

3rd July 2016

SMBE Council Meeting

9:00am - 2:00pm Room 1

Registration

2:00pm - 5:30pm Foyer

Masatoshi Nei Lecture - George Zhang

5:00pm - 6:00pm Arena 1B

5:00 PM **Jianzhi Zhang**

Testing the neutral hypothesis of phenotypic evolution *abs# 1*

Welcome Reception

6:00pm - 7:30pm Hall 1

4th July 2016

Registration

8:00am - 5:00pm Foyer

Extracting Evolutionary Patterns and Processes from Genomic Data

8:30am - 10:30am Arena 1B

Chairs: Lars Jermiin & Arndt von Haeseler

8:30 AM **Bastien Boussau**

Branch-heterogeneous models of sequence evolution *abs# 2*

9:00 AM **Rob Lanfear**

Methods to find similar sites in alignments *abs# 3*

9:30 AM **Omar Rota-Stabelli**

Among genes heterogeneity of the phylogenetic signal in genome data: causes, symptoms, and treatments *abs# 4*

9:45 AM **Daisy Shepherd**

Assessing Methods for Outlier Detection in Phylogenetic Inference *abs# 5*

10:00 AM **Zhengting Zou**

Morphological and molecular convergences in phylogenetic inference *abs# 6*

10:15 AM **David J Balding**

Decay of Accuracy of Genomic Prediction with Genetic Distance *abs# 227*

Developmental and cellular genetics

8:30am - 10:30am Room 5

Chair: Philip Batterham

8:30 AM **Christen Mirth**

Coordinating robust with plastic developmental responses in the developing fly wing
abs# 8

8:45 AM **Dong Yang**

The role of complex and young genes in the formation of organismal complexity during embryonic development *abs# 9*

9:00 AM **Josh Alpern**

Transcriptomics of developmental evolution following long term selection *abs# 10*

9:15 AM **Jaroslav Krzywinski**

The transcriptional and developmental landscape of male and female mosquitoes
abs# 11

9:30 AM **Coral G Warr**

Natural variation in expression and function at a *Drosophila melanogaster* odorant receptor locus alters olfactory responses *abs# 12*

9:45 AM **Michael Hammond**

Title: The molecular language of peptide communication in the marine sponge
abs# 13

10:00 AM **Lydia Bright**

Early stages of diversification in the Rab GTPase gene family revealed by genomic and functional studies in *Paramecium* species *abs# 14*

10:15 AM **Maja Adamska**

Transcriptional activation of Wnt and Tgfb signaling pathways in regeneration of sponges *abs# 15*

Mitochondria in the age of genomics: genome architecture, inheritance, and functions

8:30am - 10:30am Room 6

Chair: Marco Passamonti

8:30 AM **Dennis V. Lavrov**

Animal mtDNA as we don't know it: unusual mt-genomes in non-bilaterian lineages
abs# 16

9:00 AM **Andrew Pomiankowski**

Mitochondrial variation and the evolution of the germline *abs# 17*

9:30 AM **Ricardo J Pereira**

Mito-nuclear incompatibilities at early stages of species formation *abs# 18*

9:45 AM **Fabrizio Ghiselli**

The Doubly Uniparental Inheritance of Mitochondria: a useful model for mitochondrial biology and evolution. *abs# 19*

10:00 AM **Logan W. Cole**

Unexpectedly high and variable tempo of plastid DNA integration in mitochondrial genomes of angiosperms *abs# 20*

10:15 AM **Paul Sunnucks**

A mitonuclear 'supergene' explains mitonuclear discordance and nuclear gene flow between two climate-associated forms of a bird species *abs# 21*

Beyond Selective Sweeps

8:30am - 10:30am Room 7

Chair: Kelley Harris

8:30 AM **Patricia J Wittkopp**

Evolution of gene expression: from mutation to polymorphism to divergence *abs# 22*

9:00 AM **Jonathan Pritchard**

Detection of human adaptation during the past 2,000 years *abs# 23*

9:30 AM **Gavin Sherlock**

Yeast populations adapt at different rates, with a different DFE under different nutrient limitations *abs# 24*

9:45 AM **Federica Pierini**

Functional characterization of evolutionarily advantageous sequence divergence between MHC alleles *abs# 25*

10:00 AM **Katherine S Xue**

Cooperation between distinct viral variants promotes growth of H3N2 influenza in cell culture *abs# 26*

10:15 AM **Josep Comeron**

Causes and consequences of recombination rate variation across the *Drosophila melanogaster* genome *abs# 27*

Morning Tea

10:30am - 11:00am Hall 1

Plenary - Kathy Belov

11:00am - 12:00pm Arena 1B

Chair: Rebecca Johnson

11:00 AM **Katherine Belov**

Saving the Tasmanian devil from extinction *abs# 28*

Lunch

12:00pm - 1:30pm Hall 1

Workshop: BEAST

12:00pm - 1:00pm Room 5

GSA Executive Meeting

12:00pm - 1:00pm Organisers office

Extracting Evolutionary Patterns and Processes from Genomic Data

1:30pm - 3:30pm Arena 1B

Chairs: Lars Jermiin & Arndt von Haeseler

1:30 PM **Michael Hendy**

Disentangling Kimura's 3-parameter model of nucleotide evolution. *abs# 29*

1:45 PM **Stephen M Crotty**

GST: A mixture model for phylogenetic inference of heterogeneously evolved sequence data *abs# 30*

2:00 PM **Annika Lamb**

Incipient speciation of the grey shrike-thrush, *Colluricincla harmonica*, revealed by multi-locus phylogeography *abs# 31*

2:15 PM **Naoko Takezaki**

Resolving the Phylogenetic Position of Coelacanth: The Closest Relative Is Not Always the Most Appropriate Outgroup *abs# 32*

2:30 PM **Heather Bracken-Grissom**

The evolution of bioluminescence and light detection in deep-sea decapods *abs# 33*

2:45 PM **Mathieu Fourment**

The Impact of Migratory Flyways on the Spread of Avian Influenza Virus in North America *abs# 34*

3:00 PM **Hua Chen**

Demographic Inference Using the Large Sample Joint Frequency Spectrum *abs# 35*

3:15 PM **Kelley Harris**

Temporary pulses of accelerated mutagenesis in human and great ape population history *abs# 36*

Gene regulation and epigenetics

1:30pm - 3:30pm Room 5

Chair: Emily Remnant

1:30 PM **Berrit Kiehl**

Sperm-mediated epigenetic effects in Zebrafish (*Danio rerio*) *abs# 37*

1:45 PM **Megan Wilson**

Establishing bipotentiality for gonadal differentiation. *abs# 38*

2:00 PM **Paul D Waters**

DNA methylation and sex chromosome dosage compensation *abs# 39*

2:15 PM **Timothy A Hore**

Epigenetic memory in vertebrates *abs# 40*

2:30 PM **Erica V Todd**

Whole-transcriptome profiling in a model sex-changing fish identifies genes that maintain flexible sexual phenotypes. *abs# 41*

2:45 PM **Ja-Rang Lee**

Aging-associated DNA methylation changes through long term follow-up in African green monkey *abs# 42*

3:00 PM **Bridget Martinez**

Deiodinase type 3 methylation increases in response to thyroid stimulating hormone in a fasting adapted mammal *abs# 43*

3:15 PM **David Gokhman**

The regulatory evolution of the human vocal tract *abs# 44*

Molecular evolution of avian species

1:30pm - 3:30pm Room 6

Chair: Lee Rollins

1:30 PM **David W Burt**

Avian genome evolution and the origins of species diversity *abs# 45*

2:00 PM **Christopher Balakrishnan**

Speciation and domestication in the zebra finch, an avian model system for evolutionary genomics *abs# 46*

2:30 PM **Yuanyuan Cheng**

Evolution of antimicrobial peptides in birds *abs# 47*

2:45 PM **Takeshi Kawakami**

Localisation of recombination hotspots at gene promoters and retrotransposons in avian genomes *abs# 48*

3:00 PM **Nicolas Dussex**

Genomic basis of tool manufacture and use in New Caledonian crows *abs# 49*

3:15 PM **Kees van Oers**

Avian ecological epigenetics: the role of DNA methylation in the evolution of avian personality *abs# 50*

Causes and consequences of nonrandom mating

1:30pm - 3:30pm Room 7

Chairs: Amy Goldberg & Chris Gignoux

Output Session Sponsor Type

1:30 PM **Elsa G Guillot**

Modeling the biological cost of cousin alliance on human population genetics *abs# 51*

2:00 PM **Daniel Matute**

The genetic basis of female choice in *Drosophila* *abs# 52*

2:30 PM **Marleen Cobben**

Evolving mutation rate advances invasion speed of sexual species *abs# 53*

2:45 PM **Mathieu Joron**

Disassortative mating maintains inversion polymorphism and changes the rules of speciation in a mimetic butterfly *abs# 54*

3:00 PM **Nina Marchi**

Inbreeding avoidance and dispersal behaviours in humans from Inner Asia *abs# 55*

3:15 PM **Marcy K Uyenoyama**

Evolution of effective population size and sex ratio under inbreeding *abs# 56*

Afternoon Tea

3:30pm - 4:00pm Hall 1

Extracting Evolutionary Patterns and Processes from Genomic Data

4:00pm - 6:00pm Arena 1B

Chairs: Lars Jermiin & Arndt von Haeseler

4:00 PM **Severine Vuilleumier**

Evolution through successive population isolation and reconnection events: process and signature *abs# 57*

4:15 PM **Yoichiro Nakatani**

Probabilistic macrosynteny model for inferring the structure of ancient pre-WGD genomes *abs# 58*

4:30 PM **Benjamin D Kaehler**

Standard Codon Substitution Models Overestimate Purifying Selection for Non-Stationary Data *abs# 59*

4:45 PM **Aarti Venkat**

Multiple nucleotide mutations cause rampant false positive inferences of selection on the human lineage *abs# 60*

5:00 PM **Claudia C Weber**

Assessing structural awareness in models of protein evolution *abs# 61*

5:15 PM **Greg Slodkowicz**

Patterns of adaptive evolution: a structural perspective *abs# 62*

5:30 PM **Rachel Agolia**

Disentangling Sources of Selection on Exonic Transcriptional Enhancers *abs# 63*

5:45 PM **Emily R Ebel**

Malaria parasites drive adaptation in mammalian genomes *abs# 64*

Gene regulation and epigenetics

4:00pm - 5:00pm Room 5

Chair: Emily Remnant

4:00 PM **Vincent Castric**

Evolution of dominance/recessivity interactions between self-incompatibility alleles in Arabidopsis. *abs# 65*

4:15 PM **Olin Silander**

Evolutionary changes in the regulatory behaviour of the lac operon *abs# 66*

4:30 PM **Guy Barry**

Mechanisms underpinning the rapid functional evolution of the human brain *abs# 67*

4:45 PM **D. Allan Drummond**

Evolutionary constraints reveal stress-triggered gene regulation by poly(A)-binding protein *abs# 68*

Medical and human genetics

5:00pm - 6:00pm Room 5

Chair: Jeremy Brownlie

5:00 PM **Daniel M Jordan**

Recessive selection in complex disease and implications for variant discovery
abs# 69

5:15 PM **Emily Wong**

Genomic signatures of soft selective sweeps at human complex traits *abs# 70*

5:30 PM **Reed A Cartwright**

Molecular Evolution of Human Breasts *abs# 71*

5:45 PM **Bianca Haase**

A dominant TRPV4 variant underlies osteochondrodysplasia in Scottish fold cats
abs# 72

The Molecular Evolution of Venom

4:00pm - 6:00pm Room 6

Chair: Yehu Moran

4:00 PM **Baldomero Olivera**

The Evolution of Venoms: Lessons from Cone Snails *abs# 73*

4:30 PM **Michael K Richardson**

Evolution and Development of Venom in Snakes *abs# 74*

5:00 PM **Kartik Sunagar**

The rise and fall of an evolutionary innovation *abs# 75*

5:15 PM **Michela L. Mitchell**

Toxin composition in the tentacles of the Australian cold temperate sea anemone,
Oulactis sp. *abs# 76*

