2022 east **Genetics** Meeting

August 17–21, 2022

PROGRAM BOOK







Table of Contents

Genetics Society of America
Yeast22 Organizers
Sponsors
General Information
Registration Desk and Badges
Registration Desk Schedule
Conference App
Presenting Author Index
Oral Presenters
Poster Presentations
In-person Poster Presentations
Viewing Sessions Online
Exhibitor and Sponsor Information
Safety Protocols
COVID-19 Testing
Meals
Internet Access
Job and Meeting Postings
Slack Chat Channels
Security/Lost and Found
Conference Policies
Code of Conduct
Accessibility
Diversity and Inclusion
Social Media/Photo/Video Policy
Schedule of Events
Oral Presentation and Workshop Session Listings22
Poster Session Listings
Sponsor Ads

Genetics Society of America

Genetics Society of America



GSA is an international scientific society representing more than 5,000 researchers and educators around the world. As well as connecting researchers through conferences and career programs, we publish two peeredited scholarly journals, GENETICS and G3: Genes |Genomes |Genetics. We encourage you to join GSA so you can make use of exclusive member benefits and get involved in the Society's many programs, including professional development training, awards, advocacy, and more. Join us as we work to advance the field and serve our community. Visit <u>genetics-gsa.org</u> for more information.





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

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

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Yeast22 Organizers

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Conference Sponsors

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General Information

Registration Desk and Badges

You should have received your registration badge in advance via email and printed it out. Badges will not be printed onsite. In the registration area in De Neve Lecture Auditorium, you will need to show your green check mark obtained from 42Chat (indicating you uploaded your vaccination verification and negative test results), and you will be given a badge cover and lanyard. For admission to the sessions, posters, exhibits, and receptions, you must have your official conference badge.

You can download the Program and Abstract Books on the conference website or access all the information in the Conference App. Certificates of Attendance and Participation are available online.

Registration Desk Schedule

Wednesday, August 17	3:30 p.m.–9:00 p.m.
Thursday, August 18	7:00 a.m.–12:00 p.m.
	1:00 p.m.–5:30 p.m.
Friday, August 19	8:00 a.m.–12:00 p.m.
	1:00 p.m.–4:00 p.m.
Saturday, August 20	8:00 a.m.–12:00 p.m.

Conference App

In-person participants: Download the GSA Meetings app to your smartphone (available on both iOS and Android platforms) to have meeting information at your fingertips. Once you download the App, you will not need an internet connection to access previously downloaded information. You will only need an internet connection to download updates. Blackberry users and Windows Mobile Device users can access the App through the web desktop version available on the conference website.

Virtual participants: Virtual attendees will use the App to participate in the conference. Sign into the App using your registration badge ID number and last name. The App is available in two formats: Desktop App (for desktop and laptop computers), or Mobile App (for Apple iOS and Android mobile devices).

You can find your registration badge ID in your conference registration confirmation email, which was sent from the address <u>NoReply@Convention-Mail.com</u>.

Presenting Author Index

To search for specific oral and poster presenters, please use the search function in the Conference App.

Access the app at: genetics-gsa.org/yeast-2022/conference-app

General Information

Oral Presenters

NEW PROCEDURES THIS YEAR—All speakers must upload their presentation with the technical operator located in the back of De Neve Lecture Auditorium **24 hours before the start of your session**. Presenters will upload and review your presentation, and become familiar with the equipment that will be in the session room. You will NOT be able to use your own computer or upload your presentation in the session room. The day of your presentation, arrive 30 minutes before the start of your session (not your talk) and let the session chair know that you are there.

Poster Presentations

All posters are available from August 15 to September 9 as a PDF with an (optional) two-minute audio overview in the Conference App. Be sure to view all the posters in the app and leave feedback. To view a poster, look for the "Virtual Poster" link near the bottom of each poster's entry in the App. If provided, the presenter's personal calendar link is included so that you can set up individual meetings with them.

Poster presenters who are attending the conference in person have been assigned a presentation time according to the schedule below. Poster sessions will be in the Palisades Room, which is located in Carnesale Commons. Two posters will share a 4' high x 8' wide poster board. Each author will have a net usable space of 3' 10" (116.8 cm) high x 3' 10" (116.8 cm) wide.

All posters will be displayed through Friday at 10:00 p.m. Presenters should remove their posters at the end of the poster session on Friday, August 19. If you do not remove your poster, it may be lost or thrown away. The meeting does not take responsibility for posters that are not removed on time.

In-person Poster Presentations

Wednesday, August 17		
View all the virtual posters while traveling to the meeting and leave comments for the authors in the app. Posters will be available until September 9.		
Thursday, August 18–All A posters will present		
7:00 p.m.–8:00 p.m.	Even-numbered A posters	
8:00 p.m.–9:00 p.m.	Odd-numbered A posters	
9:00 p.m.–10:00 p.m.	Open Viewing	
Friday, August 19–All B posters will present		
7:00 p.m.–8:00 p.m.	Even-numbered B posters	
8:00 p.m.–9:00 p.m.	Odd-numbered B posters	
9:00 p.m.–10:00 p.m.	Open Viewing	
10:00 p.m.	Remove posters	

Viewing Sessions Online

Remote attendees can view sessions via the Online Planner:

Plenary sessions–Registrants access live plenary sessions through the App. Five minutes before a plenary session starts, log in using your registration badge ID number and last name. Tap the "Join Webinar" button on the session. The "Join Webinar" button will be visible 10 minutes before the start of the session. A recording of each session will be available in the session listings on the App within 24 hours after the session ends. The recordings will be available until September 9.

Poster Sessions–PDFs and audio overviews of all of the posters will be available via the App August 15 through September 9.

Exhibitor and Sponsor Information

Please be sure to visit with the company representatives during the poster sessions.

Genetics Society of America

www.genetics-gsa.org

GSA is an international scientific society representing more than 5,000 researchers and educators around the world. Advance your career, discover new resources, and learn about publishing in GENETICS and G3: Genes Genomes Genetics.

Singer Instruments

www.singerinstruments.com

For over 85 years, Singer instruments remains a mainstay of the yeast research community. Our dedication to listening to you has enabled us to develop innovative robotics for yeast research. From ROTOR+ PIXL enabling high-throughput screening and picking, to the msm 400 for tetrad dissection.

Safety Protocols

In-person attendees are required to wear the most protective masks they can access, ideally N95s or KN95s, while attending the conference. If you do not have access to a high-quality mask, a limited supply of complimentary masks are available at the Conference Registration Desk

Hand sanitizers will be available in the meeting rooms.

Please keep your mask on while in line for coffee and only remove to drink your coffee.

