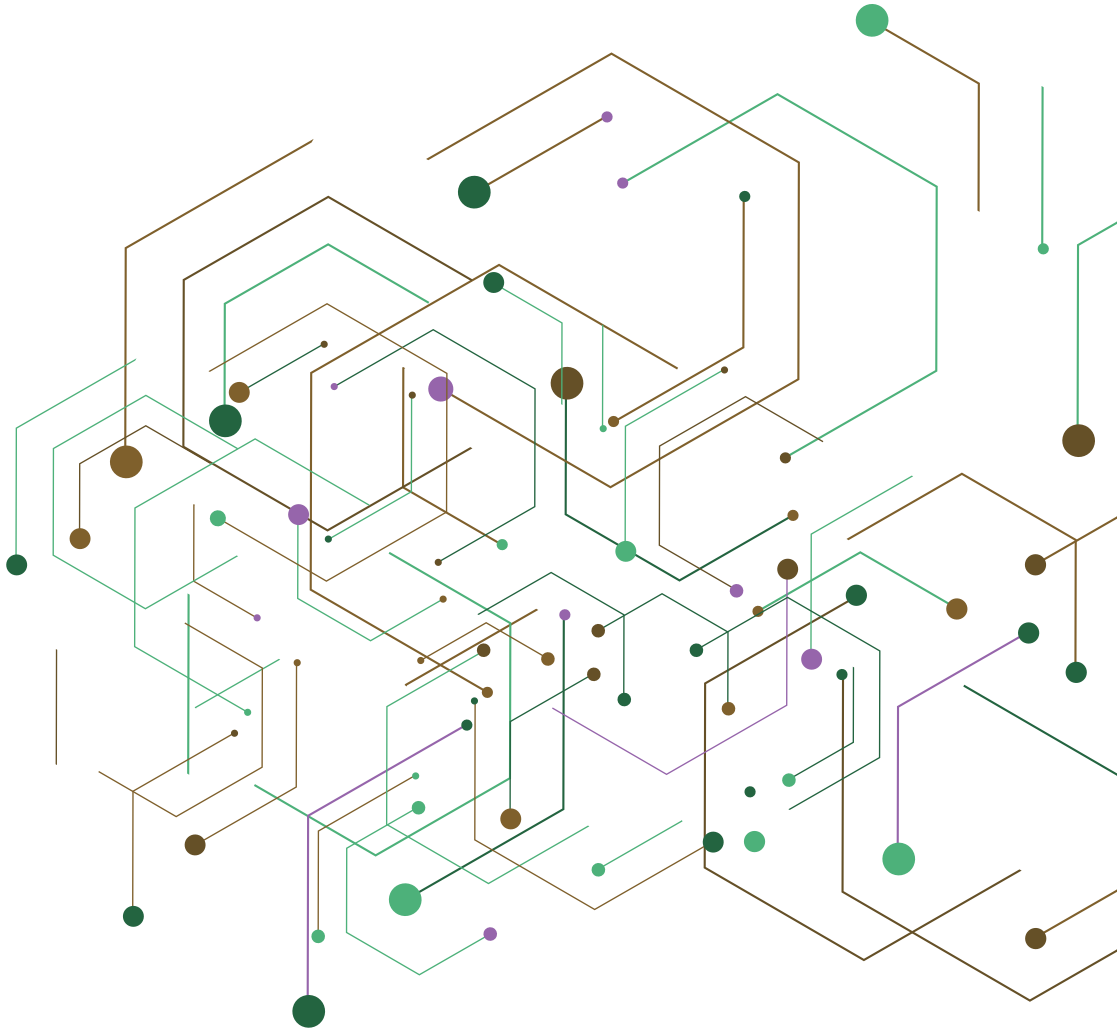# Population, Evolutionary, and Quantitative Genetics Conference

May 13–16, 2018 | Madison, Wisconsin

PROGRAM BOOK

GENETICS

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WELCOME TO #PEQG18!

GSA has long served the community of population, evolutionary, and quantitative geneticists through *GENETICS* and *G3*, advocacy, professional development programs and more. So we are delighted to be able to bring you together at a conference dedicated to promoting cross-disciplinary links between these broad fields.

This is only the second time this meeting has been held, and it's the first as a stand-alone event. The first was part of The Allied Genetics Conference 2016 (TAGC), a multi-community GSA meeting that combined PEQG with six model organism groups. We hope we'll see you again at the next PEQG meeting at TAGC 2020, which will be held April 22–26, 2020 at Gaylord National Resort & Convention Center, Metro Washington DC.

We also know that not everyone who wanted to join us was able to. It's always hard to gauge demand for a new meeting, but we apologize that we underestimated the venue size we would need. Although we were able to negotiate some extra room to accommodate those on the waiting list, please bear with us as we try to make the most of the space. Let me or any other GSA staff member know if you need help or just want to give us some feedback.

Finally, I want to acknowledge the dedicated and thoughtful organizing committee for all the work they put into making this meeting a success. Thank you for your service to the field!

Tracey DePellegrin
Executive Director, Genetics Society of America
Executive Editor, GSA Journals

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GENETICS SOCIETY OF AMERICA

The Genetics Society of America (GSA) is an international scientific society representing more than 5,000 researchers and educators around the world. We work to advance the field and foster the research community. The Society has a deep commitment to supporting the next generation of geneticists, providing professional development opportunities, training, travel grants, and more. We work with our members and partner organizations to communicate the value of genetics and fundamental research to the public and policymakers; we advocate for our scientific community and the vital work they do.

As well as encouraging communication among researchers through conferences, GSA publishes two peer-edited scholarly journals:

GENETICS

GENETICS has been innovating since 1916, publishing high quality original research across the breadth of the field.

G3 Genes|Genomes|Genetics

G3: Genes|Genomes|Genetics is an open access journal that publishes high quality, useful results regardless of perceived impact.

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SCHEDULE OF EVENTS

SUNDAY, May 13		
1:30 p.m. - 5:30 p.m.	***GENETICS* PEER REVIEW TRAINING WORKSHOP** *Pre-registration required*	Assembly Room
5:00 p.m. - 9:00 p.m.	**REGISTRATION OPEN**	2nd Floor
6:45 p.m. - 8:00 p.m.	**WELCOME AND KEYNOTE 1: Jonathan Pritchard**	Capitol Ballroom
8:00 p.m. - 10:00 p.m.	**OPENING MIXER**	University Rooms
10:00 p.m. - 11:00 p.m.	**POSTER SET-UP, GROUP M (Monday)** *Posters can be displayed beginning at 10 p.m. Sunday until 10 p.m. on Monday.*	Madison/ Wisconsin Ballroom
MONDAY, May 14		
7:30 a.m. - 8:45 a.m.	**CONTINENTAL BREAKFAST**	1st and 2nd Floors
8:00 a.m. - 5:00 p.m.	**REGISTRATION**	2nd Floor
9:00 a.m. - 10:30 a.m.	**PLATFORM SESSION 1**	Capitol Ballroom
11:00 a.m. - 1:00 p.m.	**JAMES F. CROW EARLY CAREER RESEARCHER AWARD SESSION**	Capitol Ballroom
1:00 p.m. - 2:30 p.m.	**LUNCH WORKSHOPS** *Limited seating; accommodated on a first come, first served basis*	
	A community-oriented approach to build and support women in science	Senate Room
	Developing your teaching philosophy	Conference Room I
	GENETICS discussion 1	Conference Room II
	Navigating the career decision-making process	Conference Room III
1:00 p.m. - 2:30 p.m.	**BREAK FOR LUNCH** *Conference lunch and seating available on the 1st and 2nd floors*	1st and 2nd Floors
2:30 p.m. - 4:00 p.m.	**PLATFORM SESSION 2**	Capitol Ballroom
4:00 p.m. - 5:00 p.m.	**LIGHTNING TALKS 1**	Capitol Ballroom
5:00 p.m. - 7:00 p.m.	**BREAK FOR DINNER** *Meal not provided*	
7:00 p.m. - 8:00 p.m.	**KEYNOTE 2: Catherine Peichel**	Capitol Ballroom

8:00 p.m. - 10:00 p.m.	**POSTER PRESENTATIONS (Group M)** *8–9 p.m. Even Numbers* *9–10 p.m. Odd Numbers*	Madison/ Wisconsin Ballroom
10:15 p.m. - 11:00 p.m.	**POSTER SET-UP, GROUP T (Tuesday)** *Group T can begin to display their posters beginning at 10:15 p.m. Monday through 10 p.m. Tuesday. Group M should take their posters down at 10 p.m.*	Madison/ Wisconsin Ballroom
TUESDAY, May 15		
7:30 a.m. - 8:45 a.m.	**CONTINENTAL BREAKFAST**	1st and 2nd Floors
8:00 a.m. - 5:00 p.m.	**REGISTRATION**	2nd Floor
9:00 a.m. - 10:30 a.m.	**PLATFORM SESSION 3**	Capitol Ballroom
11:00 a.m. - 1:00 p.m.	**PLATFORM SESSION 4**	Capitol Ballroom
1:00 p.m. - 2:30 p.m.	**LUNCH WORKSHOPS** *Limited seating; accommodated on a first come, first served basis*	
	Publishing Q&A	University Rooms
	Data management for reproducibility and re-usability	Assembly Room
	Looking for a mentor to help you incorporate active learning in classrooms?	Conference Room I
	GENETICS discussion 2	Conference Room II
	Talk science to me: How to start science outreach in your own community	Conference Room III
	GENETICS discussion 3	Conference Room V
	Beyond the scholarly article: Reaching a broad audience through book publishing	Senate Room
1:00 p.m. - 2:30 p.m.	**BREAK FOR LUNCH** *Conference lunch and seating available on the 1st and 2nd floor*	1st and 2nd Floors
2:30 p.m. - 4:00 p.m.	**PLATFORM SESSION 5**	Capitol Ballroom
4:00 p.m. - 5:00 p.m.	**LIGHTNING TALKS 2**	Capitol Ballroom
5:00 p.m. - 7:00 p.m.	**BREAK FOR DINNER** *Meal not provided*	
7:00 p.m. - 8:00 p.m.	**KEYNOTE 3: Trudy Mackay**	Capitol Ballroom

Time	Event	Location
8:00 p.m. - 10:00 p.m.	**POSTER PRESENTATIONS (Group T)** *8-9 p.m. Even Numbers* *9-10 p.m. Odd Numbers*	Madison/ Wisconsin Ballroom
WEDNESDAY, May 16		
7:15 a.m. - 8:15 a.m.	**CONTINENTAL BREAKFAST**	1st and 2nd Floors
8:30 a.m. - 10:00 a.m.	**PLATFORM SESSION 6**	Capitol Ballroom
10:15 a.m. - 11:15 a.m.	**PLATFORM SESSION 7**	Capitol Ballroom
11:15 a.m. - 11:45 a.m.	**AWARD CEREMONY**	Capitol Ballroom
11:45 a.m. - 1:00 p.m.	**SCIENCE SLAM**	Capitol Ballroom
11:45 a.m. - 1:00 p.m.	**LUNCH WORKSHOPS** *limited seating, accommodated on a first come-first served basis*	
	GENETICS discussion 4	Conference Room II
	Careers in publishing	Conference Room III
	Writing scientific papers	Conference Room IV
11:45 a.m. - 1:00 p.m.	**BREAK FOR LUNCH** *Conference lunch and seating available on the 1st and 2nd floors*	1st and 2nd Floors
1:00 p.m. - 4:00 p.m.	**KEYNOTE SESSION 4: Session Chairs**	Capitol Ballroom
1:00 p.m.	**The Aging Proteome: Is Aging Programmed in our Genes?** Gary Churchill	
1:30 p.m.	**Genetics and evolution of hybrid lethality between sympatric species of *Mimulus*** Andrea L. Sweigart	
2:00 p.m.	**Heterochromatin and adaptive evolution** Andrew G. Clark	
2:30 p.m.	**The role of parallel genetic changes for plant mating system shifts - on the genetic basis of a recent loss of self-incompatibility in *Capsella orientalis*** Tanja Slotte	
3:00 p.m.	**Distal expression QTLs: statistical challenges and opportunities** Barbara E. Engelhardt	