5:30 PM **Eivind Undheim**

When sex matters: Dramatic sexual dimorphism in the venom and venom system of
the centipede *Scolopendra hardwickei* *abs# 77*

5:45 PM **Giulia Zancolli**

Going with the flow? The genetic basis for snake venom evolution *abs# 78*

Sexual selection on the gamete level: the evolution of egg-sperm interactions

4:00pm - 6:00pm Room 7

Chair: Christina Zakas

4:00 PM **Leonie C Moyle**

Green eggs and sperm: gamete chemoattraction and sexual isolation in wild
Solanum species *abs# 79*

4:30 PM **Asher D Cutter**

The evolution of sperm size and post-mating pre-zygotic reproductive isolation
abs# 80

5:00 PM **Damien B Wilburn**

A "sexy" co-evolutionary arms race: insights from structural and biochemical studies
of egg-sperm interactions in Pacific abalone *abs# 81*

5:15 PM **Neil Gemmell**

Sexual selection for genetic compatibility: new insights into the genetic basis of
cryptic female choice in Chinook salmon *abs# 82*

5:30 PM **Daryn A Stover**

The case for selection at coevolving human gamete-recognition genes (*ZP2*, *ZP3*, and *C4BPA*) *abs# 83*

5:45 PM **Emily E Killingbeck**

"Fishing" for vertebrate fertilization genes: proteomic and biochemical characterization of rapidly evolving threespine stickleback egg proteins *abs# 84*

Poster session A + Refreshments

6:00pm - 8:00pm Hall 1

Output Session Sponsor Type

Mateja Hajdinjak

Genetic analyses of five late Neandertal individuals *abs# 300*

Thiseas Christos Lamnidis

Insights into South American population history, from ancient DNA from Tierra del Fuego. *abs# 301*

Hiroki OOTA

The preliminary report for the deep sequencing of the prehistoric Jomon genome from the Japanese archipelago *abs# 302*

Luca Pagani

Genome-wide allele frequency estimates from population level ultra-low coverage aDNA samples. *abs# 303*

Zoe Patterson Ross

Uncovering long-term evolutionary dynamics of hepatitis B virus using ancient DNA *abs# 304*

Alexander Peltzer

EAGER: Efficient Ancient Genome Reconstruction *abs# 305*

Cosimo Posth

The mitochondrial genome of an archaic hominin from southwestern Germany *abs# 306*

Fernando Racimo

Signatures of archaic adaptive introgression in present-day human populations *abs# 307*

Michael S Rosenberg

FINGERPRINT: Computational filtering of targeted sequences from environmental contaminants *abs# 308*

Sriram Sankararaman

The combined landscape of Neanderthal and Denisovan ancestry in present-day humans *abs# 309*

Veronika Siska

The Neolithic in Northeast Asia in light of a 7,700 year-old genome *abs# 310*

Emma M Svensson

Signs of mobility and migration in the megalithic graves of Western Sweden? *abs# 311*

Ray Tobler

The Aboriginal Heritage Project: Reconstructing the Genetic History of Aboriginal Australia with Ancient DNA *abs# 312*

Aida M Andres

Positive selection on balanced standing variation *abs# 313*

Jack Da Silva

Hill-Robertson Interference Maintained by Red Queen Dynamics Favours the Evolution of Sex *abs# 314*

Josephine Daub

Detection of pathways affected by positive selection in primate lineages ancestral to humans *abs# 315*

Angeles de Cara

The impact of genetic architecture, demography and genetic load in natural selection inferences *abs# 316*

Yuseob Kim

Temporal clustering of allele frequency trajectories in asexual population under neutral equilibrium versus positive selection *abs# 317*

Xuebin Qi

Sherpas share genetic variations with Tibetans for high-altitude adaptation *abs# 318*

Charles Robin

Genome wide association studies with insecticide resistance lead us to selective sweep loci and beyond. *abs# 319*

Thi Ha My Vy

Analyzing the “snapshots” of directional selection spreading over space from incomplete selective sweeps in African *Drosophila melanogaster* *abs# 320*

Kyria Roessler

The evolution of genomic content over generations of inbreeding maize lines *abs# 321*

Chow Lih Yew

Loss of self-incompatibility in the allotetraploid *Arabidopsis kamchatica* by degradation of the male component *abs# 322*

Samuel Elley

An experimental test of the emergence of Cellular Complexity by Constructive Neutral Evolution *abs# 323*

Alicia Lai

Emergence of RNA editing in an evolution experiment *abs# 324*

Shaun Lehmann

New insight into human evolution from character compatibility analysis of the mitochondrial genomes of three primate taxa *abs# 325*

David Penny

The Origin of Life; solvable problems. *abs# 326*

Alannah Rickerby

Experimental evidence that translation initiation in bacteria was invaded by a selfish genetic element. *abs# 327*

Nellie Sibaeva

Exploring the origin of DNA through synthetic biology: is ribonucleotide reduction essential for deoxyribonucleotide synthesis *in vivo*? *abs# 328*

Michael Woodhams

Time-reversible vs. Lie-Markov phylogenetic models in the presence of inhomogeneous substitution processes. *abs# 329*

Bojian Zhong

Chloroplast Phylogenomic Inference of Green Algae Relationships *abs# 330*

Marcin Adamski

Developmental Genomics of Sponges *abs# 331*

Nagayasu Nakanishi

Investigating neuropeptide function during cnidarian development *abs# 332*

Kanokwan Srirattana

The generation of somatic cell nuclear transfer embryos with different oocyte mtDNA haplotypes *abs# 333*

Brandon D Velie

Identification of the locus responsible for polydactyly in horses using whole-genome re-sequencing *abs# 334*

Qais Abdullah Suliman AlRawahi

Investigating the genetic diversity of the Arabian Oryx from Oman *abs# 335*

Vanessa Arranz Martinez

Connectivity among New Zealand coastal marine communities *abs# 336*

Tina Berry

Planktonic Relationships of Rottneest Island – A 5-year metabarcoding survey *abs# 337*

Amanda Y Chong

Sequence capture arrays for studying immunogenetic variation in non-model species *abs# 338*

Laurence J Clarke

Marker choice for zooplankton DNA metabarcoding studies *abs# 339*

Megan Coghlan

Archaeological forensics: estimating the provenance of ivory from two 17th and 18th century shipwrecks. *abs# 340*

Bruce E Deagle

Counting with DNA: can species proportional biomass be estimated using high-throughput amplicon sequencing? *abs# 341*

Kyle M Ewart

Clarifying the phylogeny and phylogeography of two commonly traded cockatoo species and the development of a wildlife forensic toolbox to identify illegal trade in these species *abs# 342*

Elise Furlan

Species detection at extremely low densities: the role of environmental DNA surveys *abs# 343*

Bertrand B Gauffre

Impact of dams on neutral and adaptive genetic diversity in an Australian freshwater fish *abs# 344*

Bernd Gruber

Optimising the sampling design of landscape genetic analyses using resistance surfaces *abs# 345*

Jessica F Gurr

Exploiting conserved genomic elements to create a universal amplicon resource for use in amniote species with no genome assembly *abs# 346*

Takeshi Igawa

Comparative transcriptome analyses of eight endangered amphibians in Ryukyu Archipelago: expression patterns and repertoire of immunity related genes *abs# 347*

Elzbieta Iwaszkiewicz

Patterns of gene expression of natural hybrids and parental species of *Cottus* in different seasons *abs# 348*

Elizabeth A James

Approaches to restoration of *Phragmites australis* in the salinizing wetlands of the Gippsland Lakes, southeastern Australia *abs# 349*

Gert-Jan Jeunen

Maximizing environmental DNA capture and extraction in the marine environment. *abs# 350*

Michael Knapp

Soaring on the wings of giants - rapid evolution of island gigantism in extinct New Zealand birds of prey *abs# 351*

Torsten Nygaard TNK Kristensen

The N_e to N ratio is dependent on census population size *abs# 352*

Jennifer M Lamb Alport

Population genetics and relatedness of Afro-Malagasy *Otomops* (Chiroptera: Molossidae) at lineage and colony level *abs# 353*

Quintin Lau

Selection acting on major histocompatibility complex class I genes in Japanese Ranidae frogs *abs# 354*

Jing-Yi Lu

Gene duplication and relax from selective constraints of *Gcyc* genes create high flower diversity in Didymocarpoideae (Gesneriaceae) *abs# 355*

Caitlin Morrison

Phylogeny and innate immune gene diversity within the Australian parrot genus *Neophema* *abs# 356*

Dáithí Conall Murray

Molecular Archaeology: Recycling the rubbish *abs# 357*

Ann-Marie Oppold

Support for the evolutionary speed hypothesis from intraspecific population genetic data in the non-biting midge *Chironomus riparius* *abs# 358*

Genevieve A. C. Phillips

Multiple genetic mechanisms contribute to visual sensitivity variation in the Labridae *abs# 359*

Florian Pichlmüller

Replicated island invasions of an invasive species (*Rattus rattus*). *abs# 360*

Kimberly Pinch

Naive predators and toxic prey: A population genetic analysis of yellow-spotted goannas (*Varanus panoptes*) across Australia *abs# 361*

Peter J Prentis

Comparative analysis of the thermal stress response in two intertidal *Neritid* snails *abs# 362*

Yoshimoto Saito

Comprehensive evolutionary study of Bacteriorhodopsin using prokaryotic genomes and metagenomes *abs# 363*

Yoshimoto Saito

Evolutionary study of bacteriorhodopsin using genomes and metagenomics *abs# 364*

Daniel J Schmidt

Population genetics/genomics of the Australian lungfish (*Neoceratodus forsteri*). *abs# 365*

Sonal Singhal

Museum occurrence data predicts genetic diversity in a species-rich clade of desert lizards *abs# 366*

Michael Stat

Towards marine ecosystem based management through metabarcoding eDNA *abs# 367*

Megan A Supple

Is there genomic support for assisted migration of *Eucalyptus marginata* provenances? *abs# 368*

Jamie Tedeschi

Sea turtle embryos may be able to adapt to climate change through molecular responses to thermal stress *abs# 369*

Jessica E Thomas

An aukward story of evolution and extinction - the disappearance of the Great Auk *abs# 370*

Beata Ujvari

The role of immunoglobulins in the Tasmanian Devil Facial Tumour Disease *abs# 371*

Petra Villette

Metabarcoding of Bacterial Pathogens in a Rodent Pest: Which Organ? *abs# 372*

Lu Wang

The geographical distribution of grey wolves in China *abs# 373*

Nicole E White

Black-cockatoos and molecular ecology approaches for conservation *abs# 374*

Ticao Zhang

Transcriptome sequencing of *Crucihimalaya himalaica* (Brassicaceae) reveals how *Arabidopsis* close relative adapt to the Qinghai-Tibet Plateau *abs# 375*

Michael Ørsted

The genetic architecture of cold tolerance plasticity in the *Drosophila Genetic Reference Panel* *abs# 376*

Nicole T Perna

DNA Sequence Evolution Simulation and Phylogenetic Reconstruction Using Pen and Paper *abs# 377*

Von Bing Yap

Re-imagining the Hardy-Weinberg Law *abs# 378*

Marta Barluenga

Molecular characterization of MHC class IIB genes of sympatric Neotropical cichlids in crater lakes of Nicaragua *abs# 379*

Cemalettin Bekpen

Birth of a new gene: the problem of self-tolerance versus autoimmune reaction *abs# 380*

Jason Bragg

A phylogenomic study of speciation dynamics in a large radiation of Australian skinks *abs# 381*

Karen L Carleton

Gene regulatory networks underlying the diversity of cichlid fish vision *abs# 382*

Renee Catullo

Compositionally heterogeneous codon evolution, concatenation, and cytonuclear discordance significantly alter phylogenetic reconstructions in rapidly diversifying *Drosophila* *abs# 383*

Felipe de Mello Martins

population differentiation, adaptability and heritability in the common sunskink *Lampropholis coggeri* *abs# 384*

