University of Nebraska Causes of parallel molecular adaptation: insights from reverse genetics
5:00pm	Tzachi Hagai Rapidly-evolving innate immune genes are younger, transcriptionally noisier and more pathologically dysregulated	Erez Levanon DNA editing of LTRs by APOBECs accelerate vertebrates' genome evolution	David Diez-del-Molino A palaeogenomic perspective of near-extinction population dynamics	Neda Barghi All roads lead to adaptation: Genomic signatures of parallel evolution in <i>Drosophila simulans</i>
5:15pm	Sabyasachi Das Evolutionary modification of the VLR-based adaptive immune system in jawless vertebrates	Wendy Wong Clustered de novo mutations with large intra-mutational distance contribute to the maternal age effect	Maria Laura Parolin Ancient mitogenomes of Argentine Patagonia (6070-310 YBP) reveal the early contribution of lineages not previously found in South America	Kristin Lee Detecting signatures of convergent adaptation in genomic data
5:30pm	Nicolas Strauli Using time-series sequence data to characterize the interaction between the host antibody repertoire and pathogens	Kadir Akdemir Spatial chromatin organization and distribution of somatic mutations in cancer genomes	Yassine Souilmi Paleo-population genetics: Illuminating the role of selection in shaping human diversity	Wynn Meyer Ancient convergent loss of a metabolic gene's function yields deleterious consequences for modern marine mammals
5:45pm	Julia Saltz, Rice University Genetic variation in social interactions leads to outbreaks of a sexually-transmitted fungus in <i>D. melanogaster</i>	Kateryna Makova, Penn State University Polymerization kinetics deciphered using PacBio sequencing: Non-B DNA affects polymerase progression and error rate	Johannes Krause, Max Planck Institute Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods	Sarah Kocher, Princeton University Comparative methods offer powerful insights into social evolution in halictid bees

Thursday, 6th July 2017

	Genomic mechanisms of speciation Session 1 <i>Jeffrey Good, Elen Oneal</i>	Mechanisms of phenotypic evolution Session 1 <i>Raquel Assis, Melissa Wilson Sayres</i>	Symbiosis and interactions <i>Becky Chong, Chih-Hong Kuo</i>	Computation and reproducibility in molecular evolution <i>Anton Nekrutenko, Sergei Kasakovsky Pond</i>
8:00am	Mary Gehring, Whitehead Institute Mechanisms and evolution of imprinting in plants	Joseph Thornton, University of Chicago Deep mutational scanning of an ancient protein: the many roads not taken in protein evolution	Theresa Pawlowska, Cornell University Evolutionary stability in fungal-bacterial symbioses	Simon Frost, University of Cambridge Engineering a real-time HIV surveillance platform
8:30am	Jason Wolf, University of Bath Gene interactions and coadaptation in the evolution of genomic imprinting	Daniel Weinreich, Brown University Distinguishing between mechanistic tradeoffs and mutational entropy in protein evolution	Daniel Sloan, Colorado State University Rates of organelle genome evolution and their effects on cytonuclear interactions	Dan Stanzione, Texas Advanced Computing Center The new advanced computing landscape: Opportunities for molecular biology
9:00am	Morgane Roth, ETH Zürich Hybrid seed failure among wild tomato lineages: perturbed expression and imprinting in the endosperm	Eaaswarkhanth Muthukrishnan, Dasman Diabetes Institute Complex evolutionary roots of skin-barrier function in humans	Richard Cordaux, CNRS/Université de Poitiers Does <i>Wolbachia</i> drive the diversity and evolution of sex determination systems in terrestrial isopods?	Andreina Castillo Siri, University of Arizona Comparative genomics of <i>Plasmodium</i> parasites using the web-based CoGe platform
9:15am	Elen Oneal, Duke University Isolating parent-of-origin effects causing hybrid inviability in <i>Mimulus</i>	Anna Ullastres, Institute Of Evolutionary Biology (CSIC-Universitat Pompeu Fabra) Elucidating the mechanisms driving immune response in <i>Drosophila</i> through the analyses of transposable element-induced mutations	Alejandro Manzano Marin, INRA, UMR1062 (INRA, CIRAD, IRD, Montpellier SupAgro) - Centre de Biologie pour la Gestion des Populations (CBGP) Joining the team: Co-obligate symbionts of aphids evolving from distantly related bacteria	Jaime Huerta-Cepas, EMBL Heidelberg Reproducible reconstruction, analysis and visualization of phylogenomic data using ETE
9:30am	Louis-Marie Bobay, The University of Texas at Austin Biological species are universal across Life's domains	Philip Kleinart, Max-Planck-Institut Phenotypic adaptation by positive selection on long-term balanced alleles	Tamara Hasekorn, Department of Biology, University of Central Arkansas The symbiotic potential of Paraburkholderia bacteria in the social amoeba <i>Dictyostelium discoideum</i>	Laurence Loewe, University of Wisconsin-Madison Why versioning is crucial for evolutionary systems biology
9:45am	Mikkel Heide Schierup, Aarhus University Human X and Y chromosome co-evolution, ampliconic gene evolution, selective sweeps and speciation	Isabel Alves, Ontario Institute for Cancer Research The role of individual transcriptomes in the expression of potentially harmful variation	Eva Novokova, University Of South Bohemia Symbiosis in the Triatominae subfamily: dynamics, specificity and evolutionary (in)stability of the kissing bug microbiomes	Alex Smith, University of Michigan Infectious disease dynamics inferred from genetic data via sequential Monte Carlo