3:30 p.m.	**Phenotypic Plasticity in Recombination Frequency** Nadia Singh	
6:30 p.m. - 9:30 p.m.	**MIXER ON LAKE MENDOTA** *Ticketed event* *University of Wisconsin Memorial Union*	Off site
THURSDAY, May 17		
9:00 a.m. - 4:30 p.m.	**NEW FACULTY FORUM** *Pre-registration required*	Assembly Room
12:30 a.m. – 2:00 p.m.	**NEW FACULTY FORUM LUNCH** *Pre-registration required*	Caucus
3:00 p.m. - 4:30 p.m.	**NEW FACULTY FORUM RECEPTION** *Pre-registration required*	Caucus

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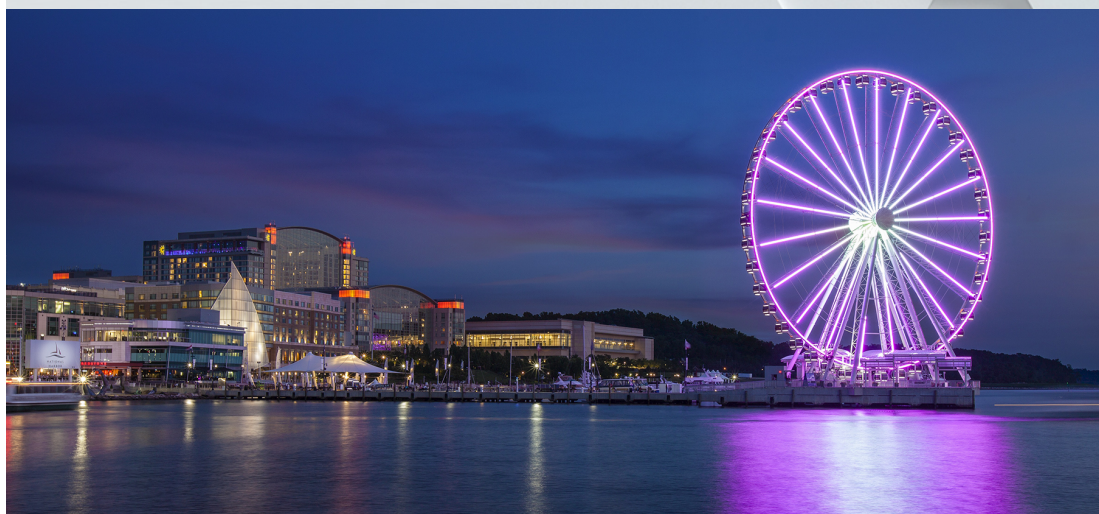
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Badges are required for admission to all sessions. If you lose your badge, please request a replacement at the conference registration desk.

Oral Presenters
All those giving oral presentations in Keynote and Platform sessions must upload and test their talk the day before their presentation in the Capitol Ballroom. Talk upload times are as follows:

Sunday	5:00 p.m. – 6:15 p.m.
	8:15 p.m. – 10:15 p.m.
Monday	7:00 a.m. – 8:30 a.m.
	1:00 p.m. – 2:00 p.m.
	5:00 p.m. – 6:00 p.m.
Tuesday	7:00 a.m. – 8:30 a.m.
	1:00 p.m. – 2:00 p.m.
	5:00 p.m. – 6:00 p.m.

All Lightning Talks must be uploaded no later than 9:00 p.m. on Sunday

Posters – Madison/Wisconsin Ballroom
Poster presentations will be in the Madison/Wisconsin Ballroom on the second floor. The room will be open to registrants from 8 a.m.–11 p.m. on Monday and Tuesday. Authors in **Group M (Monday presentations)** can display their posters beginning Sunday, May 13 at 10:00 p.m. and must remove their posters on Monday, May 14 at 10:00 p.m. Authors in **Group T (Tuesday presentations)** can display their posters beginning Monday at 10:15 p.m. and must remove their poster on Tuesday at 10:00 p.m.

Authors should be at their posters to present according to the following schedule:

GROUP M

Monday	8:00 p.m. – 9:00 p.m.	Even-numbered posters
	9:00 p.m. – 10:00 p.m.	Odd-numbered posters
	10:00 p.m. – 10:15 p.m.	Remove posters

GROUP T

Tuesday	8:00 p.m. – 9:00 p.m.	Even-numbered posters
	9:00 p.m. – 10:00 p.m.	Odd-numbered posters
	10:00 p.m. – 10:15 p.m.	Remove Posters

All posters must be removed from poster boards **no later than 10:15 p.m. on Tuesday, May 15.** After that time, remaining posters will be removed and recycled. Posters may only be removed by their authors. Posters that are not collected may not be taken by someone who is not an author on that poster.

Mobile App
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Registration and T-shirt sales
You can pick up your registration materials and Certificates of Attendance and Participation at the registration desk on the second floor. Conference T-shirts can be purchased at the desk and during poster sessions. The registration desk is open during the following times:

Sunday	5:00 p.m. – 9:00 p.m.
Monday	9:00 a.m. – 5:00 p.m.
Tuesday	9:00 a.m. – 5:00 p.m.

Social Media/Photo/Video Policy
Live tweeting of presentations is allowed unless the speaker explicitly opts out by stating so at the start of his or her talk. Taking or sharing photos or videos of posters is permitted only with the presenter's consent during the assigned poster session. Taking photos of posters while the presenter is not present is strictly prohibited.

Attendees are asked to be respectful of their colleagues by turning off or muting all mobile devices before entering meeting rooms.

Security/Lost and Found

For all emergencies and lost and found items contact hotel security by dialing 0 from any house phone. The conference registration desk will be able to assist you as well.

Meals

A continental breakfast and box lunch Monday through Wednesday are included with your registration. Seating will be available on the first floor in the Assembly, Caucus, and Senate rooms. There will also be seating available in the University and Conference rooms on the 2nd floor. You will be free for dinner each day. The Concourse Hotel is in the center of everything, so there are many restaurants for all budgets within walking distance. The hotel concierge can help you find just what you want. But don't forget to come back for the Keynote and Poster sessions. There will be a cash bar available during the posters on Monday and Tuesday night.

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Self-parking is available for hotel guests on a complimentary basis.

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A private room for nursing mothers is located on the third floor of the hotel. To access the room, which is provided compliments of the hotel, please go to the hotel front desk and sign out the key. The room has a full bathroom and refrigerator. Please note that parents and guardians are responsible for providing infant care supplies. The Lactation Room is unsupervised and the Genetics Society of America is not responsible for any accidents or injuries that may occur.

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screen any of the childcare services and assumes no responsibility with respect to these services and accepts no liabilities.

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Children must be accompanied by a parent or guardian at all times. Under no circumstances are children under the age of 18 allowed in the poster area during set-up and dismantle times.

Code of Conduct

GSA expects attendees and exhibitors to respect each other, GSA staff, and hotel staff, and to behave in a courteous fashion. Attendees should adhere to common sense rules for public behavior, personal interaction, common courtesy, and respect for private property. Abusive, harassing, or threatening behavior towards any other attendee, GSA staff, or hotel staff will not be tolerated. When at the meeting, immediately report any incidents in which you feel a meeting attendee is abusive, insulting, intimidating, bothersome, or acting in an unsafe or illegal manner at the meeting registration desk or to Suzy Brown at sbrown@genetics-gsa.org. Please contact: society@genetics-gsa.org if you need to file a formal complaint.

James F. Crow Early Career Researcher award

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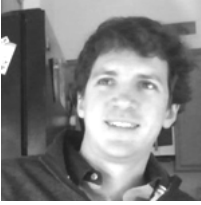
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North Carolina State University

Katherine Xue
University of Washington

The Award honors the legacy of James F. Crow, whose contributions to the field of genetics were impactful and innumerable. Finalists will present their research in the Crow Award session at the conference, and the overall winner will be selected by the keynote speakers.

Help ensure the sustainability of this community award by contributing to the Crow Award Fund. Visit the conference website to learn more: **conferences.genetics-gsa.org/peqg/2018/conference-and-travel-awards**

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Genetics Society of America

KEYNOTE, PLATFORM, LIGHTNING SESSIONS

2nd Floor, Capitol Ballroom

Sunday, May 13
7:00 p.m. – 8:00 p.m.

Keynote 1: Jonathan Pritchard

7:00 Omnigenic Architecture of Human Complex Traits. **Jonathan Pritchard**

Monday, May 14
9:00 a.m. – 10:30 a.m.

Platform Session 1

1 - 9:00   PacBio genome sequencing reveals rampant structural mutation in the malaria parasite. **Emily Ebel**

2 - 9:15   Deep taxon sampling and epigenetic profiling reveal the evolutionary dynamics of nematode orphan genes. **Ralf Sommer**

3 - 9:30   Cytonuclear coordination and evolution in allotetraploid wheat. **Joel Sharbrough**

4 - 9:45   Hostile genomic takeover by transposable elements in the Strawberry poison frog. **Rebekah Rogers**

5 - 10:00   The X chromosome of the German cockroach, *Blattella germanica*, is homologous to a fly X chromosome despite 400 million years divergence. **Richard Meisel**

6 - 10:15   piRNA-mediated silencing of an invading TE evolves rapidly through abundant beneficial *de novo* mutations. **Shuo Zhang**

Monday, May 14
11:00 a.m. – 1:00 p.m.

James F. Crow Early Career Researcher Award Session

7 - 11:00   A mechanistic model of assortative mating in a hybrid population. **Amy Goldberg**

8 - 11:20   Detecting polygenic adaptation in maize. **Emily Josephs**

9 - 11:40   Population genetic models for highly polygenic disease. **Jeremy Berg**

10 - 12:00   Evolutionary dynamics of influenza across spatiotemporal scales. **Katherine Xue**

11 - 12:20   Intra-patient evolutionary dynamics of HIV drug resistance evolution in time and space. **Alison Feder**

12 - 12:40   Genetic variation at a conserved non-coding element contributes to microhabitat-associated behavioral differentiation in Malawi African cichlid fishes. **Emily Moore**

Monday, May 14
2:30 p.m. – 4:00 p.m.

Platform Session 2

Notes

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13 - 2:30   Dissecting complex life-history trait in *Arabidopsis thaliana* using extremely large segregating population. **Wei Yuan**

14 - 2:45   GWAS reveals antagonistic pleiotropy, polygenic adaptation and fluctuating selection within a natural population. **John Kelly**

15 - 3:00   Patterns of genetic variation at the *FLO11* locus suggest a form of kin recognition in the yeast, *Saccharomyces cerevisiae*. **Helen Murphy**

16 - 3:15   Genetic dissection of chromatin accessibility and transcript abundance underlying ground state pluripotency in mouse embryonic stem cells. **Steven Munger**

17 - 3:30   Modeling ancestry-dependent phenotypic variance accurately corrects for population structure and detects variance effects. **Shaila Musharoff**

18 - 3:45   A mitochondrial-nuclear interaction compromises immune function and reveals life-history tradeoffs in females. **Kristi Montooth**

Monday, May 14
4:00 p.m. – 5:00 p.m.