Paolo Franchini

The role of microRNAs in the repeated parallel diversification of lineages of Midas cichlid fish from Nicaragua *abs# 385*

Leon Hilgers

The genetic basis of an adaptive key trait – radula genes in the radiation of *Tylomelania* *abs# 386*

Milan Malinsky

Whole genome sequencing studies of speciation and selection in the Lake Malawi cichlid radiation *abs# 387*

Simon H Martin

Species boundaries among *Heliconius* butterflies reflect the genetic architecture of speciation *abs# 388*

Henry L North

Microgeographic adaptation drives the evolution of reproductive isolation in parapatry *abs# 389*

Fabrizia Ronco

Genomics, Morphology and Ecology of the Lake Tanganyika Cichlid radiation *abs# 390*

Philipp M. Schlüter

Speciation gene evolution and the origin of chemical mimicry in a sexually deceptive orchid *abs# 391*

Yosuke Seto

Comparative RNA-seq analysis of antifungal immune responses among *Drosophila* species *abs# 392*

Yohey Terai

Speciation with extensive gene flow in Lake Victoria cichlid species *abs# 393*

Alexandra A.-T. Weber

Genomics of adaptive divergence in East African cichlid fishes: a comparative approach *abs# 394*

Daniel J Balick

Dominance and selection coefficients inferred from large-scale population data identify candidate recessive genes *abs# 395*

fabia ursula battistuzzi

Profiles of low complexity regions in Apicomplexa *abs# 396*

Chris Ward

Assessing the fitness cost of Bt insecticidal toxin resistance over time. *abs# 397*

Jae Young Choi

Using evolutionary rate covariation to detect novel evolutionary patterns in the eudicot (Brassicaceae) and monocot (Poaceae) plant lineages *abs# 398*

Matthew J Christmas

Finding needles in a genomic haystack: targeted capture to identify signatures of selection in a non-model plant species *abs# 399*

Sabyasachi Das

Evolution of Tumor Necrosis Factor Superfamily (TNFSF) genes TNFSF 12 and 13: Phylogenetic clues for the emergence of *in genomic* fusion of *TNFSF12-TNFSF13* *abs# 400*

Aurélie Désamoré

Large scale phylogenetic patterns in waterbeetles *abs# 401*

James Fleming

Untying the Evolution of Vision Using the Gordian Worms *abs# 402*

Nikki E Freed

Combining Shigella Tn-seq data with Gold-standard E. coli Gene Deletion Data Suggests Rare Transitions between Essential and Non-essential Gene Functionality *abs# 403*

Cian Glenfield

Origins and conservation of mammalian BRAF pseudogenes. *abs# 404*

Jun Gojobori

Transient Receptor Potential Gene Family Evolution in two echinoderms, sea urchin and starfish *abs# 405*

Laura F Grice

Evolution of Animal Allorecognition: A Case Study in Sponges *abs# 406*

Jayla Harvey

Worldwide Genetic Variation in Serotonin Pathway Genes Associated with Bipolar Disorder *abs# 407*

Kate E Ihle

Transcriptional evidence for a reproduction_immunity trade-off in Japanese quail (*Coturnix japonica*) *abs# 408*

Jun Inoue

A genomewide survey of genes for muscle structural proteins that enabled the rise of chordates *abs# 409*

Kangchon Kim

Population genetic processes affecting the genomic pattern of sequence diversity in influenza virus H3N2 *abs# 410*

Akihiko Koga

Rapid replacement of centromeres by a variant-type repetitive DNA in a primate taxon *abs# 411*

Verena E. Kutschera

Demographic impact on genome-wide signatures of selection *abs# 412*

Yuping Li

Fitness pleiotropy and the phenotypic basis of adaptation in experimentally evolving yeast *abs# 413*

Zhen Li

Gene Duplicability of Core Genes Is Highly Consistent across All Angiosperms *abs# 414*

Yves Van de Peer

Tangled up in two: a burst of genome duplications at the end of the Cretaceous and the consequences for plant evolution *abs# 415*

Jinn-Jy Lin

Rises and falls of opsin genes in 46 fish genomes and their implications for environmental adaptation *abs# 416*

Anders E Lind

Single cell and metagenomics help understand early stage archaeal endosymbionts *abs# 417*

Jesus Lozano-Fernandez

A molecular palaeobiological approach of arthropod terrestrialisation *abs# 418*

Xuemei Lu

Diversity in gene expression in cell populations in relation to the selectionism view of tumor evolution *abs# 419*

Adam J Orr

Phylogenies derived from somatic mutations agree with physical topologies in *Eucalyptus* *abs# 420*

Hardip R Patel

Evolution of olfactory receptor gene family in vertebrates *abs# 421*

Mateus Patricio

TreeFam and Ensembl: Phylogenetic resources *abs# 422*

Davide Pisani

Sponges, not the comb jellies, are the sister group of all the other animals: further evidence from the analyses of compositional biases *abs# 423*

Sally Potter

Chromosomal speciation in rock-wallabies: linking population processes to evolutionary processes across the phylogeny *abs# 424*

Rahul Rane

Lineage specific expansions in detoxification-related and transporter gene families and sub-classes are strongly associated with polyphagy in herbivorous insects *abs# 425*

Vyodianathan Ravi

Phylogenetic relationships of the three major teleost lineages *abs# 426*

Alan M Rice

Patterns of gene duplication and loss in the mammalian lineage mirror association with pathogenic CNVs in human *abs# 427*

Jack Scanlan

Building an evolutionary framework for the functional characterisation of an arthropod-specific gene family *abs# 428*

Shawn Rupp

Characterizing Sex-Biased Gene Expression in the Green Anole *abs# 429*

Mrudula Sane

Experimental Analysis of GC Content Evolution in Bacteria *abs# 430*

Andrew Storfer

Rapid evolutionary response to Tasmanian devil facial tumor disease *abs# 431*

Yanbo Sun

Whole-genome sequence of the Tibetan frog *Nanorana parkeri* and the comparative evolution of tetrapod genomes *abs# 432*

Setareh Tasdighian

The impact of dosage sensitive gene families on plant evolution *abs# 433*

Jakob Triebel

The number of prolactin cleavage sites generating vasoinhibins varies in primates *abs# 434*

Aleksia Vaattovaara

Evolution of the CRKs and other DUF26-containing gene families in plants *abs# 435*

Kai Wang

Genome-wide analysis of bitter taste receptor genes in birds and the genomic basis of adaptation to a microclimate contrast in the spiny mouse *abs# 436*

Megan J Wilson

Evolutionally conserved mechanisms of regeneration in chordates: Uncovering signaling pathways required for WBR in *Botrylloides leachi*. *abs# 437*

Marie Lisandra Zepeda Mendoza

Hologenomic adaptations underlying the evolution of sanguivory in the vampire bat *abs# 438*

Agustin L. Arce

Epigenetic variation in interspecific hybrids of the genus *Arabidopsis*. *abs# 439*

Wenqing Cao

The evolutionary optimization of polyadenylation by 3' UTR *abs# 440*

Michael Charleston

Alignment of biological networks *abs# 441*

Siyu Chen

The role of synonymous codon usage in regulating mRNA level explains the well-known correlation between them in genomes *abs# 442*

Se-Hee Choe

Identification and Characterization of *TYR* gene in Cynomolgus Monkey (*Macaca fascicularis*) *abs# 443*

Xiao Chu

The sequence determinants of translational readthrough constrains the evolution of 3' UTR *abs# 444*

Alex de Mendoza

Early evolution and dynamics of DNA methylation in animals *abs# 445*

Irene Gallego Romero

Patterns of chromatin accessibility and transcription factor binding in human and chimpanzee pluripotent stem cells. *abs# 446*

Emily C Glassberg

Estimating the distribution of effect sizes of variants affecting human gene expression *abs# 447*

David Gresham

Adaptive Rewiring of a Gene Regulatory Network *abs# 448*

Qing Huan

Translational regulation constrains the evolution of coding sequences after the start codon in *Saccharomyces cerevisiae* *abs# 449*

Jae-Won Huh

Genome-wide expression profiling analysis identifies aging-associated gene expression change *abs# 450*

Katia Jindrich

Functional diversity of bZIP transcription factors in the sponge *Amphimedon queenslandica*: insights into the

ancestral animal regulatory genome *abs# 451*

Zoé Joly-Lopez

Developing maps of fitness consequences for plant genomes *abs# 452*

Izabela Makalowska

Instability of 5' overlaps between protein-coding genes *abs# 453*

Jeremy RB Newman

Sequence uniqueness determines the accuracy of isoform resolvability from short read RNA-seq data
abs# 454

Andrea Polanowski

Epigenetic age estimation of humpback whale populations *abs# 455*

Wenfeng Qian

Regulation of mRNA level by codon usage bias *abs# 456*

Shrutii Sarda

High-Throughput Identification of *Cis*-Regulatory Rewiring Events in Yeast *abs# 457*

mengyi sun

Adaptive RNA editing in squid and octopus *abs# 458*

Andrew H.Y. Wang

Creating a New Code: Constructing a Synthetic Epigenetic Memory System in Mammalian Cells *abs# 459*

Alex Capraro

Waking the sleeping dragon - molecular insights into the hibernation of the central bearded dragon *abs# 460*

William B Horspool

Evidence for post-transcriptional regulation of dosage compensation in platypus *abs# 461*

Kim L McIntyre

Unravelling marsupial X inactivation with shRNA knockdowns *abs# 462*

Shaohuan Wu

Genomic evidence for elevated translational efficiency through mRNA looping *abs# 463*

Luohao Xu

Partial Translational Gene Regulation in Chicken revealed by Quantitative Mass Spectrometry *abs# 464*

Daqi Yu

Underrepresentation of active histone modification marks in evolutionarily young genes *abs# 465*

Nami Arakawa

Comparative Study of Skin Gene Expression Patterns between Humans and Apes *abs# 466*

Maxime Chantreau

Emergence of functional novelties in a molecular lock-and-key system: allelic diversification at the self-incompatibility locus in Arabidopsis. *abs# 467*

Julie Collet

A genome-wide test of the modular structure of pleiotropy *abs# 468*

Fabio Cortesi

Seeing colour in the dark: Lessons learned from the evolution of vision in 100 fish species *abs# 469*

Federico Gaiti

Genomic innovations at the onset of animal multicellularity: insights from the sponge histone PTM landscape *abs# 470*

Alexandrea M Kranz

Light environment change induces differential expression of guppy *opsins* *abs# 471*

Carmel McDougall

Expansions of ependymin-related proteins in diverse invertebrate taxa and their co-option into novel functions *abs# 472*

Fanwei Meng

Brain of the Blind: Transcriptome evolution in the golden-line cavefish *abs# 473*

Zuzana Musilova

Color vision re-evolution in deep-sea fishes: multiple rhodopsin genes as adaptation to an extreme environment *abs# 474*

Chen Siang Ng

Genome-wide detection of morphotype-specific alternative splicing in chicken feather transcriptomes *abs# 475*

Juan Pascual-Anaya

Vertebrate Hox genes evolution: insights from the embryonic transcriptome of the hagfish *abs# 476*

Qing Sunny Shen

From Origination to Function: Life-course of Human-specific *De Novo* Protein *abs# 477*

Shunsuke Sogabe

Cell-type specific transcriptomes in the sponge *Amphimedon queenslandica* sheds light on the ancestral metazoan body plan *abs# 478*

Nicholas M Wade

Rapid expansion of pigmentation genes in Penaeid prawns with absolute conservation of gene function. *abs# 479*

Julia Weissenbach

Functional diversification of chaperonin paralogs in cyanobacteria with cell differentiation *abs# 480*

Portia Westall

Preliminary insights into selection in the platypus *abs# 481*

Camilla M Whittington

Live birth and the genetic basis of evolutionary innovation *abs# 482*

Melanie J Wilkinson

Parallel evolution of the auxin pathway in an Australian wildflower *abs# 483*

Christina Zakas

The genetic basis of evolutionary transitions in early development *abs# 484*

Jane R Allison

Re-categorising the protein structure universe *abs# 485*

Matt AB Baker

Domain-swap polymerization drives the self-assembly of the bacterial flagellar motor *abs# 486*

