

BAPG XVIII Information

Location: Valley Life Sciences Building (VLSB) Floor 2, UC Berkeley, Berkeley CA.

Time: Saturday, November 9, 2019, 9am-5pm

Contact: ajstern@berkeley.edu, rasmus_nielsen@berkeley.edu

Parking: Most affordable paid parking is found at 2450 Durant Ave. Otherwise, free street parking can sometimes be found near the North and South sides of campus.

Tentative schedule

8:30am Check-in / poster setup / breakfast
(Thanks to our sponsors: 23andMe and AncestryDNA!)

9:00am Session 1: Full length talks

Opening remarks

Landen Gozashti (UCSC) - A Systematic Search for Introner Elements

Erin Calfee (Davis) - Admixture and selection in the Africanized honey bee invasion

Greg Owens (Berkeley) - Massive haplotypes underlie ecotypic differentiation in sunflowers

Manuel Lujan (Cal Academy of Sciences) - Population genomics on rare Australian Cycas

10:15am Break

10:30am Session 2: Full length talks

David Gokhman (Stanford) - Reconstructing Denisovan Anatomy Using DNA Methylation Maps

Lesly Lopez Fang (Merced) - Leveraging Both Ancestral and Derived Information to Detect Local Introgression

Chenlu Di (U. Arizona) - The causes of strongly depleted recent adaptation in human disease genes

Saurabh Belsare (UCSF) - Evaluating reference databases for imputation in humans

Luong Nguyen (AncestryDNA) - Highly accurate clustering of AncestryDNA relatives into parental sides

12:00pm Lunch

(Thanks to our sponsors: 23andMe and AncestryDNA!)

12:40pm Session 3: Full length & lightning talks

Kirsten Verster (Berkeley) - Horizontal transfer of cytolethal distending toxin B genes in insects

Kaho Tisthammer (SFSU) - In vivo mutation frequencies and fitness costs of Hepatitis C Virus

QinQin Yu (Berkeley) - Determinants of genetic drift in microbial range expansions

Matt Metzger (Berkeley) - The Evolutionary Trajectory of the Saccharomyces Clade in Response to Pseudomonas Antifungal Pressure

1:30pm Break

1:45pm Session 4: *Lightning talks*

Emilie Richards (Berkeley) - Major stages of vertebrate adaptive radiation are assembled from a disparate spatiotemporal landscape

Michelle Stitzer (Davis) - Transposable elements as deleterious alleles in maize

Kevin Wei (Berkeley) - The theory and practice of measuring broad-range recombination rate from marker selected pools

Nick Altemose (Berkeley) - A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination

Ziyue Gao (Stanford) - Ancient Rome: a genetic crossroads of Europe and the Mediterranean

David Poznik (23andMe) - Identifying human population structure in South Asia, West Asia, and North Africa

Minhui Chen (USC) - Evidence of polygenic adaptation at height-associated loci in mainland Europeans and Sardinians

2:45-5:00pm Poster session & happy hour
(Thanks to our sponsors: 23andMe and AncestryDNA!)

Poster presenters (+lightning talks)