Lightning Talks 1

130M- 4:00   Uncovering the genotype-phenotype-fitness map of microbes adapting to novel environments. **Grant Kinsler**

394M- 4:05   The potential of regularized regression to provide more accurate multivariate selection estimates. **Jacqueline Sztepanacz**

318M- 4:10   The genomic and molecular basis of rapid and polygenic response to selection for long leg length in mice. **Yingguang Frank Chan**

368M- 4:15   Gene, environment and cellular interctions underlying behavioral variance and their relation to fitness in a long-term *Caenorhabditis elegans* evolution experiment. **Luke Noble**

75M- 4:20   Gene expression drives the evolution of dominance. **Kirk Lohmueller**

98M- 4:25   The unreasonable effectiveness of population genetic inference via image recognition. **Daniel Schrider**

56M- 4:30   Methods for detecting selection in admixed populations. **Erin Calfee**

390M- 4:35   Population complexity trumps model complexity in understanding trait variation. **Mark Sterken**

182M-4:40 Selection minimizes introresession around incmopatabilitie and regions under strong linked selection in Capsella. **Yaniv Brandvain**

171M-4:45 To TE, or not to TE, that is the question: transposable element dynamics in hybrid and naïve genomes. **Caiti Smukowski**

Monday, May 14
7:00 p.m. – 8:00 p.m.

Keynote 2: Catherine Peichel

7:00 Genetics of Adaptation in Sticklebacks

Tuesday, May 15
9:00 a.m. – 10:30 a.m.

Platform Session 3

19 - 9:00   The evolution of locally adaptive seasonal camouflage in snowshoe hares. **Matthew Jones**

20 - 9:15   Speciation genes are more likely to have discordant gene trees. **Richard Wang**

21 - 9:30   Speciation, sex chromosomes, and the sensitivity of spermatogenesis. **Erica Larson**

22 - 9:45   The snowball effect requires simple epistasis. **Ricardo Azevedo**

23 - 10:00   The optimal mating distance resulting from heterosis and genetic incompatibility. **Xinzhu Wei**

24 - 10:15   Population genetic tests for the direction and relative timing of introgression. **Mark Hibbins**

Tuesday, May 15
11:00 a.m. – 1:00 p.m.

Platform Session 4

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25 - 11:00   Tracking short-term evolution in a pedigreed wild population. **Nancy Chen**

26 - 11:15   Massive variation of short tandem repeats with functional consequences across strains of *Arabidopsis thaliana*. **Maximilian Press**

27 - 11:30   Linked genetic variation and not genome structure causes widespread differential expression associated with chromosomal inversions. **Russ Corbett-Detig**

28 - 11:45   How brown rats adapted to life in NYC's concrete jungle. **Arbel Harpak**

29 - 12:00   Representing population structure with effective migration surfaces. **John Novembre**

30 - 12:15   Detection of shared balancing selection in the absence of trans-species polymorphism. **Xiaoheng Cheng**

31 - 12:30   Direct estimation of mutation rates in owl monkeys shows that life history is the main determinant of rate variation in primates. **Gregg Thomas**

32 - 12:45   The genomics of conflict: X-chromosome drive in the fly *Drosophila neotestacea*. **Kelly Dyer**

Notes

Tuesday, May 15
2:30 p.m. – 4:00 p.m.

Platform Session 5

33 - 2:30   The effect of strong purifying selection on mutational trajectories and genetic diversity. **Ivana Cvijovic**

34 - 2:45   A population genetic interpretation of GWAS findings for human quantitative traits. **Yuval Simons**

35 - 3:00   The polygenic basis of an ancient divergence in yeast thermotolerance. **Carly Weiss**

36 - 3:15   Detecting signatures of convergent adaptation in population genomic data. **Kristin Lee**

37 - 3:30   Selfing can facilitate transitions between pollination syndromes. **Carolyn Wessinger**

38 - 3:45   A temporal signal of linked selection. **Vincent Buffalo**

Tuesday, May 15
4:00 p.m. – 5:00 p.m.

Lightning Talks 2

376T- 4:00   A phylogenetic analysis of the *Drosophila* metabolome. **Daniel Promislow**

267T- 4:05   Population genetics of meiotic drive and its suppression. **Carl Veller**

302T- 4:10   Comprehensive identification of *cis*-regulatory variants in yeast promoters. **Frank Albert**

417T- 4:15   A Bayesian approach to quantitative genetics for high-dimensional traits. **Daniel Runcie**

62T- 4:20   Genome-wide characterization of differences in mutation fitness effects between populations. **Ryan Gutenkunst**

92T- 4:25   A map of highly constrained coding regions in the human genome. **Aaron Quinlan**

275T- 4:30   Convergent regressive evolution of the eye and the identification of eye-specific regulatory elements. **Nathan Clark**

331T- 4:35   Pleiotropic genetic effects percolate through underlying networks of traits. **Kerry Geiler-Samerotte**

415T- 4:40   Variance QTLs as a means to identify epistatic interactions in genome-wide association studies. **Andrew Marderstein**

90T - 4:45   Combining population genomics and fitness QTL to identify the genetics of local adaptation in *Arabidopsis thaliana*. **Nicholas Price**

Tuesday, May 15
7:00 p.m. – 8:00 p.m.

Keynote Session 3: Trudy Mackay

7:00 Context-Dependent Effects of Alleles Affecting Genetic Variation of Quantitative Traits

Wednesday, May 16
8:30 a.m. – 10:00 a.m.

Platform Session 6

39 - 8:30   Selection against LTR retrotransposons is balanced by locally adapted transposable element alleles in *Arabidopsis thaliana*. **Michelle Stitzer**

40 - 8:45   Identifying the molecular basis of convergent adaptation to herbivorous diets in mammals. **Wynn Meyer**

41 - 9:00   Understanding Adaptation and Fitness Trade-offs in Yeast. **Yuping Li**

42 - 9:15   Validated SNP for bone strength in laying hens show strong GxE. **Dirk Jan de Koning**

43 - 9:30   The genomic basis of environmental adaptation in house mice. **Michael Nachman**

44 - 9:45   Genetic architecture of parallel adaptation across spatially explicit population samples. **Angela Hancock**

Notes

Wednesday, May 16
10:15 a.m. – 11:15 a.m.

Platform Session 7

45 - 10:15   Periodic variation of mutation rates in bacterial genomes associated with replication timing. **Marcus Dillon**

46 - 10:30   Multi-environment fitness landscapes of a tRNA gene. **Chuan Li**

47 - 10:45   The architecture of an empirical genotype-phenotype map. **Jose Aguilar Rodriguez**

48 - 11:00   Surprising mechanisms underlying evolution in a classic system: Revisiting ADH in *Drosophila*. **Mohammad Siddiq**

Wednesday, May 16
1:00 p.m. – 4:00 p.m.

Keynote Session 4: Session Chairs

1:00 - The Aging Proteome: Is Aging Programmed in our Genes? **Gary Churchill**

1:30 - Genetics and evolution of hybrid lethality between sympatric species of *Mimulus*. **Andrea Sweigart**

2:00 - Heterochromatin and adaptive evolution. **Andrew Clark**

2:30 - The role of parallel genetic changes for plant mating system shifts - on the genetic basis of a recent loss of self-incompatibility in *Capsella orientalis*. **Tanja Slotte**

3:00 - Distal expression QTLs: statistical challenges and opportunities. **Barbara Engelhardt**

3:30 - Phenotypic Plasticity in Recombination Frequency. **Nadia Singh**

Notes

MONDAY POSTER PRESENTATIONS

Population Genomics

49M Severe population crashes decrease genome-wide diversity in an already genetically depauperate insular mammal. **Nicole Adams**

50M The effect of spatially varying selection on transposable element insertions in Drosophila. **Jeffrey Adrion**

51M Predicting the selective importance of genes in Drosophila melanogaster by simultaneous modeling of DNA sequence features, expression level, biological function and pathway features. **Hosseinali Asgharian**

52M Seasonal Selection across a Fine Temporal Timescale. **Alyssa Bangerter**

53M CODIS loci STR's could contain more information than previously assumed. **Mayra Banuelos**

54M Population genetic structure of a UK *Daphnia pulex* meta-population using whole genome resequencing. **Karen Barnard-Kubow**

55M Genome-wide markers reveal a complex evolutionary history involving divergence and asymmetric patterns of introgression in the Abert's squirrel (*Sciurus aberti*) species group. **Jeremy Bono**

56M Methods for detecting selection in admixed populations. **Erin Calfee**

57M Epigenetic regulation of aging in *Drosophila melanogaster*. **Qichuan Chen**

58M Inference of Admixture for Cattle with Complex Ancestry. **Tamar Crum**

59M Population genomic signatures of selection during freshwater invasions by a saline copepod (*Eurytemora affinis*). **Tiago da Silva Ribeiro**

60M Extensive negative linkage disequilibrium between amino acid changing variants suggests interference among deleterious mutations in the human genome. **Jesse Garcia**

61M Array design and SNP ascertainment bias. **Johannes Geibel**

63M Inferring global population structure and genetic diversity in wild house mice (*Mus musculus*) using a genome-wide SNP array. **Jonathan Hughes**

64M Population Genetic Analysis of Autophagy and Phagocytosis Genes in *Drosophila melanogaster* and *simulans*. **Joo Hyun Im**

65M Identifying recurrent mutations from unphased population-level sequencing data. **Kelsey Johnson**

66M Estimating the contemporary effective population size of *Hypomesus transpacificus* using RAD sequence data. **Shannon Joslin**

67M Limited evidence for selection at linked sites in wild populations of *Mus musculus domesticus*. **Michael Kartje**

68M Two opposite haplotypes that regulate *FADS1* expression underwent recurrent diet-dependent adaptation in worldwide human populations. **Alon Keinan**

69M Fine-scale localization of sites under balancing selection. **Evan Koch**

70M From soil to stein; population genomics of wild and domesticated lineages of the Lager-brewing ancestor; *Saccharomyces eubayanus*. **Quinn Langdon**

71M Impacts of recurrent hitchhiking on divergence and demographic inference in *Drosophila*. **Jeremy Lange**

72M Conserved patterns of somatic mutations in human blood cells. **Luther Liggett**

73M Phenotypically wild barley plants show evidence of extensive introgression from cultivated barley. **Chaochih Liu**

74M Human prehistoric demography revealed by polymorphic pattern of CpG transitions. **Xiaoming Liu**

75M Gene expression drives the evolution of dominance. **Kirk Lohmueller**

76M Effects of unsampled "ghost" populations on estimation of evolutionary history. **Melissa Lynch**

77M *Brassica oleracea*: The dog of the plant world. **Makenzie Mabry**

78M The evolutionary history and population structure of the *Drosophila nasuta* clade. **Dat Mai**

79M Long-Term Population Dynamics of 'Candidatus *Accumulibacter phosphatis'* in Enhanced Biological Phosphorus Removal Sequencing-Batch Reactors. **Elizabeth McDaniel**

80M The ash dieback invasion of Europe highlights huge adaptive potential of the causal fungus, *Hymenoscyphus fraxineus*. **Mark McMullan**

81M Estimating the prevalence of Wolbachia across arthropod and nematode taxa. **PALOMA MEDINA**

82M Population genomics of copy number variation in a natural population of maize wild relative teosinte. **Wenbin Mei**

83M Understanding the Hidden Complexity of Latin American Population Isolates. **Jazlyn Mooney**

84M Estimating the relative contribution of deleterious and neutral SNPs to agronomic phenotypes. **Peter Morrell**

85M Inter-species variation in the gut microbiota controls gene regulation in primates. **Amanda Muehlbauer**

86M Localizing and classifying adaptive targets with trend filtered regression. **Mehreen Mughal**