Diego A Hartasánchez

To convert or not to convert: homology requirements for meiotic gene conversion *abs# 487*

Thomas Shafee

Extreme convergent evolution in defensin proteins and quantitative maps of their sequence space *abs# 488*

Sara Stieb

How Nemo sees its colourful world: variability of visual pigment genes (opsins) in anemomefish (Amphiprioninae) *abs# 489*

Viviane Slon

Retrieval of ancient mammalian mitochondrial DNA from Middle and Late Pleistocene sediment *abs# 490*

Anne C Stone

The landscape of mitochondrial genetic diversity in chimpanzees from Gombe National Park and across the

genus *Pan* abs# 491

Sally Wasef

DNA capture of mitogenomes from Sacred Ibis Mummies of Ancient Egypt abs# 492

Lauren C White

Historical phylogeography of mainland and Tasmanian thylacines (*Thylacinus cynocephalus*) using ancient mitochondrial genomes abs# 493

5th July 2016

Registration

8:00am - 5:00pm Foyer

Medical and human genetics

8:30am - 10:30am Arena 1B

Chair: Emily Wong

8:30 AM **Bing Su**

Down-regulation of EPAS1 transcription explains genetic adaptation of Tibetans to high-altitude hypoxia abs# 85

8:45 AM **Casper-Emil T. Pedersen**

Extreme distribution of deleterious variation in a historically small and isolated population – insights from the Greenlandic Inuit abs# 86

9:00 AM **Christopher Gignoux**

The African roots of Mexico: Genetic structure and health of Mexicans of African descent abs# 87

9:15 AM **Trevor Martin**

Dynamic Genetic Control of Gene Expression and DNA Methylation in Human Aging abs# 88

9:30 AM **Yicheng ZHU**

Diagnostic sequence motifs distinguish all point mutations in humans abs# 89

9:45 AM **Julian R Homburger**

A novel approach for assessing genetic burden and constraint in protein structures leveraging large sequencing cohorts: insights from MYH7 and hypertrophic cardiomyopathy abs# 90

10:00 AM **David Gokhman**

Gene ORGANizer: Linking Genes to the Organs They Affect abs# 91

10:15 AM **Donate Weghorn**

Probabilistic inference of positive and negative selection in cancer abs# 92

David Penny and Mike Hendy Symposium

8:30am - 10:30am Room 5

Chair: Barbara Holland

8:30 AM **David Penny and Michael Hendy**

David Penny & Mike Hendy abs# 93

8:45 AM **Anthony Poole**

RNA evolution is dominated by rapid turnover, not molecular fossils. *abs# 94*

9:00 AM **Frederic Delsuc**

"The data are good but the models are bad!": examples from recent phylogenomic studies. *abs# 95*

9:15 AM **Michael Charleston**

Hadamard conjugation and phylogenetic inference. *abs# 96*

9:30 AM **Matthew J Phillips**

Geomolecular Dating and the Origin of Placental Mammals *abs# 97*

9:45 AM **Lindell Bromham**

From the genome to biodiversity: molecular evolutionary insights into macroevolution *abs# 98*

10:00 AM **Alan Cooper**

Synergistic roles of rapid warming events and human impacts in the megafaunal extinctions *abs# 99*

10:15 AM **David Bryant**

The problems with distance-based phylogenetic relationships *abs# 100*

The origin and early evolution of eukaryotes: new pieces of an enigmatic puzzle

8:30am - 10:30am Room 6

Chair: Thijs Ettema

8:30 AM **Thijs J.G. Ettema**

The archaeal ancestry of eukaryotes *abs# 101*

9:00 AM **Eugene V Koonin**

Natural history of eukaryotic viruses and transposons: What do they tell us about eukaryogenesis? *abs# 102*

9:30 AM **Chuan Ku**

Endosymbiotic origin and differential loss of eukaryotic genes *abs# 103*

9:45 AM **Sven B Gould**

Mitochondrial origin of eukaryotic membrane complexity *abs# 104*

10:00 AM **Philip J L Bell**

The early origin of the eukaryotic cell according to the Viral Eukaryogenesis hypothesis: an update in light of recent discoveries *abs# 105*

10:15 AM **Sandra L Baldauf**

Origin of the *Andalucia godoyi* mitochondrial *cox15* gene by horizontal transfer from bacteria *abs# 106*

Structural variation in the light of new sequencing technologies

8:30am - 10:30am Room 7

Chair: Hideki Innan

8:30 AM **Esther Betran**

Do retroCNVs resolve intralocus sexually antagonistic conflicts in *Drosophila*? *abs# 107*

9:00 AM **Stefan Dennenmoser**

Accumulation of structural mutations in an invasive fish of hybrid origin *abs# 108*

9:15 AM **Arbel Harpak**

Non-allelic gene conversion is ten times faster than the rate of point mutations in humans *abs# 109*

9:30 AM **Ellen M Leffler**

Characterizing complex structural variation at the human glycoporphin receptors for Plasmodium falciparum *abs# 110*

9:45 AM **Eric Smith**

Structural variation at the TEP anti-pathogen locus in African malaria mosquitoes
abs# 111

10:00 AM **Lukas FK Kuderna**

A second look at the chimpanzee genome *abs# 112*

Morning Tea

10:30am - 11:00am Hall 1

Plenary - Sally Dunwmoodie

11:00am - 12:00pm Arena 1B

Chair: Jeremy Brownlie

11:00 AM **Sally L Dunwoodie**

Identifying genetic and environmental factors causing developmental defects in humans and mice *abs# 114*

Lunch

12:00pm - 1:30pm Hall 1

Workshop: Writing for the Conversation

12:00pm - 1:00pm Room 5

GSA AGM Meeting

12:00pm - 1:00pm Room 6

SMBE Business Meeting

12:00pm - 1:00pm Room 7

Ecological and conservation genetics

1:30pm - 3:30pm Arena 1B

Chair: Lee Rollins

Output Session Sponsor Type

1:30 PM **Dianne Gleeson**

An environmental DNA (eDNA) based method for monitoring spawning activity: a case study using the endangered Macquarie perch (*Macquaria australasica*) *abs# 115*

1:45 PM **Anna J MacDonald**

From faeces to foxes: using genetics to manage an invasive predator for wildlife conservation *abs# 116*

2:00 PM **Justin O Borevitz**

Landscape Conservation Genomics: from invasive to foundation species *abs# 117*

2:15 PM **Lotte A van Boheemen**

Adaptive and neutral genomic diversity of the global invader *Ambrosia artemisiifolia* *abs# 118*

2:30 PM **Sarah Hendricks**

Source dynamics of the naturally re-established carnivore, *Canis lupus* *abs# 119*

2:45 PM **Emily J Remnant**

Discovery of new RNA viruses in healthy honeybee populations with *Varroa* infection *abs# 120*

3:00 PM **Helen R Taylor**

Seeds of destruction? The relationship between inbreeding and male fertility in two threatened bird species *abs# 121*

3:15 PM **Katherine A Farquharson**

Pedigree analysis reveals a generational decline in reproductive success of captive Tasmanian devil (*Sarcophilus harrisii*) *abs# 122*

Open Symposium

1:30pm - 3:30pm Room 5

Chair: Barbara Holland

1:30 PM **Sandra Oliveira**

Revisiting an old evolutionary question: did the S mutation of the β -globin gene result from a single or multiple mutations? *abs# 123*

1:45 PM **Simone Higgin**

Trans-domain horizontal gene transfer from bacterium to animal: the post-transfer evolution of the aspzincins in the sponge *Amphimedon queenslandica* *abs# 124*

2:00 PM **Manuel Irimia**

Tiny changes, big effects: the impact of microexons on neuronal differentiation, function and evolution *abs# 125*

2:15 PM **Amelia Lindsey**

Genome evolution of a parthenogenesis-inducing *Wolbachia* symbiont *abs# 126*

2:30 PM **Xinzhu Wei**

Patterns and mechanisms of diminishing returns of advantageous mutations *abs# 127*

2:45 PM **Xu Wang**

Divergent patterns of marsupial-eutherian genomic imprinting revealed from RNA-seq analysis in the opossum, *Monodelphis domestica* *abs# 128*

3:00 PM **Joanna L Kelley**

Transcriptional changes and the genomics basis of adaptation to an extreme environment *abs# 129*

3:15 PM **Sankar Subramanian**

Patterns of nucleotide changes in human populations *abs# 280*

Understudied, Undervalued, But Amazingly Interesting: Microbial Eukaryotic Genomic Evolution

1:30pm - 3:30pm Room 6

Chair: Xianfa Xie

1:30 PM **Jane Carlton**

Using genomics to study evolutionary biology of the trichomonads *abs# 130*

2:00 PM **Anna L Kretzschmar**

On the quest of elucidating polyketide synthases responsible for ciguatoxin production *abs# 131*

2:15 PM **Rajeev K. Azad**

Fragmented evolution of an extremophilic red alga: Massive influx of bacterial DNAs revealed by the segmental landscape of the *Galdieria sulphuraria* genome *abs# 132*

2:30 PM **Christian Woehle**

Evolution of the eukaryotic redox sensitive proteome via endosymbiosis *abs# 133*

2:45 PM **EmilyClare P Baker**

Genetics and evolution of early branching *Saccharomyces*. *abs# 134*

3:00 PM **Xianfa Xie**

Systems Biology Studies of Yeast Gene Evolution at the Genomic Level Reveal Drivers of Evolution *abs# 135*

Understanding domestication in the genomic era

1:30pm - 3:30pm Room 7

Chairs: Laurent Frantz & Guo-Dong Wang

1:30 PM **Jeffrey Ross-Ibarra**

Domestication, demography, and deleterious alleles in maize. *abs# 136*

2:00 PM **Claire M Wade**

Domestication of the dog *abs# 137*

2:30 PM **Ricardo C Rodríguez de la Vega**

What makes the fungi cheesy: the adaptive genomic toolbox of *Penicillium* molds revealed by between- and within-species comparisons *abs# 138*

2:45 PM **Johan Bélteky**

Selection for tameness in Red Junglefowl causes wide changes in brain gene expression *abs# 139*

3:00 PM **Anna V Kukekova**

Genome analysis of the red fox reveals genetic basis of domesticated behavior. *abs# 140*

3:15 PM **Jazmin Ramos Madrigal**

The genome sequence of a 5300-year-old maize cob recovered from the Tehuacan Valley provides insights into the early stages of maize domestication *abs# 141*

Afternoon Tea

3:30pm - 4:00pm Hall 1

Walter Fitch Symposium

4:00pm - 6:00pm Arena 1B

Chair: Laura Landweber

4:00 PM **Isabel Alves**

The effect of archaic admixture on inferred human population history *abs# 142*

4:15 PM **Kristin Lee**

Mutation, migration, standing variation: the where and how of convergent adaptation
abs# 143

4:30 PM **Joshua Christie**

Uniparental inheritance promotes adaptive evolution in the mitochondrial genome
abs# 144

4:45 PM **Liisa Loog**

Holy Chicken! Selection analysis applied to time series of ancient genotype data reveals how medieval religious reform shaped the genomes of modern chickens.
abs# 145

5:00 PM **Oren Avram**

A novel algorithm for selective sweeps detection in bacteria *abs# 146*

5:15 PM **Hugh K Haddock**

High-throughput experimental estimation of the effects of all amino-acid mutations to HIV's envelope protein on viral replication in cell culture *abs# 147*

5:30 PM **Benjamin Jack**

Functional Sites Induce Long-Range Evolutionary Constraints in Enzymes *abs# 148*

5:45 PM **Katya Kosheleva**

Weakly selected standing variants dominate adaptation for 1000 generations in sexual, laboratory evolved yeast populations *abs# 149*