Daily self monitoring: If you experience any of the listed symptoms, do not enter the meeting space. Contact <u>gsaconferences@genetics-gsa.org</u> to have a rapid test brought to you. Symptoms requiring a rapid test: fever or chills, cough, shortness of breath, fatigue, muscle or body aches, headache, new loss of taste or smell, sore throat, congestion or runny nose, nausea or vomiting or diarrhea.

COVID-19 Testing

Rapid antigen tests are available at the conference registration desk for those experiencing symptoms. Please contact CVS pharmacy, 1001 Westwood Boulevard, Los Angeles, CA at 310-209-9141 to schedule a PCR test if needed for return travel.

Meals

Meals are not included in the conference registration fee. Guests staying at UCLA and those who purchase meal tickets are invited to eat in De Neve Cafeteria. Meal tickets, for those staying off site, can be purchased at the De Neve front desk.

Cafeteria Hours

Breakfast-7:00 a.m.-10:00 a.m.

Lunch-11:00 a.m.-3:00 p.m.

Dinner-5:00 p.m.-8:00 p.m.

Bruin Cafe is open Wednesday through Friday for grab and go dining for breakfast and lunch.

Bruin Cafe Hours of Operation

Breakfast-1:00 a.m.-10:00 a.m.

Lunch-11:00 a.m.-3:00 p.m.

Internet Access

Complimentary Wi-Fi is available throughout the UCLA campus. Select UCLA_Web. This is a public connection. No login is required but you will need to reconnect every 24 hours.

You can also set up an account for access throughout the conference. Complete this online form: <u>https://accounts.iam.ucla.edu/register</u>.

Job and Meeting Postings

Individuals and institutions offering or seeking employment and organizers of meetings may post notices and resumes on the "Community Notices" bulletin board in the Poster Sessions. Employers are also welcome to post listings in the #jobs channel in the #Yeast22 Slack workspace.

Slack Chat Channels

The #Yeast22 Slack workspace is the place to meet other attendees online during the conference. You can join and create chat channels based on your interests. There are channels for getting technical help, discussing new papers and preprints, sharing job ads, and connecting with other attendees around shared interests.

Security/Lost and Found

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

Conference Policies

Code of Conduct

The Genetics Society of America Conferences foster an international community of geneticists and provide an opportunity to discuss scientific advances and form new collaborations.

GSA values your attendance and wants to make your experience productive and inspiring by fostering an open exchange of ideas in a professional setting. Our Code of Conduct was established to communicate a transparent set of standards and guidelines for acceptable behavior at GSA Conferences and to provide a positive, safe, and welcoming environment for all attendees, vendors, volunteers, and staff.

All conference participants (regardless of their role) are expected to follow the Code of Conduct while attending any portion of the meeting, including but not limited to meeting rooms, the exhibit/poster hall, meeting areas in the official conference venue, and social events provided by the meeting or vendors.

Unacceptable Behaviors

Unacceptable behaviors include, but are not limited to:

- Intimidating, harassing, abusive, discriminatory, derogatory, or demeaning speech or actions by any participant and at all related events
- Harmful or prejudicial verbal or written comments or visual images related to gender, gender expression, gender identity, marital status, sexual orientation, race, religion, political orientation, socioeconomic, disability or ability status, or other personal characteristics, including those protected by law
- Inappropriate use of nudity and/or sexual images in public spaces (including presentation slides and posters)
- Deliberate intimidation, stalking, or following
- Violating the rules and regulations of the conference hotel
- Sustained disruption of scientific sessions or other events
- Unwelcome and uninvited attention or contact
- Physical assault (including unwelcome touching or groping)
- Real or implied threat of physical harm
- Real or implied threat of professional or financial damage or harm
- Harassing or unwanted photography
- Photographing slides of oral presentations and posters without permission
- Recording of scientific and other sessions without permission

Taking Action or Making a Report

Need to file a complaint? For instructions on how to confidentially report a Code of Conduct violation, please visit <u>genetics-gsa.ethicspoint.com</u>. In addition, GSA staff is available to assist participants in contacting our Ethics Committee to make a report. Please email Tracey DePellegrin, GSA Executive Director, at <u>tracey.depellegrin@genetics-gsa.org</u>.

Consequences of Non-compliance

Anyone asked by GSA staff, a Session Chair, Workshop Leader, Moderator, Presenter, or Zoom representative to stop unacceptable behavior is expected to comply immediately. Retaliation toward GSA or toward someone reporting an incident or after experiencing any of the following consequences will not be tolerated and may result in additional sanctions.

The consequences of non-compliance with GSA's Code of Conduct may include:

- Immediate removal from accessing the online meeting and Slack channels without warning
- Restrictions from future GSA meeting attendance
- Termination of GSA membership or positions on GSA Boards or Committees
- Incidents may be reported to the proper authorities

Accessibility

GSA is committed to assisting attendees with special needs. If you have accessibility questions or requests, please email <u>gsaconferences@genetics-gsa.org</u>.

Diversity and Inclusion

GSA is committed to promoting equality, diversity, and inclusion to create greater opportunity for any individual to fulfill their scientific potential, irrespective of their background, gender, or circumstances. This diversity leads to innovation by attracting the widest possible talent to the community and fostering a greater diversity of ideas, approaches, and perspectives. The Organizing Committee aims to select speakers and session chairs that represent the breadth and diversity of the discipline and conference participants. GSA especially encourages the Committee to select excellent speakers from groups traditionally underrepresented in science.

Social Media/Photo/Video Policy

Live tweeting of presentations is allowed unless the speaker explicitly opts out by stating so at the start of their 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. By attending a GSA conference, you grant GSA the right to use your photograph, name, and likeness for use in GSA educational, news, or promotional materials.

Schedule of Events

Schedule of Events

All times are listed in Pacific Daylight Time (PDT)

Monday, August 12		
10:00 a.m.–11:30 a.m.	Careers in Academia/Industry Panel	Virtual
12:00 p.m.–1:00 p.m.	Virtual Social Hour	Virtual
1:30 p.m.–2:30 p.m.	Multilingual Networking	Virtual
Wednesday, August 1	.7	
2:30 p.m.–9:00 p.m	Registration	De Neve Lecture Auditorium
2:30 p.m.–9:00 p.m	Conference success tips and welcome	De Neve Lecture Auditorium
3:30 p.m.–5:30 p.m.	Review Virtual Posters Available online until September 9	Virtual
4:00 p.m.–9:30 p.m.	Speaker Check-in	De Neve Lecture Auditorium
4:30 p.m.–5:30 p.m.	Multilingual Networking	De Neve Lecture Auditorium
5:30 p.m.–6:30 p.m.	Dinner	De Neve Cafeteria
6:45 p.m.–7:00 p.m.	Conference Welcome	De Neve Lecture Auditorium
7:00 p.m.–8:30 p.m.	Tools and approaches for understanding the yeast genome	De Neve Lecture Auditorium
8:30 p.m.–9:00 p.m.	Winge-Lindegren Address, Trisha Davis	De Neve Lecture Auditorium
9:00 p.m.–10:00 p.m.	Opening Mixer sponsored by Singer Instruments	Palisades Room, Carnesale Commons
Thursday, August 18		
7:30 a.m.–6:00 p.m.	Speaker Check-in	De Neve Lecture Auditorium
8:30 a.m.–10:00 a.m.	Genetic networks of complex traits	De Neve Lecture Auditorium