	Genomic mechanisms of speciation Session 2 <i>Jeffrey Good, Elen Oneal</i>	Mechanisms of phenotypic evolution Session 2 <i>Raquel Assis, Melissa Wilson Sayres</i>	Host-parasite coevolution <i>Daniel Bolnick, Jesse Weber, Natalie Steinel</i>	Evolutionary genomics of domestication <i>Jae Young Choi, Zoé Joly-Lopez</i>
11:30am	Yaniv Brandvain, University of Minnesota - Twin Cities How imprinted and imprinting incompatibilities impact introgression	Alejandro Couce, French Institute of Health and Medical Research (INSERM) Probing the determinants of fitness effects using transposon insertion sequencing in bacteria	Peter Fields, University of Basel Empirical examination of the genomic signatures of host-parasite coevolution in the diversity panel of <i>Daphnia magna</i>	Adam Boyko, Cornell University Y-chromosome haplotype diversity in a global sample of free-ranging and companion dogs
11:45am	Colin Meiklejohn, University of Nebraska-Lincoln Dissecting the special role of sex chromosomes in <i>Drosophila</i> speciation: genetic mapping of hybrid male sterility genes	Christopher Martin, University of North Carolina at Chapel Hill From candidate variants to fitness landscapes: investigating the rare origins of novel trophic specialists during adaptive radiation		
12:00pm	Alejandro Burga, University of California, Los Angeles A wolf in sheep's clothing: how a killer selfish element was disguised as a developmental gene in <i>C. elegans</i> .	Xueyuan Jiang, Pennsylvania State University Natural selection drives rapid neofunctionalization of <i>Drosophila</i> duplicate genes	Andrea Graham, Princeton University Worlds within worlds: Scaling from molecules to populations in co-evolutionary dynamics	Brandon Gaut, University of California, Irvine Annuals, perennials and the cost of domestication
12:15pm	William Murphy, Texas A&M University Insights into the epigenetic basis of the Large X-Effect from studies in cat interspecific hybrids.	Meng Lin, Stony Brook University Rapid evolution of lighter skin pigmentation in Southern Africa		
12:30pm	Xu Wang, Cornell University The origin and evolution of genomic imprinting in the placenta of therian mammals from marsupial-eutherian comparative genomic analyses	Laura Hayward, Columbia university Selection on polygenic traits	Lei Yang, The Pennsylvania State University Extensive recombination during colonization of cervid endogenous gammaretrovirus and implications to host genome evolution	Miguel Andrés Vallebuena Estrada, Cinvestav, The Center for Research and Advanced Studies of the National Polytechnic Institute The earliest maize from Tehuacan Mexico: paleogenomic evidence of gradual domestication in a 5,300 year old crop.
12:45pm	Andrius Jonas Dagilis, The University of Texas at Austin The Spectrum of Epistasis and its Consequences for Hybrid Fitness and Speciation	Fan Han, Uppsala University Gene flow, ancient polymorphism and ecological adaptation shape the genomic landscape of divergence among Darwin's finches	Edward Schrom, Princeton University Network architecture is a fundamental constraint on optimal immunity during coevolution with a signal-disrupting parasite	Amanda Pendleton, University Of Michigan Selective sweep analysis using village dogs highlights the pivotal role of the neural crest in dog domestication
1:00pm	Vrinda Venu, FML, Max Planck Society, Tuebingen The molecular genetic basis of recombination variation in adaptively diverging stickleback fish	Aida Andres, Max Planck Institute for Evolutionary Anthropology Local adaptation of a human cold receptor along a latitudinal cline	Alexander Mikheyev, Okinawa Institute of Science and Technology Using historical collections to understand the evolutionary response of bees to an emergent parasite	Srilakshmi Raj, Cornell University Adaptation to nine thousand years of diet in Asia
1:15pm	Jeffrey Good, University Of Montana Genomic Imprinting and Speciation in Mammals	Rebecca Young, The University of Texas at Austin Transcriptomic architecture influences phenotypic diversification across vertebrates	Helen Piontkivska, Kent State University Molecular evolution of the Zika virus (ZIKV; Flaviviridae): role of RNA editing	Maud Tenaillon, Centre National de la Recherche Scientifique, France Evolutionary genomics of European maize and its American counterparts