Poster session B + Refreshments

6:00pm - 8:00pm Hall 1

Output Session Sponsor Type

Christopher J Graves

Yeast populations adapted to periodic stress trade fast growth for stress resistance *abs# 500*

Ann-Christin Honnen

Changes in clock-gene expression, activity, and fecundity in the mosquito *Culex pipiens* f. *molestus* exposed to artificial light at night *abs# 501*

Bethan Littleford-Colquhoun

What can the gut microbiota community of eastern water dragons (*Intellagama lesueurii*) tell us about adaptation to urbanisation? *abs# 502*

Alessandra AL Loria

Evidence for genetic adaptation to pollution *abs# 503*

yi peng

HMOX2 functions as a modifier gene for high-altitude adaptation in Tibetans *abs# 504*

Shigeru Saito

Evolutionary trajectory of a heat sensor TRPV1 in clawed frogs inferred from multispecies comparison and ancestral protein reconstruction *abs# 505*

Frederik Valeur Seersholm

DNA evidence of bowhead whale exploitation by Greenlandic Paleo-Inuit 4000 years ago *abs# 506*

Guangying Wang

Comparison of adaptive mechanism between sexual and asexual reproduction in *Tetrahymena thermophila* based on the experimental evolutionary genomics *abs# 507*

Jatin Arora

HIV epitope prediction provides functional link between HLA genotype and viral load *abs# 508*

Gabriela-Oana Bodea

The role of LINE-1 retrotransposition in Parkinson's disease *abs# 509*

Magdalena Gayà-Vidal

Food and pathogen adaptations: tracing the spread of lactase persistence and human African trypanosomiasis resistance into southwestern Africa *abs# 510*

Christopher R Gignoux

Insights on Array Design and Genotyping of over 50,000 Diverse Individuals for the Next Generation of Association Studies *abs# 511*

Marie-Jeanne H.C. Kempen

Understanding schizophrenia: the role of LINE-1 retrotransposition in disease aetiology *abs# 512*

Hilary C Martin

Effects of rare gene knockouts in a highly endogamous population *abs# 513*

Marco Telford

Target enrichment as a tool for wide-scale genome-wide comparison, intra-strain variation and stratification, in genome-integrated Human Herpesvirus 6 *abs# 514*

Michael C Turchin

Bayesian multivariate analysis of large genetic studies identifies novel associations *abs# 515*

Olivia Davies

Mitochondrial heteroplasmy in Australian hylaeine bees and its association with the parasite *Wolbachia* *abs# 516*

Weilong Hao

Investigating the evolutionary pathways towards extremely AT rich mitochondrial genomes *abs# 517*

Liliana Milani

Mitochondrial membrane potential: a trait involved in organelle inheritance? *abs# 518*

Anton Nekrutenko

Detection of ultra-rare mitochondrial variants *abs# 519*

Marco Passamonti

Mitochondrial selfish elements and the evolution of biological novelties *abs# 520*

Andrea Pozzi

SmithRNAs: could mitochondria 'bend' nuclear regulation? *abs# 521*

Sarah Schaack

Evolutionary Dynamics of the Mitochondria in Dwarf and Giant Rattlesnakes *abs# 522*

Renfu Shao

Splits and merges of minichromosomes shaped the complex and dynamic mitochondrial genome organization of the sucking lice (Anoplura, Insecta) *abs# 523*

Tesha Tsai

Mitochondrial DNA genetic diversity within Australian domestic pigs and their role in determining reproductive capacity. *abs# 524*

Dayana Yahalomi

Insight into the evolution of the partitioned mitochondrial genome of Myxozoa (Metazoa, Cnidaria). *abs# 525*

Samuel C. Andrew

Population differentiation and local adaptation in the Australian house sparrow. *abs# 526*

Toni I Gossmann

Tracing the presence of an enzyme essential for de-novo biosynthesis of NAD in the avian lineage: A case study for missing sequences in bird genomes *abs# 527*

Yoonsoo Hahn

Frequent Inactivation of *MOXD2* Genes in Birds *abs# 528*

Kerensa McElroy

Local adaptation of the red-browed finch *Neochmia temporalis* across climatic zones *abs# 529*

Joshua V Penalba

Genomic divergence in allopatry vs. parapatry through the speciation process *abs# 530*

Furong Qi

Delineating the gene birth and death for Mx homologs confers divergent antiviral activity to Influenza Virus *abs# 531*

Nynke Raven

The evolution of RNA recognizing Toll-Like Receptors in migratory waders *abs# 532*

Tim Sackton

Evolutionary dynamics of old, homomorphic sex chromosomes in Paleognathous birds. *abs# 533*

Ashlee Shipham

A genomic approach to examining two avian hybrid zones *abs# 534*

Amy L Slender

Sand dunes drive asymmetric gene flow between arid-zone Thick-billed grasswren subspecies *abs# 535*

Huabin Zhao

Molecular evolution of dietary diversification in birds *abs# 536*

Haim Ashkenazy

Averaging over alternative multiple sequence alignments increases the accuracy of phylogenetic tree reconstruction *abs# 537*

Guillaume Bernard

Alignment-free networks: One step further into the next generation phylogenomics *abs# 538*

Arman Bilge

Estimating Mutation Parameters and Population History Simultaneously from Temporally-Spaced Genome Data *abs# 539*

Andreas Futschik

Estimating the Effective Population Size from Experimental Evolution Data *abs# 540*

Jaime Gongora

Evolution and diversity of complement genes in crocodilians *abs# 541*

Mariangela Iannello

A transcriptome annotation pipeline for non-model organisms *abs# 542*

Manuel Irimia

VAST-DB: an Atlas of Alternative Splicing Profiles in Vertebrate Tissues and Cell Types *abs# 543*

Lars S Jermiin

ModelFinder: A new model-selection method that greatly improves the accuracy of molecular phylogenetic estimates *abs# 544*

Prabhav Kalaghatgi

MST -> P: A scalable and accurate method for reconstructing phylogenetic trees *abs# 545*

Carolin Kosiol

A reversible Polymorphism-aware phylogenetic Model (revPoMo) for species tree estimation *abs# 546*

Tommy Tsan-Yuk Lam

Phylogeny-guided genome assembly method for short nucleotide reads from deep sequencing of mixed microbial samples *abs# 547*

Carol Lee

Evolution of the Major Histocompatibility Complex (MHC) class I in wild pigs and peccaries *abs# 548*

Louis Ranjard

Haplotype reconstruction from Short Read Sequences using Vector Quantization *abs# 549*

David F Clarke

Comprehensive Annotation of Multigenic Protein-Family Structures (CAMPS) *abs# 550*

Hyunjin Shim

Time-sampled population genetics: an experimental investigation of drug-induced mutational meltdown as an antiviral treatment strategy *abs# 551*

Hannes Svardal

Enrichme – a gene set enrichment tool that naturally corrects for gene length and clustering *abs# 552*

Ashley K. Tehranchi

Measuring Natural Selection on Chromatin Accessibility in 1000 Humans From 10 Populations. *abs# 553*

Filipe G. Vieira

Estimating Identical-By-Descent tracts from low coverage NGS data *abs# 554*

Daryi Wang

MetaMIS: a metagenomic microbial interaction simulator based on a microbial community profiles *abs# 555*

Thomas K F Wong

HAL-HAS 2: A new algorithm that estimates evolution process for heterogeneity across lineages as well as convergent evolution *abs# 556*

Deepa Agashe

Evolution of the Shine-Dalgarno (SD) motif in prokaryotes *abs# 557*

Luke Ambrose

Population structure of widespread *Anopheles* mosquitoes in New Guinea, Australia and the Solomon Islands *abs# 558*

Ali Amiryousefi

Nonmetric ANOVA for Assessing Phylogenies *abs# 559*

Rajeev K. Azad

Deciphering evolutionary strata on plant sex chromosomes and fungal mating-type chromosomes through compositional segmentation *abs# 560*

Beth J Brittain

Experimental evolution with recombining and non-recombining *Acinetobacter baylyi* *abs# 561*

Amanda M.V. Brown

Inferring symbiotic innovation through a shotgun metagenomics lens: progress and pitfalls of the latest techniques *abs# 562*

Jose L. Campos

The relative role of positive and background selection in shaping genetic variability at linked sites in *Drosophila melanogaster* *abs# 563*

David Clarke

Comprehensive Annotation of Multigenic Protein-Family Structures (CAMPS) *abs# 564*

Sabyasachi Das

Evolution of Tumor Necrosis Factor Superfamily (TNFSF) genes TNFSF 12 and 13: Phylogenetic clues for the emergence of *in genomic* fusion of *TNFSF12-TNFSF13* *abs# 565*

Kristina Duan

Mechanism and fitness benefits of pyruvate kinase: a recurrent target of evolution *abs# 566*

Elizabeth Eyermann

Genetic basis of Lactase Persistence in Ethnically diverse African Populations *abs# 567*

Jaime Gongora

Genetic origins of bushpigs from Madagascar *abs# 568*

Jane Hawkey

COMBINE, bringing together Australian students and early-career researchers in bioinformatics and computational biology *abs# 569*

Clare Holleley

Biogeography of sex reversal and the effects of climate on sex determination *abs# 570*

Flora Honoré

The Hsp90 chaperone protein is essential in the *Shewanella oneidensis* bacteria under stress condition *abs# 571*

Josephine C A Hyde

Illuminating *Limbodessus*: speciation of sister species within a genus of subterranean dytiscid beetles in Western Australia. *abs# 572*

Emory Ingles

Testing the parent-of-origin hypothesis in dasyurid telomere length dimorphism *abs# 573*

Arpit Jain

An evolutionary perspective of AMPK-TOR signaling in the three domains of life *abs# 574*

Chris Kimber

Life history evolution in response to condition-dependent juvenile selection *abs# 575*

Kristina Vanessa Klaus

Historical biogeography of the ancient genus *Selaginella* – Early adaptation to xeric habitats on Pangea *abs# 576*

Nicholas Matzke

Trait-dependent dispersal models for phylogenetic biogeography, in the R package BioGeoBEARS *abs# 577*

Fernando L Mendez

Comparison of Neanderthal and modern human Y chromosomes: implications for reproductive isolation *abs# 578*

Katsuhiko Mineta

Evolutionary insights from the marine metagenomics in the Red Sea *abs# 579*

Portia Mira

Adaptive Landscapes of Resistant Genes change as Antibiotic Concentration Changes *abs# 580*

Katrina Morris

Host response to highly pathogenic avian influenza infection in quails *abs# 581*

Sally Mortlock

Risk loci on CFA13 associated with lymphoma in Bullmastiffs *abs# 582*

Saotoshi Oota

Experimental and theoretical approaches to elucidate isochore evolution by ENU mutagenesis *abs# 583*

Helen Piontkivska

Molecular co-evolutionary insights into the HIV-1 pre-integration complex *abs# 584*

Andrew M Ritchie

Robustness of Bayesian molecular dating to tree prior misspecification *abs# 585*

Marc Ritter

Coinfection study reveals immune modulatory effects of a cestode in its vertebrate host *abs# 586*

Isobel Ronai

The Mechanistic, Genetic, and Evolutionary Basis of Worker Sterility in the Social Hymenoptera *abs# 587*

Emily Roycroft

Sex-biased dispersal in the short-tail stingray *abs# 588*

Arunraj Saranya Prakashrao

Evolutionary implications of gene duplication in plant secondary metabolism *abs# 589*

Helmut Simon

Genetic Drift in Variable Size Haploid and Diploid Populations *abs# 590*

Edi Sudianto

Revisiting the plastid phylogenomics of Pinaceae with two complete plastomes of *Pseudolarix* and *Tsuga* *abs# 591*

Shiho Takahashi-Kariyazono

Evolution and genetic basis of *Acropora* species fluorescence *abs# 592*

John S Taylor

Eighteen non-visual opsins in the ancestor of vertebrates, astonishing duplication in ray-finned fish and loss in Amniota *abs# 593*

Markus Tondl

Dynamic cis-regulatory module recruitment during cardiac evolution *abs# 594*

Chloe A van der Burg

The evolution of the innate immune system: insights from an early-divergent lineage *abs# 595*