Schedule of Events

All times are listed in Pacific Daylight Time (PDT)

Thursday, August 18 (continued)			
10:30 a.m.–12:15 p.m.	Membrane trafficking, organelles and intracellular signaling	De Neve Lecture Auditorium	
12:15 p.m.–1:30 p.m.	Lunch	De Neve Cafeteria and Bruins Cafe	
1:30 p.m.–3:00 p.m.	Disease models and aging	De Neve Lecture Auditorium	
3:30 p.m.–4:00 p.m.	Lee Hartwell Lecture, Michael Desai	De Neve Lecture Auditorium	
4:00 p.m.–5:45 p.m.	Evolution and population genomics I	De Neve Lecture Auditorium	
5:45 p.m.–6:45 p.m.	Dinner	De Neve Cafeteria	
7:00 p.m.–10:00 p.m.	Posters and exhibits "A" posters will present	Palisades Room, Carnesale Commons	
Friday, August 19			
7:30 a.m.–3:30 p.m.	Speaker Check-in	De Neve Lecture Auditorium	
8:30 a.m.–10:00 a.m.	Keeping it together in a stressful world: yeast as a model for genome stability	De Neve Lecture Auditorium	
10:30 a.m.–12:00 p.m.	The editable genome	De Neve Lecture Auditorium	
12:00 p.m.–12:30 p.m.	Ira Herskowitz Award, Maya Schuldiner	De Neve Lecture Auditorium	
12:30 p.m.–1:30 p.m.	Lunch	De Neve Cafeteria and Bruins Cafe	
1:30 p.m.–2:30 p.m.	DEI Discussion: identifying ways to improve inclusion in science	De Neve Lecture Auditorium	
3:00 p.m.–5:00 p.m.	BREWMOR Workshop	Hermosa, Carnesale Commons	

Schedule of Events

All times are listed in Pacific Daylight Time (PDT)

Friday, August 19 (continued)			
3:00 p.m.–5:00 p.m.	Getting more out of SGD	De Neve Lecture Auditorium	
5:00 p.m.–6:45 p.m.	Dinner	De Neve Cafeteria	
7:00 p.m.–10:00 p.m.	Posters and exhibits "B" posters will present	Palisades Room, Carnesale Commons	
Saturday, August 20			
7:30 a.m.–5:30 p.m.	Speaker Check-in	De Neve Lecture Auditorium	
8:30 a.m.–10:00 a.m.	Evolution and population genomics II	De Neve Lecture Auditorium	
10:30 a.m.–12:00 p.m.	Mechanisms of gene regulation	De Neve Lecture Auditorium	
12:00 p.m.–1:30 p.m.	Lunch	De Neve Cafeteria and Bruins Cafe	
1:30 p.m.–3:00 p.m.	Protein Homeostasis and network conservation	De Neve Lecture Auditorium	
3:30 p.m.–5:00 p.m.	Cell cycle and metabolism	De Neve Lecture Auditorium	
5:00 p.m.–6:45 p.m.	Dinner	De Neve Cafeteria	
7:00 p.m.–7:30 p.m.	GSA Presentations	De Neve Lecture Auditorium	
7:30 p.m.–8:00 p.m.	YGM Lifetime Achievement Award, Tom Petes	De Neve Lecture Auditorium	
8:00 p.m.–9:00 p.m.	Social	Palisades Room, Carnesale Commons	
Sunday, August 21			
7:30 a.m.–10:00 a.m.	Speaker Check-in	De Neve Lecture Auditorium	
8:30 a.m.–10:00 a.m.	Gene regulation and evolution	De Neve Lecture Auditorium	

Wednesday, August 17, 2022

6:45 PM-7:00 PM

De Neve Lecture Auditorium

Welcome and Opening Remarks

Conference Organizer Peter Stirling, British Columbia Cancer Agency

GSA Welcome, Brenda Andrews, University of Toronto

Wednesday, August 17, 2022

7:00 PM–8:30 PM De Neve Lecture Auditorium

Tools and Approaches for Understanding the Yeast Genome

Session Chair Philip Hieter University of British Columbia, Canada

1 7:00 PM Identifying the targets of novel compounds using high throughput chemical-genomics in yeast **Sheena Li** University of Toronto

2 7:15 PM An ultra high-throughput, massively multiplexible, single-cell RNA-seq platform in yeasts that allows for the easy study of hundreds of genetic and environmental backgrounds. Leandra Brettner Arizona State University

3 7:30 PM The Rainbow collection–a modern set of yeast libraries for advanced microscopy **Ofir Klein** Weizmann Institute of Science

4 7:45 PM Humanization of the entire sterol biosynthesis pathway in yeast **Michelle Vandeloo** Concordia University

5 8:00 PM Profiling of RNA modifications in yeast tRNAs via direct RNA sequencing. **David** Garcia University of Oregon, Institute of Molecular Biology

6 8:15 PM Science, Brewing & Rock "n" Roll. Leah Ashley, Singer Instruments

Wednesday, August 17, 2022

8:30 PM–9:00 PM De Neve Lecture Auditorium

Winge-Lindegren Address Session Chair

Mark Rose, Georgetown University

8:30 Trisha Davis, University of WA, Seattle

Thursday, August 18, 2022

8:30 AM–10:00 AM De Neve Lecture Auditorium

Genetic networks of complex traits Session Chairs

Jing Hou Université de Strasbourg/CNRS, France; and Sean Beckwith University of Georgia, United States

6 8:30 AM The genetics of gene expression at singlecell resolution **James Boocock** UCLA

7 8:45 AM Mapping an environmental suppression network of essential genes in yeast **Núria Bosch-Guiteras** University Of Lausanne

8 9:00 AM Sc3.0 : A novel approach to minimize the synthetic yeast genome **Reem Swidah** University of Manchester

9 9:15 AM Debugging and consolidating multiple synthetic chromosomes reveals combinatorial genetic interactions **Yu Zhao** NYU Langone Health

10 9:30 AM Population-level survey of loss-of-function mutations revealed background-dependent fitness variation in yeast **Jing Hou** Université de Strasbourg/ CNRS

11 9:45 AM Explicit estimation of mRNA velocity, transcriptional output, and decay from yeast singlecell measurements improves gene regulatory network inference **Chris Jackson** New York University