87M Contrasting the genomic consequences of precipitously declining local populations of Florida scrub-jays. **Tram Nguyen**

88M Recent environmental adaptation in an invasive species: house mice in the Americas. **Megan Phifer-Rixey**

89M Antiviral enzyme APOBEC3G introduces clustered inherited mutations that fuel adaptation in human populations. **Yishay Pinto**

91M Disambiguating second degree relationship types using identity by descent sharing to third party samples. **Ying Qiao**

93M   The genomics of invasion: characterization of the red lionfish from its native and introduced range. **Emily Reed**

94M   Population genomic analyses of meiotic drive in a species pair. **Josephine Reinhardt**

95M   Demographic history influences levels of deleterious variation and explains patterns of inbreeding depression in Channel Island foxes and Isle Royale wolves. **Jacqueline Robinson**

96M   Fine-scale resolution and analysis of inbreeding tracts in domestic dogs. **Aaron Sams**

97M   *De novo* gene conversion events are enriched in sample-specific low heterozygosity regions. **Jens Sannerud**

98M   The unreasonable effectiveness of population genetic inference via image recognition. **Daniel Schrider**

99M   Rapid, phase-free detection of long identical by descent segments enables fast relationship classification. **Daniel Seidman**

100M   Population genomics of a monitored sea anemone (*Condylactis gigantea*) in Florida, U.S. **Nancy Sheridan**

101M   The Demographic and Migratory History of *Mycobacterium tuberculosis* in Canadian Northwest Territories. **Abigail Shockey**

102M   Male infertility is responsible for nearly half of the extinction observed in the mouse Collaborative Cross. **John Shorter**

103M   Minimal effects of neo-Y chromosomes on transcriptomes of house flies in spite of evidence that selection across ecological habitats maintains stable polygenic sex determination. **Jae Hak Son**

104M   Discovery of *Drosophila melanogaster* from Wild African Environments and Genomic Insights into Species History. **Quentin Sprengelmeyer**

105M   Identification of *De novo* genes created by chromosomal rearrangements in *Drosophila yakuba*. **Nicholas Stewart**

106M   African ROH Drive Enrichment of Deleterious Alleles in a Sample of Admixed Individuals. **Zachary Szpiech**

107T   Unprogrammed number

108M   Clustering of non-synonymous substitutions provides evidence for widespread epistasis and convergence in protein evolution. **Andrew Taverner**

109M   Transfer RNA genes experience exceptionally elevated mutation rates. **Bryan Thornlow**

110M   Efficient pedigree recording for fast population genetics simulation. **Kevin Thornton**

111M   Patterns of neutral genetic diversity under background selection are impacted across time by population demography. **Raul Torres**

112M   space: a tool for dynamic pca exploration. **David Turissini**

113M   Inference of demographic history provides insight into domestication and morphotype diversification in *Brassica oleracea*. **Sarah Turner**

114M   Discovering the molecular basis of polygenic local adaptation in the large Scots pine genome. **Jaakko Tyrmi**

115M Inference of selective sweep parameters through supervised learning. **Ian Vasconcellos Caldas**

116M Phylogenetic analysis and the impact of heavy metal contaminants on wild isolates of the ubiquitous ectomycorrhizal species *Cenococcum geophilum*. **Jessica Velez**

117M Haplotype-Based Method for Analyzing Ancient DNA. **Shamam Waldman**

118M Selective Sweeps in an Endemic *Drosophila serrata* Population: Insights from 110 Genomes . **Yiguan Wang**

119M Divergent fine-scale recombination landscapes between populations of threespine stickleback fish. **Michael White**

120M Mitochondrial heteroplasmy through the lens of population phylogenetics. **Peter Wilton**

121M Probing the genomic signatures of insecticide resistance in the malaria vector *Anopheles gambiae* via deep learning. **Alexander Xue**

122M Characterizing adaptive Neanderthal introgression using ancient and modern population genomic data. **Sivan Yair**

123M Mito-nuclear ancestry interactions contribute to mitochondrial DNA copy number variation in admixed populations. **Arslan Zaidi**

124M An evolutionary history of the *C. elegans* species. **Stefan Zdraljevic**

125M The evolutionary history of supergene mimicry in *Papilio* swallowtail butterflies. **Wei Zhang**

Experimental Evolution

126M Maintenance and evolutionary potential of antibiotic resistance in a long-term experiment with *E. coli*. **Kyle Card**

127M Impact of ploidy on pathogenesis depends on host immune status. **Meleah Hickman**

128M Experimental evolution of collective action despite genetic conflict and free riding in a bacterial biofilm. **Neal Jahren**

129M Transcriptome evolution of a fungal plant pathogen using an experimental evolution approach. **Arthur JALLET**

130M Uncovering the genotype-phenotype-fitness map of microbes adapting to novel environments. **Grant Kinsler**

131M Drift robustness and the evolution of genome architecture in small populations. **Thomas LaBar**

132M Host-virus genome coevolution in laboratory populations of yeast. **Gregory Lang**

133M Single cell copy number variant detection reveals the dynamics of adaptation. **Stephanie Lauer**

134M Investigating the role of population history and environment on germline mitochondrial mutagenesis. **Tess Leuthner**

135M   Invade and conquer: the spread of *wtf* meiotic drivers in yeast. **Jose Lopez Hernandez**

136M   Sign of selection on mutation rate modifiers depends on population size. **Yevgeniy Raynes**

137M   Dynamics of second order lineage competition revealed by recursive lineage tracking. **José Rojas Echenique Rojas Echenique**

138M   Tempo, mode, and fitness effects of mutation in *Caenorhabditis elegans* over 400 generations of minimal selection. **Ayush Shekhar Saxena**

139M   Effects of relaxed selection on experimentally evolved populations of *Drosophila melanogaster*. **Parvin Shahrestani**

140M   Dormancy constrains the rate and direction of adaptive evolution. **William Shoemaker**

141M   Adaptation of *Mycobacterium tuberculosis* during biofilm growth. **Tracy Smith**

142M   High accuracy haplotype-derived allele frequencies from ultra-low coverage pool-seq samples. **Susanne Tilk**

143M   Evolution in action: Understanding the phenotypes responsible for adaptation of the *C. elegans* reference strain N2 to its lab environment. **Yuehui Zhao**

Genome Evolution

144M   Determining genomic signatures of sexual selection utilizing sex hormone response elements. **Andrew Anderson**

145M   Simulating the role of L1 retrotransposons in the evolving cancer genome. **Joel Atallah**

146M   Relaxed purifying selection and family-specific transposition bursts drive transposable element dynamics following auto-polyploidization in *Arabidopsis arenosa*. **Pierre Baduel**

147M   The effects of pathogen emergence on the genome of *Mycobacterium abscessus*. **Lindsey Bohr**

148M   A "natural" mutation accumulation experiment in laboratory mouse lines provides insight into mutational processes of repetitive sequences. **Emily Brown**

149M   Abundant genome structure variation shapes heritable phenotypic variation in *Drosophila*. **Mahul Chakraborty**

150M   Genomic survey of sex determination systems in chichlids reveals an evolutionary hot-spot. **Ashley Elias**

151M   Nanopore sequencing to characterize natural variation in *Drosophila melanogaster* repeat content. **Christopher Ellison**

152M   Evolution of expression level and gene dosage following Whole-Genome Duplications in *Paramecium*. **Jean-Francois Pierre Gout**

153M   Sex Chromosome Dosage Compensation in the Monarch Butterfly. **Liuqi Gu**

154M   The Genome of the mushroom-feeding fly, *Drosophila innubila*, adapting to parasites and toxin exposure. **Tom Hill**

155M Chromosomal rearrangements during turtle evolution altered the synteny of genes involved in vertebrate sex determination. **LingSze Lee**

156M Identification and visualization of lineage-specific genomic rearrangements with R. **Doro Lindtke**

157M Characterization of a Genus-Specific Unidentified Open Reading Frame Found within the Mitochondrial Genome of *Fusarium*. **Michael MacKillop**

158M Effecs of reproductive mode and ploidy level on repetitive element evolution. **Kyle McElroy**

159M Double insertion of transposable elements provides a substrate for the evolution of satellite DNA. **Michael McGurk**

160M Effects of sex-linked variation and paternal age on recombination rate in house mice. **Andrew Morgan**

161M Properties of sex-biased gene expression in the absence of sex chromosomes. **Jane Pascar**

162M Identifying sequence heteroplasmy across entire organellar genomes of *Daucus carota* using whole genome sequence data. **Adam Ramsey**

163M Of evolutionary tuning knobs: Microsatellites as engines of adaptive evolution in common sunflower. **Chathurani Ranathunge**

164M Deep taxon sampling reveals the evolutionary dynamics of novel gene families in *Pristionchus* nematodes. **Christian Rödelsperger**

165M Transposon insertional mutagenesis in *Saccharomyces uvarum* reveals trans-acting effects influencing species dependent essential genes. **Monica Sanchez**

166M Functional parallels between programmed DNA loss in sea lamprey and Polycomb-mediated silencing. **Cody Saraceno**

167M The genome-wide rate and spectrum of spontaneous mutations differs between haploid and diploid yeast. **Nathaniel Sharp**

168M Evolution of the chromatin landscape across the young threepine stickleback Y chromosome. **Daniel Shaw**

169M Evolutiuon of X chromosome inactivation profiles in mammals. **Andrea Slavney**

170M The Sea Lamprey (*Petromyzon marinus*) Genome Provides Deep Evolutionary Perspectives on Genome Reprogramming and Stability. **Jeramiah Smith**

171M To TE, or not to TE, that is the question: transposable element dynamics in hybrid and naïve genomes. **Caiti Smukowski**

172M Methods for statistical inference of adaptive mutations, genes, and biological pathways. **Lauren Sugden**

173M Transcriptome turnover during organ evolution. **Ammon Thompson**

174M Integrative Cytogenetics of the Sea Lamprey Chromosome Elimination. **Vladimir Timoshevskiy**

175M Copy number and expression variation in ampliconic genes on the Y chromosomes in humans and other great apes. **Rahulsimham Vegesna**

176M Comparative genomic analysis of programmed DNA elimination in lamprey. **Courtney Waterbury**

177M Rapid genome shrinkage in a self-fertile nematode reveals sperm competition proteins. **Da Yin**

Speciation

178M   Female x male postcopulatory interactions and the evolution of gametic incompatibilities. **Yasir Ahmed**

179M   Simulations and genomic data from hybridizing haplodiploids reveal exceptionally heterogeneous genetic differentiation. **Emily Bendall**

180M   The genomics of behavioral evolution and speciation in the *Drosophila athabasca* species complex. **Ryan Bracewell**

181M   The molecular evolution of pheromone communication and reproductive isolation in orchid bees. **Philipp Brand**

182M   Selection minimizes introression around incmopatabilitie and regions under strong linked selection in *Capsella*. **Yaniv Brandvain**

183M   High inter- and intraspecific turnover of heterochromatin-associated repeats in great apes. **Monika Cechova**

184M   *Prdm9*-controlled meiotic chromosome interactions in hybrids between closely related mouse subspecies. **Jiri Forejt**

185M   Fine-scale ancestry switching across the genomes of wild hybrid mice. **Megan Frayer**

186M   Correlation and constraint of self and interspecific incompatibility across the range of Texas *Phlox*. **Robin Hopkins**

187M   Pairwise hybrid incompatibilities dominate allopatric speciation for a simple biophysical model of development. **Bhavin Khatri**

188M   Cytoplasmic-nuclear incompatibility between wild-isolates of *Caenorhabditis nouraguensis*. **Piero Lamelza**

189M   Developing *Drosophila melanogaster* as a model for the genetic basis of early-stage reproductive isolation. **Matthew Lollar**