Brandon D Velie

The relationship between coat colour phenotype and equine behaviour: a pilot study *abs# 596*

Yin Wang

powerful transmission of carrion beetle *microphorus vespilloides* symbiosis *abs# 597*

Yen Ting Wong

Genetic and Protein Study of Alpaca Fibre. *abs# 598*

Ge Zhang

Evolution of parent-of-origin effects on complex traits *abs# 599*

Fatemeh Ashari Ghomi

Are essential genes more likely to be conserved? *abs# 600*

Rajeev Azad

Identification of novel genomic islands in Liverpool epidemic strain of *Pseudomonas aeruginosa* using segmentation and clustering *abs# 601*

Qamar Bashir

Prevalence, evolution and concurrent infection by multiple dengue virus serotypes in patients from Pakistan *abs# 602*

Holger Bergmann

Tracing functional protein interaction networks using 'feature-aware' phylogenetic profiling *abs# 603*

Minh Duc Cao

Phylogenomics analysis of large bacterial phylogenies using whole genome information *abs# 604*

Samia Elfekih

Can adaptive radiations in the *Bemisia tabaci* species complex be revealed by co-evolving endosymbionts?
abs# 605

Paul Gardner

Avoidance of stochastic RNA interactions can be harnessed to control protein expression levels in bacteria and archaea *abs# 606*

Jeremy Glasner

Evolutionary Genomics of Plant Pathogenic Enterobacteria *abs# 607*

Chowdhury Mehedi Hasan

Testing the role of recombination in the evolution of multidrug resistance in experimental bacterial populations *abs# 608*

Rosemarie Herbert

Geographical distribution influences purifying selection on innate immune genes in *Drosophila* *abs# 609*

Honour McCann

The origin and evolution of the emergent plant pathogen *Pseudomonas syringae* pv. *actinidiae* *abs# 610*

Klaus Neuhaus

Ribosomal footprinting allows detecting and analyzing weakly translated, evolutionary young genes in EHEC
abs# 611

Daniel Tamarit

The basis of the *Bartonella* radiation: Origin and evolution of a specialized gene transfer agent *abs# 612*

Melissa Ward

Identification of source and sink populations for the emergence and global spread of the East-Asia clone of Community-Associated MRSA *abs# 613*

THIERRY WIRTH

Epidemic success and underlying driving forces of the *Mycobacterium tuberculosis* complex in a low-prevalence setting *abs# 614*

Lilly Yuen

Co-evolution of Hepatitis B Virus subgenotype C4 and Indigenous Australians for at least 53,000 years
abs# 615

Barbara Zehentner

Overexpression of overlapping ORFs in *Escherichia coli* O157:H7 reveals growth phenotype *abs# 616*

Elizabeth G Atkinson

Re-evaluating the target of selection within *FOXP2* suggests functional divergence among diverse human populations *abs# 617*

Chiara Barbieri

Reconstructing human diffusion and collapse in the Americas *abs# 618*

Anders Bergstrom

Human population genetics of Papua New Guinea *abs# 619*

Local adaptation & barriers to gene flow in *Littorina saxatilis* hybrid zones *abs# 620*

Anne Clark

Characterizing introgressed sequences in *S. cerevisiae* *abs# 621*

Angeles de Cara

Supergene evolution favoured by the introgression of an inversion in *Heliconius* *abs# 622*

Siobhan Dennison

Developing a SNP toolkit for management of the koala, *Phascolarctos cinereus*: from pedigrees to

population genomics *abs# 623*

Eran Elhaik

Localizing Yiddish and non-Yiddish speaking Ashkenazic Jews to primeval villages in ancient Ashkenaz lands *abs# 624*

Anders Eriksson

Hurdles out of Africa: how climate and terrain shaped the history of human migrations *abs# 625*

Ashley Farlow

The global evolutionary history of *Arabidopsis thaliana* *abs# 626*

Colleen Friel

Genomic analysis of coexistence and symbiosis in *Trifolium* populations *abs# 627*

Naoko T Fujito

Spread of reduced activity of *STX* promoter in modern humans *abs# 628*

Shyam Gopalakrishnan

Whole genome sequencing reveals the complex phylogeography of canids *abs# 629*

Nina Hollfelder

Demographic history of Northeast Africa revealed by genome-wide population-genetic data *abs# 630*

Risa Iwasaki

Genome-wide analysis to identify locally adapted genes in humans *abs# 631*

Latifa Jackson

Mathematical Model of Missing African Genomic Variation: A case for robust sampling *abs# 632*

Kim Jäderkvist Fegraeus

Evolution of the Coldblooded trotter breed: Where did the speed come from? *abs# 633*

Maddie E James

Parallel speciation in an Australian wildflower *abs# 634*

maryam Dr. javed

Exploring Dairy Potential of River Buffalo by Gene Based Technologies *abs# 635*

maryam Dr javed

Genomic Exploration of Poor Estrus Behavior is Imperative to Exploit Livestock Capabilities *abs# 636*

Daniel Jeffares

Structural variants in yeast have strong effects on quantitative traits and reproductive isolation, and are transient in natural populations. *abs# 637*

Jonathan T. L. Kang

Consanguinity and runs of homozygosity in Jewish populations *abs# 638*

Konrad J Karczewski

Breaking the infinite sites model: widespread mutational recurrence in exome sequence data from over 60,000 individuals *abs# 639*

Peter Keightley

Inferring the unfolded site frequency spectrum and using it to quantify adaptive molecular evolution in *Drosophila* *abs# 640*

Heebal Kim

Genome-wide association study of copy number variation for detection of genes affecting fat distribution in pig *abs# 641*

Carolin Kosiol

Experimental evolution in *Drosophila* analysed with Gaussian process models *abs# 642*

Benjamin Laenen

The impact of selection on cis-regulatory variation across the genome of an outcrossing plant *abs# 643*

Yuki Matsumoto

Selective breeding mediated genetic mapping for tameness in mouse *abs# 644*

Michael J McDonald

Can we see ecology in sequence data? *abs# 645*

Fernando L Mendez

Comparison of Neanderthal and modern human Y chromosomes: implications for reproductive isolation
abs# 646

Mait Metspalu

Large-scale whole genome sequencing of the Estonian population reveals novel loss-of-function variants and new insights into the population history *abs# 647*

Kevin Murray

kWIP: The *k*-mer Weighted Inner Product, a *de novo* estimator of genetic relatedness. *abs# 648*

Lisa Oyston

Functional Validation of Human Parkinson's Disease GWAS in the Fly *abs# 649*

Min-Sheng Peng

Mitochondrial Genomes Reveal the Complex Demographic History of Human Populations in Eastern Pamirs
abs# 650

Daniel R Schrider

Robust identification of hard and soft sweeps in humans via machine learning *abs# 651*

Alisa Sedghifar

Beyond clines: lineages and haplotype blocks in hybrid zones *abs# 652*

Lara Shepherd

A molecular investigation of the relationships of karaka (*Corynocarpus laevigatus*). *abs# 653*

Laurits LS Skov

Detecting introgressed archaic haplotypes in Oceanic population genome sequences *abs# 654*

Jan Strugnell

ddRAD-based target capture across *Jasus* lobster species to assess spatial-temporal adaptive variation
abs# 656

Jessica Stapley

Ecological divergence and reproductive isolation in a colour polymorphic *Anolis* lizard. *abs# 657*

Michal Szpak

Prioritizing Candidate Genetic Variants Driving Adaptations in Human Populations *abs# 658*

Maud I Tenaillon

Using whole genome sequencing of pooled samples to detect local adaptation of teosintes along two altitudinal gradients *abs# 659*

Ayla L van Loenen

Evolutionary history of European Bison (*Bison bonasus*) *abs# 660*

Anouk Willemsen

The factors that constrain or promote the evolution of alternative genome architectures in an RNA virus
abs# 661

Shuhua Xu

Genetic origins, population structure and admixture of Xinjiang's Uyghurs *abs# 662*

Yubin Yan

Genomic divergence between two sympatric sibling species in the mangrove genus *Rhizophora* detected by RAD sequencing *abs# 663*

Lixin Yang

A Functional MiR-124 Binding-Site Polymorphism in IQGAP1 Affects Human Cognitive Performance

abs# 664

Xiaoming Zhang

Y-chromosome diversity suggests southern origin and Paleolithic backwave migration of Austro-Asiatic speakers from eastern Asia to the Indian subcontinent abs# 665

Daniel Falush

Adaptive introgression in agricultural *Campylobacter coli* abs# 666

Hangxing Jia

Detection of *Drosophila melanogaster* line admixture through targeted barcoding sequencing abs# 667

Alejandro Manzano-Marín

Blood ties: Metabolic convergence among gammaproteobacterial endosymbionts from blood-feeding arthropods and the Mexican leech *Haementeria officinalis* abs# 668

Omar Rota-Stabelli

Using molecular clocks to investigate beneficial (and deleterious) microbe-host interactions in the agroecosystem abs# 669

Marina Brasó-Vives

Exploring the role of segmental duplications in the phenotypic differences between humans and other great apes abs# 670

Daniel L. Cameron

GRIDSS: detecting structural variation using positional de Bruijn graphs abs# 671

Ying Chen

Segregation of chromosomes during the meiosis of pentaploid in yeast abs# 672

Maryam Keshavarz

Structural variation in genome could make novel complex trait in mouse behavior abs# 673

Paul Battlay

Systems Genetics identifies two structural variants of P450 genes that confer resistance to insecticides in *Drosophila melanogaster*. abs# 674

Shengjun Tan

LINE-1-like retrotransposons contribute to RNA-based gene duplication in dicots abs# 675

Galit Blecher

The Recruitment of Proteins into a Scorpion Venom abs# 676

Ira Cooke

Comparative proteomic and transcriptomic analysis of venom producing posterior salivary glands of the blue ringed octopus (*Hapalochlaena maculosa*) and the southern sand octopus (*Octopus kaurna*). abs# 677

Ricardo C Rodríguez de la Vega

Intragenome diversity of gene families encoding toxin-like proteins in venomous animals abs# 678

Jan M Strugnell

A combined transcriptomic and proteomic approach reveals putative toxins in the slime secretions of the southern bottletail squid, *Sepiadarium austrinum* (Cephalopoda) abs# 679

Joachim M Surm

Expression patterns of cnidarian toxins reveal dynamic gene family evolution and regulation abs# 680

Daniel BB Bakari

A new glimpse on life origin abs# 681

Violette Da Cunha

Lokiarchaea is not the missing link between Archaea and Eukaryotes. abs# 682

Eva F. Caceres

Metagenomics exploration of novel archaea sheds new light on the early evolution of eukaryotes abs# 683

Joseph Larsen

Rings Reconcile Genotypic and Phenotypic Evolution within the Proteobacteria *abs# 684*

Martina Bradic

Transcriptional variation in the protist *Trichomonas vaginalis* caused by insertion of DNA transposable elements *abs# 685*

Joanna Ciomborowska

Should we reconsider the chromosomal gene movement of retrocopies? *abs# 686*

William G Dodt

Resolving kangaroo phylogeny and overcoming retroposon ascertainment bias *abs# 687*

Jeffrey Fawcett

High similarity between distantly related species of a plant SINE family is consistent with a scenario of vertical transmission without horizontal transfer. *abs# 688*

Patricia Gerdes

Identification of polymorphic L1 insertions in mice *abs# 689*

Zoé Joly-Lopez

Phylogenetic and genomic analyses resolve the origin of important plant genes derived from transposable elements *abs# 690*

Bethany R Jose

Applying complementary NGS approaches for *in silico* resolution of the present and past mobilome of *Clostridium difficile* R078 isolates *abs# 691*

Jaeun Jung

Bioinformatic Analysis of Expression and Regulation of Human Antisense transcripts by Transposable elements in Human Full-Length cDNA Sequences *abs# 692*

Young-Hyun Kim

Macaca specific exon creation event generates a novel *ZKSCAN5* transcript *abs# 693*

