

BAY AREA POPULATION GENOMICS XII

Stanford University • May 30, 2015

Schedule of Events

Registration & Light Breakfast in the Courtyard	8:30am-9:25am
Opening Remarks Dmitri Petrov (Department of Biology, Stanford University)	9:25am-9:30am
Paleogenomes illuminate multiple admixture events between polar bears and brown bears James Cahill (UC Santa Cruz)	9:30am-9:50am
Fitness-valley crossing in subdivided populations Michael McLaren (Stanford University)	9:50am-10:10am
The micro-generalist advantage: A simple condition for stable, highly polygenic allele- frequency fluctuations under seasonal selection Meike Wittmann (Stanford University)	10:10am-10:30am
Coffee-Break in the Courtyard	10:30am-11:00am
Cross-disorder analysis of Autism Spectrum Disorder Maude M. David (Stanford University)	11:00am-11:20am
Clustering of DNA shared by descent in present-day Americans reconstructs recent settlement patterns of people in the United States Eunjung (Christine) Han (Ancestry DNA)	11:20am-11:40am
Selection and explosive growth may hamper the performance of rare variant association tests Lawrence Uricchio (UCSF/Stanford University)	11:40am-12:00pm
Lunch in the Courtyard	12:00pm-1:00pm
Hsp90 buffers the phenotypic effects of standing genetic variation but not new mutations Kerry Geiler-Samerotte (NYU)	1:00pm-1:20pm
Pooled ChIP-seq identifies QTLs affecting transcription factor binding and histone modification Ashley Tehranchi (Stanford University)	1:20pm-1:40pm
Keynote • Life in tandem: The Evolution of Gene Regulation in Duplicate Genes Jonathan Pritchard (Stanford University)	1:40pm-2:10pm
Poster Session with Wine, Beer, & Cheese Reception	2:10pm-3:00pm

Registration and Meeting Location: Alway Building M106 & Alway Courtyard

For more information, see the BAPGXII Website: https://stanfordcehg.wordpress.com/2015/05/22/bapgxii/

Poster Session Presenters

Sex-biased genes and temperature-dependent sex determination in the American Alligator **Edward Rice** (Green/Shapiro Labs, UC Santa Cruz)

Tracking the effects of human genetic variation through the gene regulatory cascade **Yang I Li** (Pritchard Lab, Stanford University)

Disentangling sources of selection on exonic transcriptional enhancers

Rachel Agoglia (Fraser Lab, Stanford University)

Environment-Modulated Genetic Adaptation of RNA Editing in Drosophila

Arielle Yablonovitch (Li Lab, Stanford University)

Rapid Adaptation and Low Recombination: A Two Chromosome Model Michael Pearce (Fisher Lab, Stanford University)

Emergence of novel phenotypes in co-evolving biological systems: allelic diversification and dominance at the Self-incompatibility locus in Arabidopsis

Vincent Castric (Nielsen Lab, UC Berkeley)

Pan-genome analysis of Saccharomyces cerevisiae **Giltae Song** (Cherry Lab, Stanford University)

Privacy leaks in genomic data-sharing beacons **Suyash Shringarpure** (Bustamante Lab, Stanford University)