190M   Maintenance of reproductive isolation in sympatric *Mimulus* species. **Samuel Mantel**

191M   The role of hybridization during ecological divergence of southwestern white pine (*Pinus strobiformis*) and limber pine (*P. flexilis*). **Mitra Menon**

192M   Caught in the act? Speciation, divergence and admixture in wild tomatoes. **Laura Rose**

193M   Fitness benefits of paternal mitochondrial transmission in intra-species hybrids. **Joseph Ross**

194M   Investigating hybrid seed lethality between closely related subspecies within the *Mimulus tilingii* complex. **Gabrielle Sandstedt**

195M   The genetic and genomic basis of species divergence. **Allison Schloop**

196M   Using genome data to test the proposed hybrid origin of the bear macaque. **Laurie Stevison**

197M   Male fragility and the genetics of sex-specific hybrid incompatibility in the intertidal copepod *Tigriopus californicus*. **Eric Watson**

198M   Genetic Architecture of Hybrid Male Sterility in the Mouse. **Samuel Widmayer**

Education Initiatives

199M   Tracking the trends in white nationalist misappropriation of population genetics research. **Jedidiah Carlson**

Adaptation and Ecological Genetics

200M   Evidence that genotype-by-temperature interactions maintain polygenic sex determination in the housefly. **Kiran Adhikari**

201M   The genetic basis of morphological and behavioral island syndrome traits in deer mice. **Felix Baier**

202M   Parallel adaptation in two co-distributed species along a latitudinal cline. **Mallory Ballinger**

203M   Predation induced adaptation in *Daphnia* populations across time and space. **Doerthe Becker**

204M   Expanding functional horizons or evolutionary combat? Evaluating drivers of the rapid evolution of bag of marbles in Drosophila. **Jaclyn Bubnell**

205M   Genomic basis of adaptive island dwarfism in Boa constrictor snakes. **Daren Card**

206M   Does historical admixture predict patterns of introgression in a contemporary hybrid zone? A comparison of recent and ancient admixture in *Lycaeides* butterflies. **Samridhi Chaturvedi**

207M   Temperature adaptation of Arabidopsis thaliana rosette growth. **Pieter Clauw**

208M   Nematode sampling across the Hawaiian Islands reveals niche preferences for *C. elegans* and a new *Caenorhabditis* species. **Tim Crombie**

209M   The relative importance of phenotypic plasticity, trans-generational effects and selection in heat shock responses of the cactophilic *Drosophila mojavensis*. **Fernando Diaz**

210M   Evolutionary Adaptation at Ecological Time Scales: Seasonal Allele Frequency Changes among Microhabitats of the Killifish, *Fundulus heteroclitus*. **Moritz Ehrlich**

211M   Hybrid swarm-based association mapping and evolution of ovarian diapause in *Drosophila melanogaster*. **Priscilla Erickson**

212M   Genetics of parallel leaf shape evolution in the *Mimulus guttatus* species complex. **Kathleen Ferris**

213M   Adaptation of commensal gut bacteria in the human microbiome. **Nandita Garud**

214M   Population genomics of experimental transplants identifies the genetic basis of adaptation in Mexican maize landraces. **Daniel Gates**

215M   Host genetic control of the microbiome in wild primates. **Laura Grieneisen**

216M   Effect of gut microbiota on α-amanitin tolerance in mycophagous *Drosophila*. **Logan Griffin**

217M   Systems genetics of rice adaptation to drought stress. **Simon Groen**

218M   Predator-induced transgenerational plasticity is mediated by underlying changes in gene expression and methylation. **Nicky Hales**

219M Evolution of gene expression and plasticity in parallel cold-adapted *Drosophila* populations. **Yuheng Huang**

220M Deleterious variants and gene by environment interactions in *Zea mays*. **Asher Hudson**

221M The molecular basis of a difference in expression of a prostate-specific gene between humans and chimpanzees, and its relevance for sexual selection in hominids. **Michael Jensen-Seaman**

222M Experimental natural selection of big bluestem grass ecotypes across the Great Plains' climate gradient. **Loretta Johnson**

223M Adaptation to cadmium protects the germline from cadmium-induced mutations. **Nathan Keith**

224M A pilot study of genetic structure of *Porphyra umbilicalis* KÜTZING in the Gulf of Maine using SNP markers from RNA-Seq. **Anita Klein**

225M Eukaryotic acquisition of a bacterial operon identified through comprehensive comparative genomics in the yeast subphylum. **Jacek Kominek**

226M Environmental association in barley landraces: Identifying the genetic basis of low temperature and drought tolerance. **Li Lei**

227M The effects of oxidative stress on *Tigriopus californicus* sex-specific gene expression revealed by single individual RNA-seq. **Ning Li**

228M Mitochondrial-encoded genes contribute to thermal divergence between *Saccharomyces* species. **Xueying Li**

229M The signature of two centuries of anthropogenic change in genomes of Iberian *Arabidopsis thaliana*. **Lua Lopez Perez**

230M Divergent patterns of copy number variation in natural populations of house mice (*Mus musculus domesticus*) along an environmental gradient. **Katya Mack**

231M Genetic Architecture of Pollution Resistance in Parallel Populations of Killifish. **Jeffrey Miller**

232M Identification of isoforms and expression profile of Dmrt1 in the painted turtle, Chrysemys picta. **Beatriz Akemi Mizoguchi**

233M Divergence and convergence in Yellowstone monkeyflowers: familiar phenotypes with a new genomic basis. **Thom Nelson**

234M The adaptive landscapes of Transposable elements in grasses. **Jason Pienaar**

235M Rapid evolution and the genomic consequences of selection against interspecific mating. **Martha Reiskind**

236M The genetic basis of gut evolution across trophic levels in Malawi cichlid fish. **Reade Roberts**

318M The genomic and molecular basis of rapid and polygenic response to selection for long leg length in mice. **Yingguang Frank Chan**

368M Gene, environment and cellular interactions underlying behavioral variance and their relation to fitness in a long-term *Caenorhabditis elegans* evolution experiment. **Luke Noble**

390M Population complexity trumps model complexity in understanding trait variation. **Mark Sterken**

394M The potential of regularized regression to provide more accurate multivariate selection estimates. **Jacqueline Sztepanacz**

TUESDAY POSTER PRESENTATIONS

Adaptation and Ecological Genetics

237T   Temperature effects on Mendelian inheritance in intra-species hybrids. **Joseph Ross**

238T   Local genetic adaptation in United States *Bos taurus* beef cattle. **Troy Rowan**

239T   Analysis of *C. elegans* population dynamics to investigate the ecological significance of aging. **Andrea Scharf**

240T   Dissecting Natural Variation of Stress Signaling in *Saccharomyces cerevisiae*. **Amanda Scholes**

241T   Characterizing a novel biochemical trait, mushroom toxin tolerance, in a *Drosophila tripunctata* population. **Clare Scott Chialvo**

242T   Repeated adaptation of *Mimulus guttatus* to harsh serpentine soils. **Jessica Selby**

243T   Assessing the genetic diversity of native and non-native *Phragmites* (common reed) in Wisconsin. **Nicholas Tippery**

244T   The predictability of genomic signatures of specialization in a generalist/specialist species pair. **Kim Vertacnik**

245T   **Withdrawn**

246T   Discerning the historical and genetic relationship between the endosymbiotic bacteria *Wolbachia* and the *Drosophila* germline stem cell gene *bag of marbles*. **Miwa Wenzel**

247T   Genomics of parallel adaptation at two timescales in *Drosophila*. **Li Zhao**

Theoretical Population Genetics

248T   Reversal of dominance is the most powerful driver of stable polymorphism in fluctuating environments, but boom-bust cycles and the storage effect are more likely to stabilize many loci of large effect. **Jason Bertram**

249T   On the heterozygosity of an admixed population. **Simina Boca**

250T   The relative importance of hemiplasy and homoplasy in trait evolution. **Rafael Guerrero**

251T   Self-incompatibility haplotypes can diversify through sequential mutation and gene conversion. **Alexander Harkness**

252T   Examining the impact of mutation, selection and drift on gene expression evolution. **Mark Hill**

253T   A noval understanding of Linkage Disequilibrium and Past Effective Population Size Estimation. **Tin-Yu Hui**

254T   Updating an efficient pipeline for local ancestry inference. **Ethan Jewett**

255T   The rate of fitness valley crossing in rapidly adapting populations. **Taylor Kessinger**

256T   Simple model of the number of independent originations of recurrent mutant in very large populations. **Bhavin Khatri**

257T   Deleterious variation mimics signatures of genomic incompatibility and adaptive introgression. **Bernard Kim**

258T   Mutation load from slightly deleterious effects at many loci may be countered by beneficial mutations of larger effect, even when linkage disequilibrium restricts adaptation. **Joseph Matheson**

259T   Inversions help maintain sexually antagonistic balanced polymorphism. **Christopher McAllester**

260T   Mother's Curse and Father's Curse as Manifestations of Sexual Conflict. **Manisha Munasinghe**

261T   Somatic evolution and the inevitability of aging. **Paul Nelson**

262T   The expected distribution of fitness effects in populations rescued from extinction by evolution. **Matthew Osmond**

263T   Exact and efficient computation of linkage statistics for inference. **Aaron Ragsdale**

264T   The hidden contributions of women to theoretical population genetics. **Rochelle-Jan Reyes**

265T   The spatial allele frequency spectrum. **Daniel Rice**

266T   Estimation of genetic relatedness in admixed populations. **Arun Sethuraman**

267T   Population genetics of meiotic drive and its suppression. **Carl Veller**

268T   Sexual conflict constrains the evolution of reinforcement. **Alison Wardlaw**

Molecular Evolution

269T   Taking the measure of mutation in the light of molecular dynamics. **Gregory Babbitt**

270T   Beyond the pale ale: insights into temperature tolerance and carbon source evolution through *Saccharomyces eubayanus.* **Emilyclare Baker**

271T   The functional consequences of the rapid evolution of Matrimony, a Drosophila female meiosis-specific inhibitor of Polo kinase. **Amanda Bonner**

272T   Balancing selection is pervasive in *Drosophila* antimicrobial peptides. **Joanne Chapman**

273T   Evolution and natural variation of the major heat-shock protein network in humans. **Christina Chavez**

274T   Allelism and acetyl-CoA carboxylase gene variants in allohexaploid wild oat. **Michael Christoffers**

275T   Convergent regressive evolution of the eye and the identification of eye-specific regulatory elements. **Nathan Clark**

276T   Evolution of the recombination pathway in mammals. **Amy Dapper**

277T   A Fitness Carol: The evolutionary trajectory of a protein's past, present, and future. **Drew Doering**

278T   "mtDNA fossils" suggest that our hominine ancestors were engaged in distant interspecies hybridizations. **Zoe Fleischmann**

279T   Diamond in the garbage: A hypothesis on human evolution based on castoffs of the human genome. **Zoe Fleischmann**

280T Evidence for a substantial contribution of damage-induced mutations among human germline mutations. **Ziyue Gao**

281T Recombinant apomixis and genotypic diversity in asexual ferns. **Amanda Grusz**

282T Non-B DNA affects polymerization speed and error rate in sequencers and living cells. **Wilfried Guiblet**

283T Convergent evolution of phosphatase gene families allows for specialization in phosphate and thiamine starvation in multiple yeast species. **Bin He**

284T Pseudogenization of PON1 in Marine Mammals Implies Sensitivity to Organophosphate Pesticides. **Jerrica Jamison**

285T Widespread expression divergence of young duplicate genes in grasses. **Xueyuan Jiang**