Miriam Merenciano

Functional analysis of a natural mutational hotspot in the proximal promoter of a stress-response gene in *Drosophila melanogaster* *abs# 694*

Ann-Marie Oppold

The role of heterozygous transposable elements in reproductive isolation among *Chironomus riparius* populations *abs# 695*

Jessica Stapley

Do transposable elements facilitate adaptation? *abs# 696*

Guiling Sun

Transposons horizontally transferred between parasitic plants and hosts are still actively expressed in some recipients *abs# 697*

Peter Civián

Multiple domestications of Asian rice with limited inter-group gene flow. *abs# 698*

Anik Budhi Dharmayanthi

The Origin and Evolution of Fibromelanosis Locus in Domesticated Chickens: Comparison between Indonesian Cemani and Chinese Silky Genomes *abs# 699*

Allowen EVIN

What can morphometrics tell us about domestication at the age of genomics ? *abs# 700*

Rohan Mehta

The probability of monophyly of a sample of gene lineages given a species tree: an application to maize domestication. *abs# 701*

Marina M Naval Sanchez

Changing Patterns of Genomic Variability Following Domestication of Sheep *abs# 702*

Catherine J Nock

Cracking the nut: genome and transcriptome sequencing of *Macadamia integrifolia* (Proteaceae) *abs# 703*

Anna AR Rudzinski

A discriminative model-based approach to inferring the geographic origin of domestic species *abs# 704*

Markus G Stetter

Characterization of grain amaranth (*Amaranthus L*) domestication with Genotyping by Sequencing and whole genome sequencing *abs# 705*

Emma Svensson

The genomic signature of a 4,600 year old Scandinavian dog adds a time-depth to modern basal dog breeds *abs# 706*

Guo-Dong Wang

Out of southern East Asia: the natural history of domestic dogs across the world *abs# 707*

Penelope A Ajani

Genome variability in the ecologically significant marine diatom *Leptocylindrus* (Bacillariophyta) in a southern hemisphere upwelling system *abs# 708*

Crystal Hepp

Global phylogeography of *Coccidioides spp.*; the etiologic agent of Valley Fever *abs# 709*

Aaron Reinke

Identification of microsporidia host-exposed proteins reveals a repertoire of large paralogous gene families and rapidly evolving proteins *abs# 710*

Isheng J Tsai

Comparative and population genomics of *Phellinus noxius* causing brown root rot disease in trees *abs# 711*

Arjun Verma

Molecular ecology of palytoxin producing protist *Ostreopsis siamensis* (Alveolata) along the East Australian Current *abs# 712*

David J Winter

Why do ciliates have such low mutation rates, and why don't we? *abs# 713*

6th July 2016

Registration

8:00am - 5:00pm Foyer

Ecological and conservation genetics

8:30am - 10:30am Arena 1B

Chair: Jason Bragg

8:30 AM **Rebecca Johnson**

The Koala Genome Consortium – the utilization of *de novo* genome and transcriptome sequencing for applied conservation genomics of an iconic Australian marsupial *abs# 150*

8:45 AM **Peri E Bolton**

Colourful conservation – conservation genetics and selection on colour polymorphism in the threatened Gouldian finch *abs# 151*

9:00 AM **Catherine E Grueber**

Effects of selection on genetic diversity in threatened species breeding programs: empirical data from Tasmanian devil *abs# 152*

9:15 AM **Katie L Millette**

Broken barriers: anthropogenic disturbance leads to continental-scale levels of genetic diversity *abs# 153*

9:30 AM **Katrina M Morris**

Lack of genetic diversity across diverse immune genes in an endangered mammal, the Tasmanian devil *abs# 154*

9:45 AM **Craig Moritz**

Genomics-led biodiversity discovery in reptiles across the monsoonal tropics of northern Australia *abs# 155*

10:00 AM **Manpreet K Dhani**

Genomic insights into the mechanisms of priority effects in nectar yeast *abs# 157*

Next Generation of tools for molecular evolutionary analysis

8:30am - 10:30am Room 5

Chair: Sudhir Kumar

Output Session Sponsor Type

8:30 AM **Sudhir Kumar**

Next generation suite for molecular evolutionary genetics analysis (MEGA) *abs# 158*

9:00 AM **Remco Bouckaert**

What is new in BEAST *abs# 159*

9:30 AM **Arndt von Haeseler**

IQ-TREE: efficient phylogenomic software for maximum likelihood analysis *abs# 160*

9:45 AM **Sergei LK Pond**

Beyond software tuning: scaling up comparative coding sequence analysis using approximations and models that adapt their complexity to the data. *abs# 161*

10:00 AM **Alexander Herbig**

MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman *abs# 162*

10:15 AM **David A. Duchene**

Assessment of substitution model adequacy for phylogenomics *abs# 163*

Stronger together: powerful molecular innovation arising from partnership

8:30am - 10:30am Room 6

Chair: Amanda Brown

8:30 AM **Francisco Rodriguez-Valera**

Bacterial viruses, can't live with them, can't live without them *abs# 164*

9:00 AM **Stephanie R Weldon**

Swapping partners mid-dance: Symbiotic replacement in a tightly integrated intrabacterial, intracellular nested mutualism *abs# 165*

9:15 AM **Glen Dsouza**

Experimental evolution of metabolic dependency in bacteria *abs# 166*

9:30 AM **Mathieu Groussin**

Disentangling diet and phylogeny reveals both horizontal and vertical evolution of mammalian microbiomes *abs# 167*

9:45 AM **Bastian Greshake**

The Genomic Footprint of Lichenization: Comparative Genomics of Lecanoromycetes *abs# 168*

10:00 AM **Carolyn Frank**

Nitrogen fixation by the conifer foliar microbiome *abs# 169*

Mechanisms of transgenerational adaptation to environmental change

8:30am - 10:30am Room 7

Chair: Timothy Ravasi

8:30 AM **Ary Hoffmann**

Moving from genetics to genomics in understanding climate change adaptation in *Drosophila*: what else can we learn? *abs# 170*

9:00 AM **Luciano B Beheregaray**

Comparative Evolutionary Genomics of Adaptation to Environmental Change in Ecologically Important Aquatic Organisms *abs# 171*

9:30 AM **Celia Schunter**

Molecular signatures of transgenerational brain response to ocean acidification in a reef fish *abs# 172*

9:45 AM **Eric A Miska**

Transgenerational epigenetic inheritance: mechanisms and biology in *C. elegans* *abs# 173*

10:00 AM **Ana Marija Jakšić**

Purifying selection causes genetic canalization of gene expression at high and low larval densities in *Drosophila melanogaster* *abs# 174*

10:15 AM **Wei-Chin Ho**

Phenotypic changes in organismal adaptation to new environments: plasticity distorts while evolution restores *abs# 175*

Morning Tea

10:30am - 11:00am Hall 1

Population Genomics

11:00am - 1:00pm Arena 1B

Chair: Ashley Farlow

11:00 AM **Hannes Svoldal**

Genomic insights from two emerging model systems: Polygenic adaptation to simian immunodeficiency virus (SIV) infection in vervet monkeys, and the role of gene flow in rapid speciation in Lake Malawi cichlids *abs# 176*

11:30 AM **Anna Malaspinas**

The population history of Aboriginal Australia *abs# 177*

12:00 PM **Sharon R Browning**

Ancestry-specific estimation of recent effective population size in the Americas

abs# 178

12:15 PM **Elena Arciero**

Human population structure and genetic adaptation in the Himalayan region abs# 179

12:30 PM **Alicia R Martin**

Fine-scale identity-by-descent and birth records in Finland provide insights into recent population history abs# 180

12:45 PM **Peter Frandsen**

Demographic history and population structure of chimpanzees (*Pan troglodytes*) with implications for global conservation strategies abs# 181

Next Generation of tools for molecular evolutionary analysis

11:00am - 12:00pm Room 5

Chair: Sudhir Kumar

11:00 AM **Rachel S Schwartz**

Rapid identification of phylogenetically informative data from high-throughput sequencing reads abs# 182

11:30 AM **Milan Malinsky**

RADpainter and fineRADstructure: population inference from RAD-seq data abs# 183

11:45 AM **Vanessa Gray**

Envision: A computational tool for predicting mutational effect magnitudes abs# 184

Open Symposium

12:00pm - 1:00pm Room 5

Chair: Craig Millar

12:00 PM **Rodrigo Cogni**

Addicted? Reduced host resistance in populations with defensive symbionts abs# 185

12:15 PM **Michelle M Meyer**

Both co-evolution with protein binding-partners and RNA structural plasticity influences the evolution of bacterial RNA regulators. abs# 186

12:30 PM **Iakov I Davydov**

A new realistic codon model for genome-scale positive selection analysis with variation in DNA constraints and in selection abs# 187

12:45 PM **Jemma L Geoghegan**

Virological Factors That Increase the Transmissibility of Emerging Human Viruses abs# 188

Evolution of Aerobic Metabolisms in Archaea

11:00am - 12:00pm Room 6

Chair: Gregory Fournier

11:00 AM **Jennifer B Glass**

Thaumarchaeotal Metalloenzymes: Evolutionary History, Influence of Oxygen and

11:30 AM **Gregory Fournier**

Mapping the Physiological and Metabolic Adaptations to Oxygen across the Archaea
id# 37991

Phylogenomics and Bacterial Pathogen Evolution

12:00pm - 1:00pm Room 6

Chair: Kathryn Holt

12:00 PM **Nouri Ben Zakour**

Evolution and global dissemination of the multidrug resistant Escherichia coli ST131
clone *abs# 191*

12:30 PM **Sebastian Duchene**

Genome-scale rates of evolutionary change in bacteria *abs# 192*

12:45 PM **Tal Dagan**

Phylogenomic networks reveal limited phylogenetic range of recent lateral gene
transfer by transduction *abs# 193*

Genetic mechanisms driving morphological evolution

11:00am - 1:00pm Room 7

Chair: James Noonan

11:00 AM **Joanna Wysocka**

TBC *abs# 194*

11:30 AM **Emily S Wong**

Interplay of cis and trans mechanisms driving transcription factor binding, chromatin,
and gene expression evolution *abs# 195*

11:45 AM **Veronica Hinman**

Transcription Factor Evolution as a Mechanim for Modifying Developmental Gene
Regulatory Networks. *abs# 196*

12:00 PM **Mathilde PARIS**

Genomic basis of the evolution of wing pigmentation in Drosophila *abs# 197*

12:15 PM **Michael Hiller**

Controlling for phylogenetic relatedness improves discovering the genomic basis
underlying species' phenotypic differences *abs# 198*

Lunch

1:00pm - 2:00pm Hall 1

Workshop: Citizen Science engagement: the good the bad and the ugly

1:00pm - 2:00pm Room 5

Workshop: Wikipedia editing for scientists

1:00pm - 2:00pm Room 6

Population Genomics

2:00pm - 4:00pm Arena 1B

Chair: Ashley Farlow

2:00 PM **Leif Andersson**

Polygenic basis for ecological adaptation in the Atlantic herring revealed by genome sequencing *abs# 199*

2:30 PM **Craig R Primmer**

The genetic architecture of age at maturity in 57 Atlantic salmon populations: a large-effect locus with sex dependent dominance reduces sexual conflict and shows signals of local adaptation *abs# 200*

3:00 PM **Parul Johri**

Population genomics of *Paramecium* species *abs# 201*

3:15 PM **Sha Zhu**

Inferring population dynamics from high throughput genomic analysis of *Plasmodium falciparum* field samples *abs# 202*

3:30 PM **Luke M Noble**

Genomic correlates of inbreeding depression in outcrossing *Caenorhabditis* nematodes *abs# 203*

3:45 PM **Åsa Pérez-Bercoff**

Investigating the evolution of new biochemical pathways in baker's yeast *Saccharomyces cerevisiae* *abs# 204*

Open Symposium

2:00pm - 4:00pm Room 5

Chair: David Lambert

2:00 PM **Tin Yau Pang**

Co-functioning between horizontally transferred segments reveals exaptation in the evolution of new metabolic phenotypes in *E. coli* *abs# 205*