Last name	First name	Institution / company	Title
Abrams	Melanie	UC Berkeley	Unpacking the evolution of an ancient thermotolerance divergence in <i>Saccharomyces</i>
Aguilar Gómez	Diana	UC Berkeley	Population genomics of variegated toad-headed lizard and its adaptation to the colorful sand of the Gobi Desert
Altemose	Nicolas	UC Berkeley	A high-resolution map of non-crossover events reveals impacts of genetic diversity on mammalian meiotic recombination
AlZaben	Faisal	UC Berkeley	Finding the genetic underpinnings of an ancient thermotolerance divergence in yeast
Castaneda	Stuart	SFSU	CpG-creating mutations are costly in much of the HIV genome
Cerca	José	UC Berkeley	Genomics of Convergent Invertebrate Morphology
Chen	Minhui	USC	Evidence of polygenic adaptation at height-associated loci in mainland Europeans and Sardinians
Chintalapati	Manjusha	UC Berkeley	Reconstructing spatio-temporal patterns of admixture in human history using present-day and ancient genomes
Chuong	Julie	Buck Institute/Berkeley	Dissecting the genetic basis of an ancestral cold tolerance trait between <i>Saccharomyces</i> yeast species
Cjivovic	Ivana	Princeton	High-resolution lineage tracking reveals traveling wave of adaptation in laboratory yeast
Fergusson	Ryan	SFSU	Comparison of the Cutaneous Microbial Community Structure on Amphibians Between Regions in North and Central America
Freyman	Will	23andMe	Phased IBD: fast and accurate identity-by-descent inference despite haplotype and phasing errors
Fujito	Naoko	UCSF	Genomic variation and population histories of spotted (<i>Strix occidentalis</i>) and barred (<i>S. varia</i>) owls
Gao	Ziyue	Stanford	Ancient Rome: a genetic crossroads of Europe and the Mediterranean
Gripkey	Hans	UC Davis	Improved tools for genomic DNA library construction of small insects (2019 update)
Hilsabeck	Tyler	Buck Institute/USC	Insulin-Like Signaling and NADPH-oxidase pathways lie upstream of purine metabolism and suggest

			metabolite-centric approach to rescue uric acid-driven decreased lifespan
Karageorgi	Marianna	UC Berkeley	Genetics of adaptation in insects specialized on toxic cardiac glycoside-producing plants
Kolora	Rohit	UC Berkeley	Origins and evolution of longevity in Rockfish
Lei	Li	JGI	Population genomics of <i>Brachypodium hybridum</i>
Matsunaga	Teruyuki	UC Berkeley	Insect odorant receptors tuned to volatile mustard oils
Metzger	Matt	UC Berkeley	The Evolutionary Trajectory of the <i>Saccharomyces</i> Clade in Response to <i>Pseudomonas</i> Antifungal Pressure
Poznik	David	23andMe	Identifying human population structure in South Asia, West Asia, and North Africa
Rauchman	Courtney	UC Berkeley	Selection biases heritability estimation
Richards	Emilie	UC Berkeley	Major stages of vertebrate adaptive radiation are assembled from a disparate spatiotemporal landscape
Rocha	Joana	UC Berkeley	Life in the desert: the genomic history of extreme environment adaptation in North African foxes
Song	Shiya	AncestryDNA	Novel way of building reference panels enables finer resolution of ancestry inference among indigenous people of the Americas
Stern	Aaron	UC Berkeley	Pinpointing selection on genetically-correlated polygenic traits using within-population sequence data
Stokes	Peter	UC Berkeley	Using Ancient and Extant Genome Sequencing to Inform Domestication Dynamics of Sunflower
Svedberg	Jesper	UC Santa Cruz	Inferring Adaptive Introgression using Hidden Markov Models
Tournebize	Remy	UC Berkeley	Using two-loci statistics for inferring the properties of founder events in human history
Turissini	David	AncestryDNA	Novel way of building reference panels enables finer resolution of ancestry inference among indigenous people of the Americas
Stitzer	Michelle	UC Davis	Transposable elements as deleterious alleles in maize
Wei	Kevin	UC Berkeley	The theory and practice of measuring broad-range recombination rate from marker selected pools
Yu	QinQin	UC Berkeley	Determinants of genetic drift in microbial range expansions
Zhang	Wanchang	UC Berkeley	Deciphering the genetic mechanism of phenotypic diversity of the Siamese fighting fish and the speciation & evolutionary history in <i>Betta</i> genus based on whole genome sequencing

Information for presenters

Full length talks: 12 minutes, with 3 minutes afterwards for questions.

Lightning talks: 4 minutes, with 1 minutes afterwards for questions.

We have a very packed schedule, so please please please heed the guidelines for time.

Posters: the poster session will take place in Valley Life Sciences Building Courtyard. Presenters will have the opportunity to set up posters during the breaks/lunch. We will provide easels, posterboard, and other materials for setup. Please make your poster no larger than 36"x48". If it is not too inconvenient, please try to use portrait orientation so we can accommodate as many posters as possible.