286T Current challenges to Neo-Darwinism, molecular phylogenetics, and DNA barcoding: a solution arising from modern molecular data. **Yuri Kartavtsev**

287T Alpha-amanitin resistance in *Drosophila melanogaster*: physiology and gene expression characterizing the trait. **Prajakta Kokate**

288T The molecular evolution of spermatogenesis. **Emily Kopania**

289T Identifying genes associated with longevity in mammals using patterns of convergent evolution. **Amanda Kowalczyk**

290T Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts. **David Krause**

291T Different evolutionary dynamics revealed by functional SNP classes in global chicken groups. **Dorcus Malomane**

292T Traversing the fitness landscape of lung adenocarcinoma *in vivo* using tumor barcoding and CRISPR/Cas9-mediated genome editing. **Christopher McFarland**

293T Single locus experimental evolution of ancestral steroid receptor proteins. **Brian Metzger**

294T The tempo and mode of genome evolution across the budding yeast subphylum. **Dana Opulente**

295T Deep mutational scanning along an evolutionary trajectory. **Yeonwoo Park**

296T Developing robust evolutionary-rates-based methods for detecting convergent genomic changes underlying phenotypic adaptations. **Raghavendran Partha**

297T Natural Selection Has a Broad Impact on Codon Usage Biases across Eukaryota. **Zhen Peng**

298T Evolutionary origin of multimeric assembly in Hemoglobin. **Arvind Pillai**

299T Immune genes are hotspots of convergent positive selection in birds. **Allison Shultz**

300T Increased rates of molecular adaptation, but not divergence, in proteins of dimorphic sperm from Monarch butterflies (*Danaus plexippus*). **James Walters**

301T α-Amanitin resistance in *Drosophila melanogaster*: a genome-wide association approach. **Thomas Werner**

Quantitative and Complex Traits

302T Comprehensive identification of *cis*-regulatory variants in yeast promoters. **Frank Albert**

303T High throughput assessment of natural variation in the resistance to starvation stress in C. elegans using microfluidics. **Heather Archer**

304T Network Architecture and Mutational Sensitivity of the *C. elegans* Metabolome. **Charles Baer**

305T A tissue specific system of chromatin regulatory genes. **Christopher Baker**

306T How much of the response to selection can be attributed to discrete genes ? **Nicholas Barton**

307T Malathion resistance in the *Drosophila* genetic reference panel is associated with selective sweeps and structural variation. **Paul Battlay**

308T Genomics of larval locomotor evolution across *Drosophila mojavensis* populations. **Kyle Benowitz**

309T Distinguishing close linkage from pleiotropy in multiparental populations. **Frederick Boehm**

310T Screen for enhancers and suppressors of Parkinson's disease with the *Drosophila*-rotenone model. **Alexa Bracci**

311T Systems genetics, fine mapping, and validation of candidate genes involved in opioid and psychostimulant addiction traits in a reduced complexity cross. **Camron Bryant**

312T Modeling gene-by-treatment effects in a Replicable Genetic Reference Population: DrugX-induced liver injury in the Collaborative Cross as an example. **Yanwei Cai**

313T Identifying functional variants influencing human height variation. **Terence Capellini**

314T Antagonistic pleiotropy at a human *GDF5 cis*-regulatory variant. **Terence Capellini**

315T Unraveling fatty acid variation in oat (*Avena sativa* L.) with multivariate genome-wide association analyses. **Maryn Carlson**

316T Estimation of phenotypic and additive genetic covariance functions for function-valued traits in the presence of amplitude and phase variation. **Patrick Carter**

317T A genome-wide association study to identify genetic factors affecting resistance allele formation in CRISPR gene drives. **Jackson Champer**

319T Dissecting the genetic basis of head morphology and evolution using haplodiploid wasps. **Lorna Cohen**

320T QTL Mapping of Epicuticular Waxes to Understand the *gl* Locus of Onion. **Eduardo D. Munaiz**

321T Phenotypic clustering reveals novel genetic associations unique to distinct subtypes of polycystic ovary syndrome. **Matthew Dapas**

322T   Association analysis reveals the importance of the *Or* gene in carrot (*Daucus carota* L.) carotenoid accumulation and domestication. **Julie Dawson**

323T   Impact of early summer hair shedding on susceptibility to fescue toxicosis and heat stress in taurine cattle. **Harly Durbin**

324T   Reconstructing the history of polygenic adaptation using local coalescent trees. **Michael Edge**

325T   The genetic basis of exploration tendency in a multiparent population of *Drosophila melanogaster*. **Zachary Elkins**

326T   Genetic variation underlies differential responses to docetaxel and zinc treatments in *Caenorhabditis elegans*. **Kathryn Evans**

327T   Evolution of age-specific decline in stress phenotypes is driven by both antagonistic pleiotropy and mutation accumulation. **Elizabeth Everman**

328T   Genetic dissection of variation in copper resistance in *Drosophila melanogaster*. **Elizabeth Everman**

329T   Complex genetic interactions drive peanut allergy models. **Martin Ferris**

330T   Deciphering sex-specific genetic architectures using Bayesian methods. **Scott Funkhouser**

331T   Pleiotropic genetic effects percolate through underlying networks of traits. **Kerry Geiler-Samerotte**

332T   Discriminating primary from metastatic tumors in melanoma using Whole-Genome Gene Expression Profiles. **Agutin Gonzalez-Reymundez**

333T   The effects of IIS/TOR signaling on sex-differential gene expression in Drosophila. **Rita Graze**

334T   Uncovering the genetic basis of leaf shape, a potentially adaptive trait, in *Ipomoea trifida*. **Sonal Gupta**

335T   Single Plant GWA study validated by Bulk Segregant Analysis for plant height in the maize *Shoepeg* population. **Abiskar Gyawali**

336T   Demography obscures signatures of selection in island populations of *Drosophila santomea* and *D. yakuba*. **Clair Han**

337T   Using metabolomics to study a complex trait in *Drosophila melanogaster*. **Ben Harrison**

338T   The role of detoxification gene *Cyp12d1* in resistance to caffeine in *Drosophila*. **Dianarys Hernandez-Aquino**

339T   Sex-ratio heritability in the common snapping turtle: a reptile with temperature-dependent sex determination. **Kyle Hilliard**

340T   Detecting quantitative trait loci in mice bred for high levels of voluntary wheel running. **David Hillis**

341T   Tracking signatures of response over 20 generations of selection for long leg length in mice. **Layla Hiramatsu**

342T   Empirical distributions of mutational effects define gene-specific neutral models of regulatory evolution. **Andrea Hodgins-Davis**

343T   Genome-wide Association Study identifies genetic variants associated with facial attractiveness. **Bowen Hu**

344T Systems biology of age-related phenotypes in response to diet restriction in *Drosophila*. **Kelly Jin**

345T Haplotype Based Analysis Established *SorCS1* as a Positional Candidate Gene for Tame Behavior in a Fox Model of Animal Domestication. **Jennifer Johnson**

346T Automated measurement of ecologically-relevant social behavior in a laboratory environment. **Zachary Johnson**

347T Putting up with parasites: a developmental regulator confers tolerance of transposition in the *Drosophila* female germline. **Erin Kelleher**

348T Repeated cis-regulatory evolution of a metabolic bottleneck gene implies evolution might be predictable. **Meihua Kuang**

349T Transcriptome analysis of anterior pituitary and adrenal gland in the red fox strains with different stress-responsiveness. **Anna Kukekova**

350T Distinct Genetic Architectures for Phenotype Means and Plasticities in *Zea mays*. **Aaron Kusmec**

351T A novel sex-ratio distorter segregates at low frequency in a *D. miranda* population. **Emily Landeen**

352T The genetic basis of natural variation in chemical communication. **Daehan Lee**

353T Genetics of chromosome-X nondisjunction rate variation in *C. elegans*. **Tzitziki Lemus Vergara**

354T Exploiting natural variation in yeast stress responses to connect gene expression variation to organismal traits. **Jeffrey Lewis**

355T Losing sweetness: insights into reduced nectar in the selfing syndrome. **Irene Liao**

356T The effects of quantitative trait architecture on detection power in artificial selection experiments. **Runyang Lou**

357T Sex-specific mechanisms of paraquat susceptibility in *D. melanogaster*. **Pamela Lovejoy**

358T TRiAGE: technique for ranking genes in epistasis. **Matt Mahoney**

359T Genetic variation interacts with experience to determine interindividual differences in learned song. **David Mets**

360T Digging for genes involved in behavioral evolution. **Olivia Meyerson**

361T Observing viability selection in contemporary humans. **Hakhamanesh Mostafavi**

362T Genomic rearrangements considered as quantitative traits. **Richard Mott**

363T Environmental clustering strategies to exploit genotype-by-environment interaction for genomewide selection. **Jeffrey Neyhart**

364T Transcriptional response of a multiparent population to adult nutritional change. **Enoch Ng'oma**

365T Coevolved nucleo-mitochondrial interactions and slow growth contribute to mitochondrial genome stability. **Tuc Nguyen**

366T Networks underpinning symbiosis revealed through cross-species eQTL mapping. **Dahlia Nielsen**

367T Developing environmental region-specific genomic predictions for beef cattle breeds. **Sara Nilson**

369T Phenotypic characterization of gigantism in Gough Island mice. **Mark Nolte**

370T Effect of Transposable Element Copy Number on Maize Phenotypes. **Ellen Osborn**

371T Whole Genome Resequencing to identify QTLs for ascites in chickens. **Alia Parveen**

372T Sexual dimorphism and evolution of crossover patterning in house mice. **April Peterson**

373T Ohtadstat: A new framework for the application of Ohta's D statistics to genome-wide datasets. **Paul Petrowski**

374T Distinct distributions of mutational effects on fitness revealed by high-throughput phenotyping. **Yevgeniy Plavskin**

375T Trait correlations and environmental interactions to inform the domestication of *Silphium integrifolium*. **John Price**

376T A phylogenetic analysis of the *Drosophila* metabolome. **Daniel Promislow**

377T High-resolution mapping of candidate loci for social behavior in the red fox. **Halie Rando**

378T A model experiment of parallel selection for elucidating the architecture of complex traits. **Richard Reeves**

379T Genetic variation in shoot developmental turnover underlies climate adaptation in the perennial plant *Arabidopsis lyrata*. **David Remington**

380T Tools for studying natural variation in Akt signaling in *Drosophila melanogaster*. **Didem Sarikaya**

381T From Estimation to Prediction of Genomic Variances: Allowing for Linkage Disequilibrium and Unbiasedness. **Nicholas Schreck**

382T Genomic prediction of puberty and reproductive traits in beef cattle and its accuracy in admixed individuals. **William Shaffer**

383T Impact of genetic variation on mRNA splicing in human tissues. **Ankeeta Shah**

384T The Genetic Architecture of Morphology in Peruvian Native Potato. **Laura Shannon**

385T *Cis*-acting variants affect gene expression dynamics within and between *Saccharomyces* species. **Ching-Hua Shih**

386T Host-Pathogen QTLs underlying susceptibility to infectious disease. **Clare Smith**

387T Identifying genetic modifiers of flight performance using the Drosophila Genetic Reference Panel. **Adam Spierer**

388T Parallel Evolution of Ethanol Tolerance found in Four Populations of *Drosophila melanogaster*. **Quentin Sprengelmeyer**

389T Characterizing translational regulation in genetically diverse mouse strains. **Alexander Stanton**

391T Inferring the population genetics of polygenic adaptation through machine learning. **Markus Stetter**

392T Behavioral and Life-History Evolution in Island Mice with Extreme Body Size. **Jered Stratton**

393T Reciprocal, sparse diallels of Collaborative Cross mice for identifying effects of parent-of-origin, perinatal exposures, allelic imbalance, and X-inactivation skew. **Kathie Sun**