Thursday, August 18, 2022

10:30 AM-12:15 PM

De Neve Lecture Auditorium

Membrane trafficking, organelles, and intracellular signaling

Session Chairs Elcin Unal University of California, Berkeley; and Beatriz Gonzalez University of Buffalo

12 10:30 AM Septins interact with AP-3 during vesicle trafficking in budding yeast **Mitchell Leih** University of Colorado Boulder, CO

13 10:45 AM Cnm1 mediates nucleus-mitochondria contact site formation in response to phospholipid levels **Naama Zung** Weizmann Institute of Science

14 11:00 AM Ait1 regulates TORC1 signaling and localization in budding yeast AndrewCapaldi University of Arizona

15 11:15 AM Isc10 inhibits CMGC group kinases by dual mechanisms **Abhimannyu Rimal** Thomas Jefferson University

16 11:30 AM Identification of plasma membrane to trans-Golgi Network vesicle fusion machinery in *Saccharomyces cerevisiae* **James Grissom** University of North Carolina at Charlotte

17 11:45 AM Essential role of the yeast Golgi membrane protein Erd1 in recycling of early Golgi glycosylation enzymes **Richa Sardana** Cornell University

12:00 PM Lightning Talks

Thursday, August 18, 2022

1:30 PM–3:00 PM De Neve Lecture Auditorium

Disease Models and Aging

Session Chairs

Grant Brown Univ Toronto, Canada; and Alexandra Imre University of Debrecen, Hungary

18 1:30 PM Leveraging gametogenesis-specific rejuvenation pathways to counteract cellular aging **Tina Sing** University of California, Berkeley

19 1:45 PM Does Rnq1's evolutionarily conserved non-prion domain regulate functional aggregation of Rnq1? **Irina Derkatch** University of Nevada, Reno

20 2:00 PM Reprogramming single-cell aging in yeast **Nan Hao** University of California, San Diego

21 2:15 PM Identifying pathways that slow down the age-associated decline of mitochondrial membrane potential **Adam Waite** Calico Life Sciences LLC

22 2:30 PM Comparative proteomics of the multidrug-resistant human fungal pathogen *Candida auris* links cellular detoxification with amino acid metabolism **Karl Kuchler** Medical University Vienna

23 2:45 PM Mitochondria-dependent toxicity of aggregation prone proteins **Annabel Vivian Almazan** Wright State University

Thursday, August 18, 2022

3:30 PM–4:00 PM De Neve Lecture Auditorium

Lee Hartwell Lecture

Session Chair Maitreya Dunham, University of WA, Seattle

3:30 Michael Desai, Harvard University

Thursday, August 18, 2022

4:00 PM–5:45 PM De Neve Lecture Auditorium

Evolution and population genomics I Session Chairs

Helen Murphy William and Mary, United States; and Jennifer Molinet Universidad de Santiago de Chile

24 4:00 PM Evolutionary rescue of phosphomannomutase deficiency in yeast models of human disease **Gregory Lang** Lehigh University

25 4:15 PM Hybridization drives mitochondrial DNA degeneration and metabolic shift in a species with biparental mitochondrial inheritance **Mathieu Henault** Université Laval

26 4:30 PM Understanding the likelihood of evolutionary tradeoffs among drug resistant mutations using a large population of barcoded yeast **Kara Schmidlin** Arizona State University

27 4:45 PM Selection on plastic adherence leads to hyper-multicellular strains and incidental virulence in the budding yeast **Helen Murphy** William and Mary

28 5:00 PM Evolution of protein thermal stability between two thermally diverged *Saccharomyces* species Nilima Walunjkar University of Rochester

29 5:15 PM Quantitative genetics and biotechnological exploitation of novel yeast hybrids **Samina Naseeb** Staffordshire University

5:30 PM Lightning Talks

Friday, August 19, 2022

8:30 AM–10:00 AM De Neve Lecture Auditorium

Keeping it together in a stressful world: Yeast as a model for genome stability

Session Chairs Martin Kupiec Tel Aviv University; and Shivani Singh University of TX Health Science at Houston

30 8:30 AM Distinct patterns of aneuploidization impact the structure and stability of the *Saccharomyces cereivisae* genome **Lydia Heasley** University of Colorado, Anschutz Medical Campus

31 8:45 AM A genetic screen uncovers sister chromatid cohesion without Pds5 **Martin Kupiec** Tel Aviv University

32 9:00 AM Uncovering natural histories of mutator alleles in budding yeast **Pengyao Jiang** University of Washington

33 9:15 AM High-throughput single cell sequencing with linear amplification to study yeast recombination **Yi Yin** UCLA

34 9:30 AM DNA replication protein Cdc6 interacts with mitotic cyclin Clb2 to arrest cell cycle at metaphase under re-replication stress **Amy Ikui** Brooklyn College

35 9:45 AM A Humanized Yeast Platform Defines *in vivo* Targets of APOBEC3C Mutagenesis **Grant Brown** University of Toronto

Friday, August 19, 2022

10:30 AM–12:00 PM De Neve Lecture Auditorium

The editable genome

Session Chairs Yi Yin UCLA, United States; and Andreas Vestergaard Technical University of Denmark, Denmark

36 10:30 AM CRI-SPA–a mating based, CRISPR-Cas9 assisted method for high-throughput genetic modification of yeast strain libraries. **Paul Cachera** Denmark Technical University (DTU)

37 10:45 AM Yeast-based screening system to identify and optimize the anti-sense oligos that promote targeted base-editing in mRNA molecules by the ADAR enzymes **Ricky Steinberg** Bar Ilan university

38 11:00 AM Powerful Genome-wide Screening in any Species or Strain through Profiling of Hermes Insertion Mutations **Andrew Gale** Johns Hopkins University

39 11:15 AM A novel Cas3 base-editor for efficient directed evolution of complex metabolic pathways in *S. cerevisiae* **Anna Zimmermann** VIB

40 11:30 AM Transformation-mediated chromosome synthesis and replacement in eukaryotic cells **Alessandro Luis Venega Coradini** University of Southern California

11:45 AM Lightning Talks

Friday, August 19, 2022

12:00 PM–12:30 PM De Neve Lecture Auditorium

Ira Herskowitz Award Session Chair Michael Knop, University of Heidelberg

12:00 PM Maya Schuldiner, Weizmann Institute of Science

Friday, August 19, 2022

1:30 PM–2:30 PM De Neve Lecture Auditorium

DEI Discussion: Identifying Ways to Improve Inclusion in Science

Session Chair Tracy Johnson UCLA

Tracy Johnson will lead a discussion on ways to support inclusion in science.