2:15 PM **Meagan A Rubel**

Dietary and Environmental Factors Shaping African Gut Microbiomes *abs# 206*

2:30 PM **Marina Telonis-Scott**

Population and sex-specific transcriptomics of east Australian *Drosophila* *abs# 207*

2:45 PM **Arpit Jain**

protTrace: Predicting the evolutionary traceabilities for proteins and pathways *abs# 208*

3:00 PM **Oliver W Griffith**

Term pregnancy in marsupials is homologous to implantation in eutherian mammals: a hypothesis *abs# 209*

3:15 PM **Agnes Piecyk**

Geographic patterns of virulence in a stickleback – tapeworm system *abs# 210*

3:30 PM **Nicky Rollings**

Snakes, plugs and mating balls: Telomere dynamics in red-sided garter snakes *abs# 211*

3:45 PM **Jonathan Waters**

Ancient DNA evidence supports a 'Founder-Takes-All' model for spatial genetics.
abs# 212

Phylogenomics and Bacterial Pathogen Evolution

2:00pm - 4:00pm Room 6

Chair: Kathryn Holt

2:00 PM **Daniel J Wilson**

What is the role of within-host evolution in *Staphylococcus aureus* infection? *abs# 213*

2:30 PM **Sarah G Earle**

Genome-wide association study of carriage versus invasive disease in *Neisseria meningitidis* *abs# 214*

2:45 PM **Nicole E Wheeler**

Profile-based comparison of *Salmonella* genomes reveals signatures of invasive potential *abs# 215*

3:00 PM **Sean Schneider**

Genomic analysis of adaptation during chronic colonization in *Helicobacter pylori*
abs# 216

3:15 PM **Jane Hawkey**

Insertion sequence dynamics in the global *Shigella sonnei* population *abs# 217*

3:30 PM **Verena J Schuenemann**

Ancient leprosy genomics: Retracing the evolutionary history of *Mycobacterium leprae* from medieval genomes *abs# 218*

3:45 PM **Kirsten Bos**

Tracing the aftermath of the Black Death through analyses of ancient genomes.
abs# 219

Genetic mechanisms driving morphological evolution

2:00pm - 3:00pm Room 7

Chair: James Noonan

2:00 PM **Gregory Wray**

Building a bigger brain: the genetic basis for the human neocortex *abs# 220*

2:30 PM **Tarang K Mehta**

Evolution of modulatory regulatory programs across different tissues in cichlids
abs# 221

2:45 PM **William L Hatleberg**

Genomic insight into the evolution of larval body plans *abs# 222*

Transposable Elements and Genome Evolution

3:00pm - 4:00pm Room 7

Chair: Cedric Feschotte

3:00 PM **Laura Landweber**

Oxytricha's mobile genome *abs# 223*

3:30 PM **Robert Kofler**

Rapid establishment of a piRNA based defense system – evidence from the P-element invasion dynamics in experimentally evolving *D. simulans* populations
abs# 224

3:45 PM **Eric Miska**

piRNA vs TEs: genomic and epigenomic variation in 16 strains of mice *abs# 225*

Afternoon Tea

4:00pm - 4:30pm Hall 1

Population Genomics

4:30pm - 5:30pm Arena 1B

Chair: Ashley Farlow

4:30 PM **Matthew S Ackerman**

Estimating seven coefficients of pairwise relatedness using population genomic data
abs# 226

4:45 PM **Adam B Rohrlach**

Unsupervised Detection and Quantification of Demographic Structure in mtDNA via Multiple Correspondence Analysis *abs# 7*

5:00 PM **Daniel Falush**

A tutorial on how (not) to over-interpret STRUCTURE/ADMIXTURE bar plots
abs# 228

5:15 PM **Tom R Booker**

Hill-Robertson Interference in the Genomes of Wild Mice, *Mus musculus castaneus*
abs# 229

Graham Webb memorial symposia

5:30pm - 6:30pm Arena 1B

Chair: Jenny Graves

5:30 PM **Jenny Graves**

Weird animal genomes, epigenetics and sex chromosome turnover *abs# 230*

6:00 PM **Gregory B Peters**

Mapping the Eukaryote Chromosome: From Primary Constriction to Monia Gap.
abs# 231

6:15 PM **Janine Deakin**

Chromosome rearrangements in a second transmissible tumour in Tasmanian devils
abs# 232

Inter-disciplinary Mechanistic Models: From Biophysical Chemistry and Molecular Process to Evolution and Ecology

4:30pm - 6:30pm Room 5

Chair: David Liberles

Output Session Sponsor Type

4:30 PM **Daniel B Stouffer**

The evolutionary complexity of ecological networks *abs# 233*

5:00 PM **Julian Echave**

The biophysical origin of observed patterns of protein evolutionary divergence of sequence, structure, and motion *abs# 234*

5:30 PM **Aaron Goodman**

Stochastically varying environments promote evolution of modularity and hierarchy in simulated bacterial metabolic networks *abs# 235*

5:45 PM **Michael J Harms**

Physical origins and evolutionary effects of high-order epistasis in genotype-phenotype maps *abs# 236*

6:00 PM **Steven Maere**

The use of mechanistic genotype-phenotype mapping models to simulate the evolution of transcriptional systems *abs# 237*

6:15 PM **Ashley I. Teufel**

Functional retention of protein-protein interactions despite substantial sequence divergence. *abs# 238*

Into the great warm open - ancient DNA beyond the temperate frontier

4:30pm - 6:30pm Room 6

Chair: Marcus Thomas Gilbert

4:30 PM **Hannes Schroeder**

Out in the (not so) cold: ancient DNA and the tropics *abs# 239*

4:45 PM **Michael Bunce**

20,000 bones and counting - Insights into Past Biodiversity and Ancient DNA Preservation using Bulk-Bone Metabarcoding *abs# 240*

5:00 PM **Maria A Nieves Colon**

Ancient DNA preservation in tropical pre-contact archaeological sites in the Americas *abs# 241*

5:15 PM **Rosa Fregel**

Using whole-genome in-solution capture to infer the geographic origin of Indian Ocean enslaved people in the historical cemetery of Le Morne (Mauritius) *abs# 242*

5:30 PM **Torsten Günther**

The genomic enigma of two Medieval North Africans *abs# 243*

5:45 PM **Alicia Grealy**

Eggshell palaeogenomics: palaeognath evolutionary history revealed through ancient nuclear and mitochondrial DNA from the Madagascan elephant bird *Aepyornis abs# 244*

6:00 PM **Morten E Allentoft**

Ancient DNA preservation: cutting to the bone *abs# 245*

6:15 PM **Cesare de Filippo**

Harvesting information from ultra-short ancient DNA sequences *abs# 246*

Transposable Elements and Genome Evolution

4:30pm - 6:30pm Room 7

Chair: Cedric Feschotte

4:30 PM **Josefa González**

Functional analysis of nine retrotransposons inserted in the promoter of a stress-response gene in *Drosophila* *abs# 247*

5:00 PM **Sandra R Richardson**

Endogenous L1 Retrotransposition in the Mammalian Primordial Germline and Early Embryo *abs# 248*

5:15 PM **Kim A Steige**

The role of transposable elements for gene expression in *Capsella* hybrids and allopolyploids *abs# 249*

5:30 PM **Rachel O'Neill**

Retroelements and noncoding RNAs linked to centromere turnover during Macropodid chromosome evolution *abs# 250*

5:45 PM **Kateryna Makova**

Integration and fixation preferences of human and mouse endogenous retroviruses uncovered with Functional Data Analysis *abs# 251*

6:00 PM **Alexander Suh**

The dynamic landscape of transposition across the speciation continuum of *Ficedula* flycatchers *abs# 252*

6:15 PM **Eugene Koonin**

CRISPR-Cas and origin of adaptive immunity from selfish genetic elements *abs# 253*

Conference Dinner + Awards

7:00pm - 10:30pm Arena 1

7th July 2016

Registration

8:00am - 11:00am Foyer

Plenary - Eske Willerslev

8:30am - 9:30am Arena 1B

Chair: David Lambert

8:30 AM **Eske Willerslev**

Human migrations and megafaunal extinctions *abs# 254*

Invitation to next year's meeting

9:30am - 10:00am Arena 1B

Morning Tea

10:00am - 10:30am Hall 1

Population Genomics

10:30am - 11:30am Arena 1B

Chair: Ashley Farlow

10:30 AM **Hilary C Martin**

Insights into platypus population structure and history from whole-genome sequencing *abs# 255*

11:00 AM **Kathryn Hodgins**

Convergence in the genomics of local adaptation to climate in conifers *abs# 256*

11:15 AM **Emilie Cros**

Patterns of diversification in two babbler species from Sundaland. *abs# 257*

GSA Awards

11:30am - 1:30pm Arena 1B

Chair: Katherine Belov

11:30 AM **Aleksandra Filipovska**

Regulation of the mitochondrial transcriptome *abs# 258*

12:00 PM **Sambasivam Periyannan**

Conventional and modern genetic approaches of cloning rust disease resistance in wheat *abs# 259*

12:30 PM **Elizabeth Dennis**

'Fixation' of hybrid vigour *abs# 260*

12:45 PM **Dawn Gleeson**

An educators journey *abs# 261*

1:00 PM **Sebastian Duchene**

Understanding Evolutionary Rate Variation in Viruses *abs# 262*

The Allan Wilson Memorial

10:30am - 1:00pm Room 5

Chairs: & Neil Gemmell

10:30 AM **Rebecca Cann**

Avian Poxvirus Identified as Major Extinction Threat to Hawaiian Forest Birds
abs# 263

11:00 AM **Axel Meyer**

Genomics of parallel evolution and speciation during repeated adaptive radiations in cichlid fishes *abs# 264*

11:30 AM **Scott V. Edwards**

Convergent regulatory evolution and the origin of flightlessness in palaeognathous birds *abs# 265*

12:00 PM **James A. Lake**

Allan Wilson as I Knew Him *abs# 266*

12:30 PM **W. Kelley Thomas**

Sequencing our way towards understanding global eukaryotic biodiversity *abs#*

Ancient DNA and the effects of human innovation on genomes

10:30am - 12:30pm Room 6

Chairs: Torsten Günther & Emma Svensson

10:30 AM **Christina Warinner**

The evolution and changing ecology of the human microbiome *abs# 268*

11:00 AM **Wolfgang Haak**

Ancient DNA, archaeology and linguistics: on the chances, limitations and perils of working on the edge of time *abs# 269*

11:30 AM **Laura S Weyrich**

Insights from Neandertal microbiota on the history of human health and disease
abs# 270

11:45 AM **Johannes Krause**

Genomic History of Upper Paleolithic Europeans *abs# 271*

12:00 PM **Cristina Valdiosera**

The spread of farming across the Mediterranean to Iberia and its role in shaping ancient and modern European genomes *abs# 272*

12:15 PM **Marcos Gallego Llorente**

The Neolithic Revolution developed among geographically adjacent but genetically distinct populations *abs# 273*

Explosive radiations and the genomic basis for speciation

10:30am - 12:30pm Room 7

Chairs: Federica Di Palma & Wilfried Haerty

10:30 AM **Walter Salzburger**

The genomics of adaptive radiation *abs# 274*

11:00 AM **Chris Jiggins**

Shuffling of modular enhancers by adaptive introgression generates convergence and novelty in butterfly patterns *abs# 275*

11:30 AM **Sangeet Lamichhaney**

The genetic basis for beak diversification and adaptive evolution in Darwin's finches
abs# 276

11:45 AM **Ryan York**

Repeated evolution of behavior via polygenic adaptation in Malawi cichlid fish
abs# 277

12:00 PM **Angeles de Cara**

Testing the role of selection and demography in driving a rapid postglacial radiation in the songbird genus *Junco* *abs# 278*

12:15 PM **Giordano Botta**

High resolution populations genomics reveals an extremely complex dynamics of early speciation in Afrotropical malaria vectors. *abs# 279*