395T Assessment of sugar beet (*Beta vulgaris* L. subsp. vulgaris) elite inbred lines in Japan. **Kazunori Taguchi**

396T Epistatic networks jointly influence phenotypes related to metabolic disease and gene expression in Diversity Outbred mice. **Anna Tyler**

397T Extreme QTL Analysis of Lifespan in an Advanced Intercross Population of *Drosophila*. **Desiree Unselt**

398T The *Drosophila* model system for analyzing natural variation in resistance to *Metarhizium* spp. **Jonathan Wang**

399T Environment-dependent pleiotropic effects of mutations on growth rate and carrying capacity of population growth. **Xinzhu Wei**

400T Unprogrammed Number

401T Accurate, ultra-low coverage impuation and association studies in Hybrid Swarm mapping populations. **Cory Weller**

402T Dissecting the Genetics Basis of Learning, Memory, and Thermal Tolerance in a Multi-parental Population of Fruit Flies. **Patricka Williams-Simon**

403T Recombination in mtDNAs reveals negative mito-mito epistasis between *Saccharomcyes cerevisiae* popula tions. **John Wolters**

404T Genome-wide association for testis weight in the diversity outbred mouse population. **Joshua Yuan**

405T The genetic basis of evolutionary transitions in early development. **Christina Zakas**

406T Natural variation in *C. elegans* arsenic-induced toxicity is explained by differences in branched chain amino acid catabolism. **Stefan Zdraljevic**

407T Genetic analysis on multi-parental populations. **Luyan Zhang**

408T Using automated phenotyping to study the genetic architecture of pupation site selection in *Drosophila melanogaster.* **Wenyu Zhang**

Statistical Genetics

409T Admixture statistics for populations in space. **Gideon Bradburd**

410T Development of Genomic-Based Strategies for Screening and Selection of Accesssions from a Carrot (*Daucus carota)* Germplasm Collection. **Keo Corak**

411T Bayesian Inference of the Allelic Series in Multiparental Populations. **Wesley Crouse**

412T Assessment of population sub-structure in genetic association studies. **Nicholas DeVogel**

413T A multivariate linear mixed model for detecting GxE. **Hyeonju Kim**

414T Realized heritability in panmictic populations - evolution of the concept. **Milan Lstiburek**

415T Variance QTLs as a means to identify epistatic interactions in genome-wide association studies. **Andrew Marderstein**

416T Relatedness and differentiation in arbitrary population structures. **Alejandro Ochoa**

417T　A Bayesian approach to quantitative genetics for high-dimensional traits. **Daniel Runcie**

418T　The contribution of homeologous gene interactions to the genetic variance of allopolyploid wheat. **Nicholas Santantonio**

419T　Regulatory network inference from a dense time-course RNA-seq study of *Drosophila* innate immune response. **Maria Florencia Schlamp**

420T　Effect of fitness landscape, population structure and linkage disequilibrium on the detection of local adaptation. **Bertrand Servin**

421T　Genetic variation and ancestry in *Helicobacter pylori* and gastric cancer susceptibility in Central America. **Gloria Tavera**

422T　Pedigree Analysis of a large dog population. **Silvan Urfer**

423T　Integrated software packages of map construction and QTL mapping in various kinds of genetic populations. **Jiankang Wang**

424T　Ancestral life history and natural genetic variation shape starvation survival in *C. elegans*. **Amy Webster**

425T　Inferring parental genomes and parent-of-origin using genotypes from siblings. **Amy Williams**

426T　Genetically-informed association analysis identifies risk factors for late-onset Alzheimer's disease. **Donghui Yan**

62T　Genome-wide characterization of differences in mutation fitness effects between populations. **Ryan Gutenkunst**

90T　Combining population genomics and fitness QTL to identify the genetics of local adaptation in *Arabidopsis thaliana.* **Nicholas Price**

92T　A map of highly constrained coding regions in the human genome. **Aaron Quinlan**

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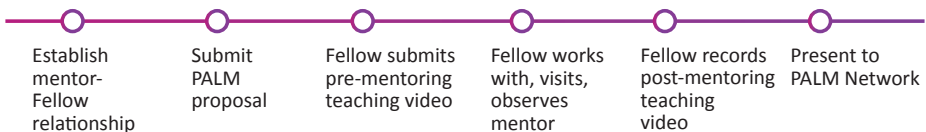
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PRESENTING AUTHOR INDEX

WORKSHOPS AND SPECIAL EVENTS

Monday Lunch
1:00 p.m. – 2:30 p.m.

A community-oriented approach to build and support women in science

1st Floor, Senate Room

Organizer:
Nadia Singh, University of Oregon

The goal of this event is to create a sense of community that empowers and inspires women to take control of their careers by building community support networks. With **Katie Peichel** (University of Bern), **Laurie Stevison** (Auburn University), **Heather Fiumera** (Binghamton University-SUNY), and Nadia Singh.

Developing your teaching philosophy

2nd Floor, Conference Room I
Organizer:
Jessica Maher, University of Wisconsin-Madison

A teaching philosophy statement is a common element in academic job or award applications, but can prove challenging to write. In this workshop, we will explore elements of compelling teaching statements, and discuss how to demonstrate evidence of effective teaching that is tailored for different audiences. Participants will have the opportunity to reflect on their own teaching practices, and consider how they might get started writing or polishing an existing teaching statement.

Monday Lunch continued
1:00 p.m. – 2:30 p.m.

GENETICS Discussion 1
2nd Floor, Conference Room II

Featured authors:
Robert L. Unckless, University of Kansas
Andrew G. Clark, Cornell University
Philipp W. Messer, Cornell University
Early Career Facilitator:
Jessica Velez, University of Tennessee,
Oak Ridge Laboratory

Featured article: Evolution of Resistance
Against CRISPR/Cas9 Gene Drive

Join featured *GENETICS* authors to
explore the stories behind the scientific
discoveries. These discussions provide
unique opportunities to talk directly to
the authors for deeper understanding of
the data, methods, advancements, and
future directions.

Navigating the career decision-making process
2nd Floor, Conference Room III

Organizers:
Sonia Hall , Genetics Society of America
Jackie Bubnell, Cornell University

This interactive career planning
workshop will engage participants in
thinking about how their skills, interests,
and values can be used to inform their
career planning and decisions.

Tuesday Lunch
1:00 p.m. – 2:30 p.m.

Publishing Q&A
2nd Floor, University Rooms

Organizers:
Tracey DePellegrin, Genetics Society of America
Mark Johnston, University of Colorado School of Medicine, Editor in Chief, *GENETICS*

Lost in publication? Not ready to publish yet, but curious about the peer-review process? Students and postdocs are invited to join journal editors, including from the GSA journals *GENETICS* and *G3: Genes|Genomes|Genetics,* to discuss the ins-and-outs of getting your articles published. All questions welcome!

Beyond the scholarly article: Reaching a broad audience through book publishing
1st Floor, Senate Room

Organizers:
Dennis Lloyd, University of Wisconsin Press
Nathan MacBrien, Northwestern University Press

Check the mobile app or website for workshop description.

Looking for a mentor to help you incorporate active learning in classrooms?
2nd Floor, Conference Room I

Organizers:
Sue Wick, University of Minnesota and **Christopher Baker**, The Jackson Laboratory

You may have seen data clearly showing how incorporation of active learning techniques increases student performance and decreases the number of D, F, and W grades in STEM courses, but feel that implementing these methods on your own can be daunting. This session will provide information about an NSF-funded, one-on-one teaching mentoring program, Promoting Active Learning and Mentoring (PALM).

Tuesday Lunch continued
1:00 p.m. – 2:30 p.m.

GENETICS discussion 2
2nd Floor, Conference Room II

Featured Authors:
Luke M. Noble, New York University
Early Career Facilitator:
Andrea Hodgins-Davis, University of Michigan

Featured article: Polygenicity and Epistasis Underlie Fitness-Proximal Traits in the *Caenorhabditis elegans* Multiparental Experimental Evolution (CeMEE) Panel

GENETICS discussion 3
2nd Floor, Conference Room V

Featured Author:
Elizabeth King
University of Missouri
Early Career Facilitator:
Ben Harrison
University of Washington

Featured article: Genetic Dissection of Nutrition-Induced Plasticity in Insulin/Insulin-Like Growth Factor Signaling and Median Life Span in a *Drosophila* Multiparent Population

Talk science to me: How to start science outreach in your own community

2nd Floor, Conference Room III
Organizers:
Adam Ramsey, Co-Chair, GSA Communication and Outreach Committee
Jessica Velez, Co-Chair, GSA Communication and Outreach Committee

Are you interested in science outreach? Perhaps you're not sure where to start, or nervous about the questions you might receive, or not sure how to target your audience. Join us as we dismantle the barriers to starting your own outreach initiations in your local community, discuss the realities of speaking with your community, and share our personal stories of science outreach success.

Tuesday Lunch continued

1:00 p.m. – 2:30 p.m.

Data management for reproducibility and re-usability

1st Floor, Assembly Room

Organizer:
Jan Cheetham, University of Wisconsin-Madison

As the research landscape continues to produce more data, practices become increasingly computational and expectations of sharing, re-usability, and reproducibility become more prevalent, research data management has become an ever increasingly popular topic. Research Data Services will introduce research data management best practices for attendees, as well as focus in on critical areas such as documentation, sharing, and minimum standards for reproducibility.

Presenters: **Jan Cheetham, Cameron Cook, Trisha Adamus**

Wednesday Lunch

11:45 a.m. – 1:00 p.m.

Science Slam

2ND Floor, Capitol Ballroom

The #PEQG18 Science Slam is your opportunity to step away from the bench and computer to show the community the importance of your work and earn bragging rights for your lab!
Even if you don't want to present, please come and cheer your peers on!

Rules:
1. 3-minute time limit
2. Presentation must be original
3. No props (including technology) permitted
4. Lab and individual entries welcome

Writing scientific papers

Conference Room IV

Organizer:
Kristi Montooth, University of Nebraska, Lincoln

Regardless of whether one loves or hates to write, writing well challenges everyone. And, while there is no one way to write a scientific paper, there are better and worse strategies to produce an excellent paper. In this workshop, we will focus on writing as a practice and debunk common myths that prevent productive writing. We will then discuss what makes a better or worse introduction. Come prepared for an active lunch hour, and bring a laptop or tablet for collaborative editing of *GENETICS* papers.

GENETICS discussion 4

2nd Floor, Conference Room II

Featured Author:
Dahlia M. Nielsen, North Carolina State University
Early Career Facilitator:
Mark G. Sterken, Wageningen University

Featured Article: Networks Underpinning Symbiosis Revealed Through Cross-Species eQTL Mapping

Careers in publishing

2nd Floor, Conference Room III

Organizer:
Toni Gunnison, Journals Manager, University of Wisconsin Press

Join us for a panel discussion to explore a diverse range of careers in publishing. Gain a deeper understanding of the skills and experience needed, day-to-day responsibilities, and pathways to success.
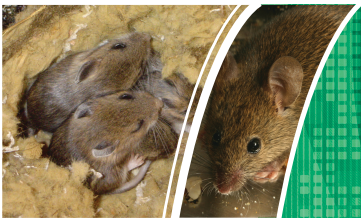
Panelists:
Amber J. Rose – Acquisitions Assistant (U of Wisconsin Press)
Danielle Pacha – Managing Editor (A-R Editions)
Elizabeth Gebhardt – Managing Editor (Alliance of Crop, Soil, and Environmental Science Societies)
Abby Morrison – Publication Systems Assistant (Alliance of Crop, Soil, and Environmental Science Societies)

GigaMUGA

High Density Mouse Universal Genotyping Array

Content and Design Characteristics

The Giga Mouse Universal Genotyping Array (GigaMUGA) provides more than 143,000 SNP markers built on the Illumina Infinium platform. The GigaMUGA improves upon the 78,000 SNP MegaMUGA and includes nearly all of the predecessor's content. A majority of the SNP markers are distributed throughout the mouse genome and were selected to be informative in most mouse populations, including wild mice and multiple *Mus* species, but with a special emphasis for markers that are informative in the Collaborative Cross and Diversity Outbred population resources. The utilization of these informative SNPs make the array a highly cost-effective tool for many genotyping applications. The GigaMUGA design criteria make it optimal for detecting heterozygous regions and discriminating between haplotypes in homozygous regions.