Panelists:

Alexa Novales, University of California, Los Angeles

Dan Pollard, Western Washington University

Gustavo Silva, Duke University

Jacob Steenwyk, Vanderbilt University

Friday, August 19, 2022

3:00 PM-5:00 PM

Hermosa

BREWMOR: Bridging Research and Education With Model ORganisms

Session Chairs Michael Law, Stockton University and Jill Keeney, Juniata College

3:00 PM-4:00 PM

Introduction

Naomi Moresi- yEvo Lab: A University-High School collaboration to Evolve Caffeine Tolerance in Yeast

Lisa Scheifele- Build-a-Genome: Cutting-edge concepts using simple model organisms

Mark Barnby and Jane Kim- Student exploration of trinucleotide repeat expansion control by genes of unknown function in the yeast Saccharomyces cerevisiae

Breakout discussion 1

4:00 PM-5:00 PM

SGD presentation and discussion

Breakout discussion 2—applying SGD tools to your course design

Wrap-up discussion

Friday, August 19, 2022

3:00 PM–5:00 PM *De Neve Lecture Auditorium*

Getting more out of SGD

Session Chair Stacia Engel, Stanford University

Saturday, August 20, 2022

8:30 AM-10:00 AM

De Neve Lecture Auditorium

Evolution and population genomics II Session Chairs

Meru Sadhu NIH, NHGRI; and Julie Rojas University of Wisconsin-Madison, United States

41 8:30 AM Gene Presence Networks Predict Novel Respiratory Genes from Multiple Losses of Mitochondrial Complex I across Yeasts John Wolters UW-Madison

42 8:45 AM Impact of structural variants on gene expression variations in a yeast natural population **Andreas Tsouris** University of Strasbourg

43 9:00 AM Pararesistance: a mutation-independent mechanism of antifungal drug resistance **Jinglin Lucy Xie** Stanford University

44 9:15 AM The evolution of killer toxin resistance in the opportunistic human pathogen *Candida glabrata* **Paul Rowley** University of Idaho

45 9:30 AM Extensive sampling of *Saccharomyces cerevisiae* in Taiwan reveals ecology and evolution of predomesticated lineages **Isheng Jason Tsai** Academia Sinica

46 9:45 AM Domestication of *S. cerevisiae* in baking: a peek into the evolutionary history of your sourdough starter **Caiti Smukowski Heil** North Carolina State University

Saturday, August 20, 2022

10:30 AM–12:00 PM De Neve Lecture Auditorium

Mechanisms of Gene Regulation

Session Chairs Gustavo Silva Duke University, United States; and Chien-Der Lee UCSF, United States

47 10:30 AM The E2 ubiquitin conjugase Rad6 is a master regulator of translation during oxidative stress **Gustavo Silva** Duke University

48 10:45 AM Pathogenic missense mutations in genes encoding structural subunits of the RNA exosome complex cause distinct transcriptomic changes as well as altered interactions with RNA exosome cofactors **Maria Sterrett** Department of Biology, Emory University

49 11:00 AM Dynamic Phosphorylation of Eukaryotic Translation Initiation Factor 4A Couples Cell Growth and Translation **Sarah Walker** University at Buffalo, SUNY

50 11:15 AM Investigating the role of G4 DNA in transcription control in budding yeast Long Duy
Duong Mc Govern Medical School, University of Texas Health Science Center at Houston

51 11:30 AM Genetic interactions between cyclin C-Cdk8 and COMPASS regulate yeast meiosis **Michael Law** Biology Program, Stockton University

52 11:45 AM Forging connections between threonine metabolism and chromatin regulation JenniferChik University of California, San Diego

Saturday, August 20, 2022

1:30 PM-3:00 PM

De Neve Lecture Auditorium

Protein homeostasis and network conservation

Session Chairs

Jolanda van Leeuwen University of Lausanne; and Harsha Garadi Suresh University of Toronto

53 1:30 PM Pulse labeling reveals the tail end of protein folding by proteome profiling Thibault Mayor University of British Columbia

54 1:45 PM Genetic Variation in the Ubiquitin System Creates Complex, Pathway-Specific Effects on Proteasomal Protein Degradation **Mahlon Collins** University of Minnesota

55 2:00 PM An orthologous gene coevolution network provides insight into eukaryotic cellular and genomic structure and function **Jacob Steenwyk** Vanderbilt University

56 2:15 PM Proteomic and phosphoproteomic analysis of the cellular response to mis-made proteins caused by mistranslating tRNA variants **Matthew Berg** University of Washington

57 2:30 PM Decoupling growth and metabolism via PKA hyperactivation is linked to alterations in lipid homeostasis **Ellen Wagner** University of Wisconsin-Madison

58 2:45 PM Humanized yeast to measure the functional impact of human genetic variation in the mevalonate kinase gene **Farhat Zafar** Concordia University

Saturday, August 20, 2022

3:30 PM–5:00 PM De Neve Lecture Auditorium

Cell cycle and metabolism

Session Chairs Jennifer Cobb University of Victoria; and Gabriela Teplitz Université de Sherbrooke

59 3:30 PM From Chemostats to Single Cells: Miniaturized Technologies for Monitoring Yeast Metabolic Cycles **Tom Mickleburgh** North Carolina State University

60 3:45 PM Cross-talk between the DNA damage response and the Mediator of transcription **Gonen Memisoglu** The University of Chicago

61 4:00 PM Cip1 tunes cell cycle arrest duration upon calcineurin activation **Mackenzie Flynn** University of Massachusetts Chan Medical School

62 4:15 PM Decoding multisite phosphorylation by CDK **Michelle Conti** University of Massachusetts Chan Medical School

63 4:30 PM Quiescent yeast cells are equipped with the regulatory mechanism that suppresses re-entry into mitosis **Hideki Nakanishi** Jiangnan University

64 4:45 PM A novel role for phosphatidylinositol-3,5-bisphosphate in mitosis **Ayse Koca Caydasi** Koç University

Saturday, August 20, 2022

7:00 PM–7:30 PM De Neve Lecture Auditorium

GSA Presentations

7:00 PM GSA Poster Awards, **Elena Kuzmin**, Concordia University and **Bryce Taylor**, Loras College

7:10 PM GSA Presentation to Brenda Andrews, G3 Editor in Chief

7:15 PM Early Career Leadership Program Overview, **Joseph Ogbede**, University of British Columbia

Saturday, August 20, 2022

7:30 PM–8:00 PM *De Neve Lecture Auditorium*

YGM Lifetime Achievement Award Session Chair

Yi Yin, University of California, Los Angeles

7:30 PM Tom Petes, Duke University

Sunday, August 21, 2022

8:30 AM–10:00 AM De Neve Lecture Auditorium

Gene Regulation and Evolution

Session Chairs Jen Gallagher West Virginia University; and Pablo Villarreal Universidad de Santiago de Chile

66 8:30 AM *S. pombe wtf* genes use dual transcriptional regulation and selective protein exclusion from spores to cause meiotic drive **Ananya Nidamangala Srinivasa** Stowers Institute for Medical Research

67 8:45 AM Species-wide exploration of the inherited gene expression variation in yeast **Joseph Schacherer** University of Strasbourg / CNRS

68 9:00 AM Evolution of Acquired Resistance for Hydrogen Peroxide Involves Differential Sensing of Phosphate by TORC1 and Activation of the Transcriptional Factor Msn4 in *C. glabrata* compared with *S. cerevisiae* **Jinye Liang** University of Iowa

69 9:15 AM Kfc1, the yeast ortholog of Virilizer, is required for mRNA m⁶A methylation and meiosis **Zachory Park** Georgetown University

70 9:30 AM Functional dissection of the RNA polymerase trigger loop by deep mutational scanning **Bingbing Duan** University of Pittsburgh

71 9:45 AM The anticodon determines the impact of mistranslating tRNA^{Ala} variants in *Saccharomyces cerevisiae* **Ecaterina Cozma** University of Western Ontario

All poster authors have been invited to upload a pdf and audio overview of their poster. These electronic files will be available through the conference app August 15–September 9. Be sure to visit the app and leave your questions for the authors. Posters numbers followed by "V" are only available online. Poster numbers followed by "A" will be presented in person on Thursday, 7:00 p.m.–10:00 p.m. and those followed by "B" will be presented on Friday, 7:00 p.m.–10:00 p.m.

Disease Models and Aging	72–89
Evolution and population genetics	90–110
Gene Regulation	111–141
Genomics and System Biology	142–168
Genome Integrity	169–192
Intracellular Dynamics	193–239
New Technology and Resources	240–259
Yeast as a Tool	260-270

Disease Models and Aging

72A rDNA copy number is a determinant of replicative lifespan and facilitates further dissection of the aging processes in yeast. **Nathaniel Thayer** Calico Life Sciences LLC

73AVariability of the probiotic yeast *Saccharomyces cerevisiae* var. *'boulardii'* in genome, phenotype, and virulence **Alexandra Imre** University of Debrecen

74A Engineering all-substitution gene variant libraries using a single Cas9 guide RNA target sequence in pooled yeast populations **Cory Weller** National Human Genome Research Institute, National Institutes of Health

75A Impact of environmental stress on self-perpetuating protein aggregation in yeast **Yury Chernoff** Georgia Institute of Technology

76A Glycan remodeling on the yeast surface to permit directed evolution of antibody Fc regions **Tatiana Chernova** Emory University, Department of Biochemistry

77A The Canadian Rare Diseases Models and Mechanisms (RDMM) Network: Connecting novel disease gene discoveries to functional characterization research in model organisms **Philip Hieter** University of British Columbia

78A Plant extract targetting α -synuclein mediated toxicity in Parkinson Disease models **SONAL KAPUR** G. N. Ramachandran Protein Centre, Council of Scientific and Industrial Research-Institute of Microbial Technology, Chandigarh, India

79A The human pathogenic yeast *Cryptococcus neoformans* can utilize ferritin as an iron source **Won Hee Jung** Chung-Ang University **87** Impact of alanyl-tRNA synthetase editing deficiency in yeast **Hong Zhang** University of Maryland **80B** tRNA synthetase inhibitors increase lifespan in a *GCN4* dependent manner **Christine Robbins** University of New Mexico Health Sciences Center

81B A structure-function method to identify pathogenic missense single nucleotide variants in *COQ5*, a gene encoding a *C*-methyltransferase in coenzyme Q biosynthesis **Sining Wang** University of California, Los Angeles

82B Genetic Polymorphism that underlies Fungal Persistence interactions across a Mammalian Host Christopher NeVille University of Southern California

83B Identifying critical PxP adaptor binding sites in the yeast Vps13 VAB domain **Kevin Jeffers** The University of British Columbia

84B Protein interactions of PAS kinase, Pbp1, and Ptc6 in yeast reveal potential targets for ALS treatment **Colleen Newey** Brigham Young University

85B Identifying Genes Required for Nuclear Rejuvenation during Gametogenesis **Ben Styler** University of California, Berkeley

86B Analyses of missense single nucleotide variants in the *COQ4*, *COQ7*, and *COQ9* genes encoding proteins essential for coenzyme Q biosynthesis **Akash Jain** UCLA

88V Impairment of yeast PRPP synthetase activity affects cell signalling–a model for management and treatment for human neuropathies? **Michael Schweizer** Heriot Watt University

89V Testing all possible CPOX missense variants to proactively detect pathogenic variation **Warren van Loggerenberg** University of Toronto

Evolution and population genetics

90A Natural variation in the consequences of gene overexpression during osmotic stress **Maria Elena Vanacloig Pedros** Great Lakes Bioenergy Research Center, UW Madison

91A Evolved lager laboratory hybrids exhibit high fermentation capacity under beer fermentation **Jennifer Molinet** Universidad de Santiago de Chile

92A Population genomics of structural variations in *Saccharomyces uvarum* **Francisco Cubillos** Universidad de Santiago de Chile (USACH)

93A Exploring the role of RNA editing in overcoming short-term extreme environmental conditions **Shay Ben-AROYA** Bar-Ilan University

94A Assessment of reproduction isolation and fitness variation across coexisting *Saccharomyces cerevisiae* pre-domesticated lineages **Chen Hsiao** Biodiversity Research Center, Academia Sinica, Taipei, Taiwan

95A Search for genes involved in adaptation to low nitrogen conditions for wine production in wild and domesticated strains of *Saccharomyces cerevisiae* **Eduardo I. Kessi-Pérez** Universidad de Santiago de Chile (USACH)

96A The evolutionary divergence of transcription start sites (TSS) is shaped by the functional impact of 5' UTR (5' Untranslated Region) length **Yu ZHAN** Saint Louis University

97A The effect of cis-acting elements on copy number variant formation and dynamics during adaptive evolution **Julie Chuong** New York University, Center for Genomics and Systems Biology

98A Homology and Disease curation at SGD: budding yeast as a model for eukaryotic biology **Stacia Engel** Stanford University

99B Reversion dynamics of copy number variants in the absence of selection **Titir De** New York University

100B Evolutionary constraints override mutational constraints in redomestication of wild *S. cerevisiae* and *S. paradoxus* **Emery Longan** University of Rochester

101 Long-term adaptation to a secondary carbon source in *Saccharomyces cerevisiae* **Artemiza Martinez** Lehigh University

102B Experimental evolution for investigating the genetic basis of freeze-thaw tolerance **Leah Anderson** University of Washington

103B Characterization of *Candida albicans* error-prone polymerases in antifungal drug resistance and DNA damage **Michelle Agyare-Tabbi** University of Guelph

104B Exploring the evolutionary arms race between human PKR and vaccinia K3L **Michael Chambers** NIH-NHGRI