The GigaMUGA includes an excess of probes in the telomeric regions of each autosome to facilitate detection of recombination events throughout the chromosome. More than 46,000 SNPs were specifically selected to flank a catalog of more than 20,000 recombination hotspots.

The array also includes more than 2,000 non-SNP probes intended for exploring copy number variation in regions selected from previously published data.

Performance

The GigaMUGA array provides robust calls for over 143,000 SNP markers in classical strains with greater than 99.7% concordance (based on over 500 reference samples).

Initial analysis in classical inbred strains shows that on average the number of informative SNPs in pairwise combinations is greater than 25,000. This number increases greatly when one or both of the strains are derived from different subspecies.

GigaMUGA allows to discriminate between closely related sister strains (e.g. C57BL/6J and C57BL/6CR) and between related wild derived strains of similar origin (e.g. PWK/PhJ and PWD/PhJ; ZALENDE/EiJ and TIRANO/EiJ).

Genotypes for many inbred strains can be viewed at the UNC Systems Genetics Core Facility website (http://www.csbio.unc.edu/CCstatus/index.py?run).
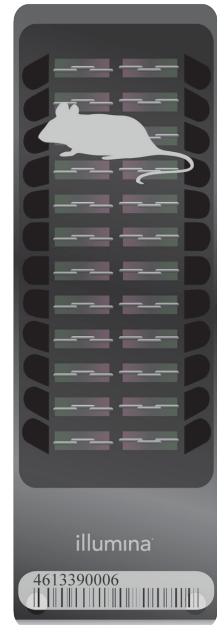
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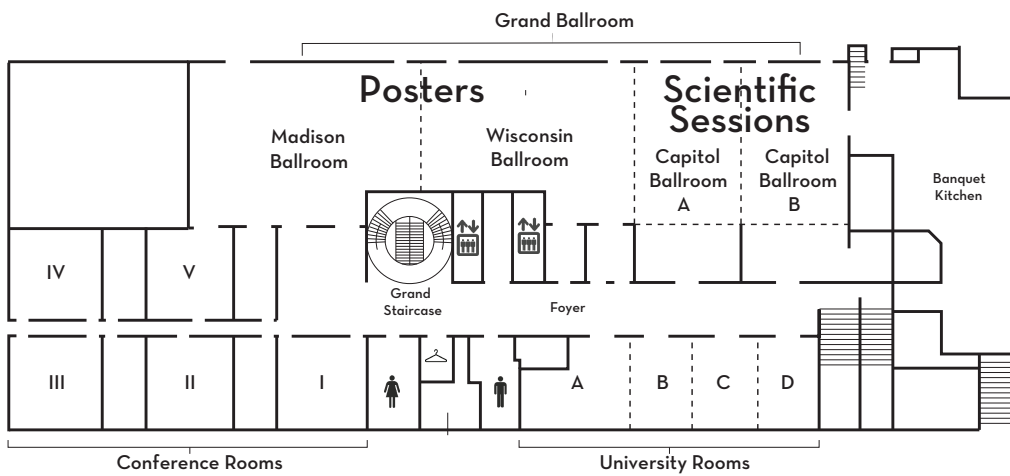
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1st Floor

Senate Room B

Senate Room A

The Bar

Kitchen

Loading Dock

Auto Lift

Caucus Room

Grand Staircase

Salad Bar

Private Dining Room

Assembly Room

Parking Entrance

Shuttle Port

Front Desk

Lobby

Seating

CIRC

Starbucks

Business Center

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Grand Ballroom

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Madison Ballroom

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Conference Rooms

University Rooms

Monday Posters

Tuesday Posters
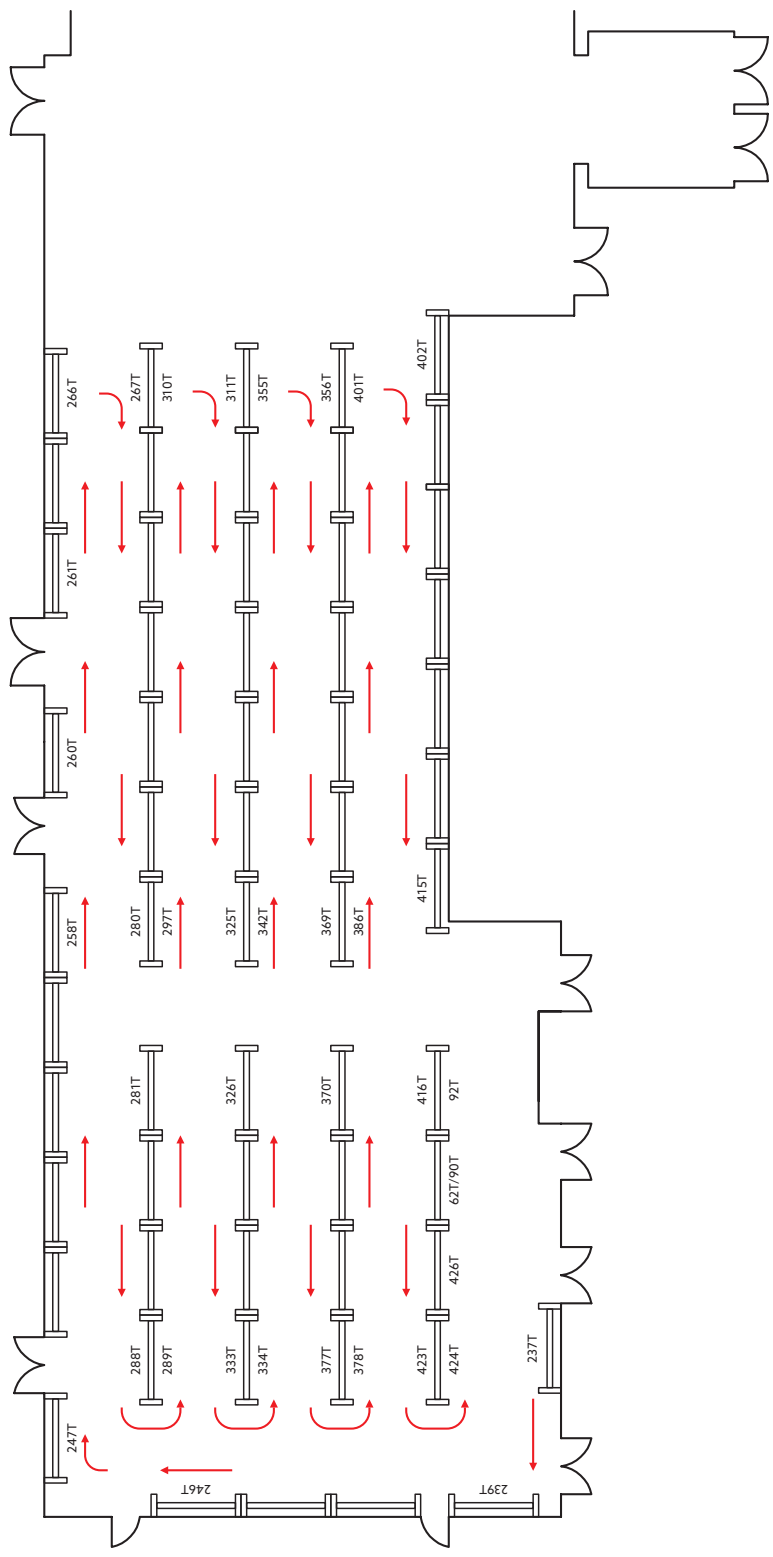
SUNDAY, May 13		
6:45 p.m. - 8:00 p.m.	WELCOME and KEYNOTE 1: Jonathan Pritchard	Capitol Ballroom
8:00 p.m. - 10:00 p.m.	OPENING MIXER	University Rooms
MONDAY, May 14		
7:30 a.m. - 8:45 a.m.	CONTINENTAL BREAKFAST	1st and 2nd Floors
8:00 a.m. - 5:00 p.m.	REGISTRATION	2nd Floor
9:00 a.m. - 10:30 a.m.	PLATFORM SESSION 1	Capitol Ballroom
11:00 a.m. - 1:00 p.m.	JAMES F. CROW EARLY CAREER RE-SEARCHER AWARD TALKS	Capitol Ballroom
1:00 p.m. - 2:30 p.m.	BREAK FOR LUNCH and WORKSHOPS	1st and 2nd Floors
2:30 p.m. - 4:00 p.m.	PLATFORM SESSION 2	Capitol Ballroom
4:00 p.m. - 5:00 p.m.	LIGHTNING TALKS 1	Capitol Ballroom
7:00 p.m. - 8:00 p.m.	KEYNOTE 2: Catherine Peichel	Capitol Ballroom
8:00 p.m. - 10:00 p.m.	POSTER PRESENTATIONS (Group M) 8–9 p.m. Even Numbers 9–10 p.m. Odd Numbers	Madison/ Wisconsin Ballroom
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7:30 a.m. - 8:45 a.m.	CONTINENTAL BREAKFAST	1st and 2nd Floors
8:00 a.m. - 5:00 p.m.	REGISTRATION	2nd Floor
9:00 a.m. - 10:30 a.m.	PLATFORM SESSION 3	Capitol Ballroom
11:00 a.m. - 1:00 p.m.	PLATFORM SESSION 4	Capitol Ballroom
1:00 p.m. - 2:30 p.m.	BREAK FOR LUNCH AND WORKSHOPS	1st and 2nd Floors
2:30 p.m. - 4:00 p.m.	PLATFORM SESSION 5	Capitol Ballroom
4:00 p.m. - 5:00 p.m.	LIGHTNING TALKS 2	Capitol Ballroom
7:00 p.m. - 8:00 p.m.	KEYNOTE 3: Trudy Mackay	Capitol Ballroom
8:00 p.m. - 10:00 p.m.	POSTER PRESENTATIONS (Group T) 8-9 p.m. Even Numbers 9-10 p.m. Odd Numbers	Madison/ Wisconsin Ballroom
WEDNESDAY, May 16		
7:15 a.m. - 8:15 a.m.	CONTINENTAL BREAKFAST	1st and 2nd Floors
8:30 a.m. - 10:00 a.m.	PLATFORM SESSION 6	Capitol Ballroom
10:15 a.m. - 11:15 a.m.	PLATFORM SESSION 7	Capitol Ballroom
11:15 a.m. - 11:45 a.m.	AWARD CEREMONY	Capitol Ballroom
11:45 a.m. - 1:00 p.m.	SCIENCE SLAM	Capitol Ballroom
11:45 a.m. - 1:00 p.m.	BREAK FOR LUNCH AND WORKSHOPS	1st and 2nd Floors
1:00 p.m. - 4:00 p.m.	KEYNOTE SESSION 4: Session Chairs	Capitol Ballroom
6:30 p.m. - 9:30 p.m.	MIXER ON LAKE MENDOTA	Off site
THURSDAY, May 17		
9:00 a.m. - 4:30 p.m.	NEW FACULTY FORUM	Assembly Room