105B Expression of heterologous ADAR enzymes in yeast indicates editing activity is affected by temperature, and identifies the mdADAR1 as a hyper transcriptome diversifier **Adi Avram Shperling** Bar Ilan University

106B Effects of domestication on the sexual reproduction of *Saccharomyces Cerevisiae* **Annamarie Steed** University of Washington

107V Evolution of the Pleiotropic Drug Resistance (Pdr) Snq2/ Pdr18 gene subfamily in the hemiascomycete yeasts **Paulo Jorge Dias** Institute for Bioengineering and Biosciences (iBB), Institute for Health and Bioeconomy (i4HB), Instituto Superior Técnico, University of Lisbon

108V *MAT*α-composing genes for sex-determining transcription factors evolved as haploinsufficient genes monitoring genome size in *Saccharomyces cerevisiae* **Kazumasa Oya** Chiba university

109V Gene whose overexpression is adaptive illuminates the missing pieces of the cell **Nozomu Saeki** Okayama University

110V The neutral rate of whole-genome duplication varies among yeast species and their hybrids **Souhir Marsit** Université du Québec À Rimouski

Gene Regulation

111A WOR1, the master transcriptional factor in the positive transcriptional feedback loop, is required for the maintenance of opaque cell type in an epigenetic manner **Chien-Der Lee** UC San Francisco

112A Using SPRITE to investigate heat shock-dependent changes in 3D chromatin architecture and genome topology in *Saccharomyces cerevisiae* **Gurranna Male** Louisiana State University Health Sciences Center

113A Identify proteins that bind to a specific mRNA in the cell cycle using dCas13d-APEX2 fusions **Michael Polymenis** Texas A&M Univ

114A Natural variation in codon bias and mRNA folding strength interact synergistically to modify protein synthesis rates in *Saccharomyces cerevisiae* **Daniel Pollard** Western Washington University

115A Transcriptome fates in response to starvation are regulated by splicing **Jen Gallagher** West Virginia University

116A Docosahexaenoic acid modulates intracellular *myo*-inositol and its biosynthetic genes. **Marlene Murray** Andrews University

117A Study of the cellular component-dependent functions of Xrn1 **José Pérez-Ortín** Universitat de València

118A Cryptic translation events target yeast ncRNA transcripts for nonsense-mediated decay **Nicholas Guydosh** NIDDK/NIH

119A Understanding the role of J domain and RRM of Cwf23 in RNA splicing **Kirpa Yadav** Indian Institute of Science Education and Research, Bhopal

120A Kar4, the yeast ortholog of Mettl14, is required for mRNA m⁶A methylation and meiosis **Zachory Park** Georgetown University

121A "Terminators at the Terminus": Novel insights into the mechanism of regulation of sub-telomeric transcripts **Kathirvel Ramalingam** University of Hyderabad

122A Transcriptional Regulation by Histone H3 Lysine 4 Methylation in *S. cerevisiae* **Neha Deshpande** Texas A&M University

123A Predicting yeast transcriptional activation domains from amino acid sequences **Ananya Bahugudumbi** UC Berkeley

124A Monte Carlo simulations of GCN4 orthologs reveal features of transcriptional activation domains that confer high and low activity **Angelica Lam** Center for Computational Biology, University of California, Berkeley

125B Meiotic Regulation of the Unfolded Protein Response **Constantine Bartolutti** University of California, Berkeley

126B The hunt for the promoter element controlling Whi5's sizeindependent transcription **Jacob Kim** Stanford University

127B Investigating the role of the Spt5 C-terminal repeat domain and its phosphorylation in transcription regulation **Sanchirmaa Namjilsuren** University of Pittsburgh

128B One carbon metabolic enzymes and cell cycle progression **Staci Hammer** Texas A&M University

129B Genome-wide Analysis of the Transcriptional Response of Wild-type and adn2 Δ Cells in Response to Perturbation of the Cytokinetic Machinery Aimaiti Aikeremu University of Western Ontario

130B Modularization, minimization, and diversification of the yeast transcription factor repertoire **Daniel Lusk** University of Southern California

131B The transcription elongation factor Rtf1 regulates distribution of the nucleosome remodeler Chd1 on active genes **Sarah Tripplehorn** University of Pittsburgh

132B Investigating transcriptional interference induced by long undecoded transcript isoform (LUTI) expression **Kate Morse** UC Berkeley

133B Genetic dissection of transcription start site selection in *Saccharomyces cerevisiae* **Payal Arora** University of Pittsburgh

134B The decrease in mRNA decay as cell size increase to compensate for non-linear transcriptional scaling **Crystal Tsui** Stanford University

135B Differential regulation of the mitotic G1/S transcriptome is required for timely meiotic entry **Amanda Su** University of California, Berkeley

136B Environmental Effects on Transcriptional Activation Domain Function **Jordan Stefani** University of California, Berkeley

137B Examining the evolution of yeast transcription factor activation domains **Giovani Pimentel-Solorio** University of California, Berkeley

138B Engineering Synthetic Transcriptional Activation Domains from Conserved Sequence Properties **Melvin Soriano** University of California, Berkeley

139V Dominant effects of the histone mutant H3-L61R on Spt16gene interactions in budding yeast **Andrea Duina** Hendrix College

140V Understanding the Role of Cdk8 in Glycolysis Gene Regulation **Mary-Elizabeth Raymond** Queen's University

141V Expression of defective human *SHQ1* variants in yeast decreases the stability of H/ACA small nucleolar RNAs and impairs ribosome biogenesis **François Dragon** University of Quebec at Montreal

Genomics and Systems Biology

142A The yeast Ty1 retrotransposon contains a prion-like domain essential for transposition **Sean Beckwith** University of Georgia

143A Modeling the fitness cost of chromosomal duplication identifies determinants of aneuploidy toxicity **Julie Rojas** University of Wisconsin–Madison

144A A CRISPRi-based approach of identifying and quantifying fitness impacts of Hsp90 client-chaperone interactions. **Kieran Collins** Stanford University

145A Protein dynamics of whole-genome duplicates using singlecell imaging and automated analysis reveals mechanisms of gene retention **Rohan Dandage** Centre for Applied Synthetic Biology, Concordia University, Montreal, Canada

146A Engineering Yeast with Catalytically Active Human Proteasome Core **Aashiq Kachroo** Concordia University

147A Fine-tuning phylogenomics for admixed *Saccharomyces cerevisiae*: problems and possible methodological solutions with short- and long-read sequencing **Walter Pfliegler** University of Debrecen

148A Pseudodiploidy enhances homology directed repair in *Saccharomyces cerevisiae* **Simone Giovanetti** NIH

149A Data Integration Through Allele Curation at SGD **Edith Wong** Stanford University

150A The *Saccharomyces* Genome Database and the Gene Ontology: Best buds **Suzanne Aleksander** Stanford University

151A Integration of SGD regulatory and expression data into the GRNmap and GRNsight applications for modeling and visualizing small-to-medium gene regulatory networks **Kam Dahlquist** Loyola Marymount Univ

152A A systematic approach to mapping bypass suppressors of essential genes and essential gene pairs in *S. cerevisiae* **Clarence Hue Lok Yeung** University of Toronto, St. George

153A Consequences of thiol oxidative stress on cytosolic proteostasis in yeast **Alec Santiago** UTHealth

154A Integrative analysis of genomic loci linked to gene expression and growth reveals causal genes and mechanisms underlying complex traits **Kaushik Renganaath** University of Minnesota

155B Contaminated medicines: The role of arginine biosynthesis in N-nitrosamine toxicity **Joseph Ogbede** University of British Columbia, Vancouver

156B Analysis of ~10,000 CRISPR interference perturbations in a yeast cross **Joseph Hale** University of Southern California

157B Quantitative trait gene discovery by genome-wide reciprocal hemizygote scanning **Randi Avery** University of Minnesota

158B Genetic-Interaction Screens Identify Functional Redundancy and Regulators of Transcription Factors in Fission Yeast **Kurtis Marno Jones** University of Calgary

159B Systematic exploration of Complex HaploInsufficiency (CHI) in *Saccharomyces cerevisiae* **Thuy Nguyen** University of Toronto

160B Detection and quantification of genetic background effects using genome-wide, double barcoded, CRISPRi perturbations in a focused yeast cross **Ilan Goldstein** University of Southern California

161B Systematic analysis of temperature-sensitive alleles of essential genes uncovers new regulators of filamentous growth in yeast **Atindra Pujari** State University of New York at Buffalo

162B Investigating the genetic and metabolic changes in response to DNA damage stress in telomerase-mutant yeast **Taizina Momtareen** West Virginia University

163B Chromosome Substitution for Characterizing Epistasis **Cassandra Buzby** New York University

164B Characterization of lysine transport at the yeast vacuolar membrane and study of its physiological role **Evi Zaremba** Université Libre de Bruxelles

165B A screen for histone mutations that affect quiescence and chronological lifespan in *S. cerevisiae*. **Eric Small** University of New Mexico Health Sciences Center

166B Genetic Network Rewiring Between Distantly Related Yeast Species **Vanessa Pereira** Centre for Applied Synthetic Biology, Concordia University

167V Production of soybean ferritin variants with cadmiumbinding affinity by *in vivo* cloning and mutagenesis in *Saccharomyces cerevisiae* **Renato Riveros** Universidad Nacional Agraria La Molina

168V Global analysis of genetic suppression of partial lossof-function alleles **Sabine van Schie** Centre for Integrative Genomics–UNIL

Genome Integrity

169A Yeast Nucleolin Nsr1 Impedes Replication and Elevates Genome Instability at an Actively Transcribed Guanine-Rich G4 DNA-Forming Sequence **Shivani Singh** University of Texas Health Science at Houston

170A Mechanisms involved in differential telomere length homeostasis. **Gabriela Teplitz** Université de Sherbrooke

171A Phosphorylation-mediated Ccp1-Ndc80 switch at the N-terminus of CENP-T regulates kinetochore assembly in fission yeast **Fei Li** New York University

172A Deletion of telomeres via genetic engineering of circular chromosomes in *S. cerevisiae* **Melissa Mefford** Morehead State University

173A Centromeric sequence variation is widespread and affects cellular fitness **Brandon Fagen** The Stowers Institute for Medical Research

174A The relationship between an euploidy and chromosome instability in wild yeast **James Hose** University of Wisconsin-Madison

175A The INO80 and SWR1 chromatin remodeling complexes function in chromosome segregation and ploidy maintenance **Ines Pinto** Univ Arkansas

176A Novel insights into how Eco1p acetylation of Smc3p inhibits Scc2p activation of cohesin **Vincent Guacci** UC Berkeley

177B Using Mutational Scanning in *Saccharomyces cerevisiae MUS81* to Identify Synthetic Lethal Interactions **Anthony Oppedisano** University of British Columbia

178B The budding yeast superoxide dismutase Sod2 preserves nuclear genome integrity under oxidative stress **Sonia Vidushi Gupta** University of South Florida

179B Mechanisms of Rad5-mediated mutagenic repair of DNA gaps **Kate Jiang** University of Toronto

180B Using single-cell tracking to define DNA damage response heterogeneity **Peter Bartlett** University of Toronto

181B Engineering yeast to combat cosmic radiation: a new trajectory to study DNA damage and genome integrity **Hamid Gaikani** University of British Columbia

182B *pol30* mutants through two pathways to dissociating Srs2 to rescue DDT defects **Li Fan** University of Saskatchewan

183B Fork reversal activity of Rad5 and the helicase activity of Rrm3 interact in the prevention of DNA double-strand breaks in yeast **Julius Muellner** University of South Florida

184B Genetically engineering a strain of *S. cerevisiae* with a single circular chromosome **Austin Lytle** Morehead State University

185B Investigating the role of post-replication repair in the resolution of transcription-associated replication stress. **Leticia Dinatto Pereira** Terry Fox Laboratory, BC Cancer Research Centre

186B Contributions of Fumarase and the Histone Variant H2A.Z during Responses to DNA Damage and DNA Replication Stress **Ann Kirchmaier** Purdue Univ

187V G1-Cyclin2 (*CLN2*) promotes chromosome hypercondensation in *eco1/ctf7 rad61* null cells during hyper-thermic stress in *Saccharomyces cerevisiae* **Robert Skibbens** Lehigh University

188V Ortholog replacement reveals a novel function of the transcription factor TFIIIC complex in mitotic chromosome segregation **Akshi Gupta** Academia Sinica

189V A non-canonical Dun1 FHA domain interaction surface contributes to ligand specificity and resistance to genotoxic stress **Geburah Straker** University of Waterloo

190V The absence of *SAF1* and *CTF8* together contributes to MMS Resistance and HU Sensitivity in S. *cerevisiae* **Narendra Bairwa** Shri Mata Vaishno Devi University

191V The absence of F-box motif Encoding Gene *SAF1* and Chromatin Associated factor *CTF8* together contributes to MMS Resistance and HU Sensitive phenotype in *S. cerevisiae* **Meenu Sharma** Shri Mata Vaishno Devi University

192V Enhanced mutagenicity during meiosis: the involvement of DNA repair and recombination genes **Ayelet Arbel-Eden** Hadassah Academic College

Intracellular Dynamics

193A A noncanonical GTPase signaling mechanism controls exit from mitosis in budding yeast **Xiaoxue Zhou** Massachusetts Institute of Technology

194A Why is the yeast lag phase so long? **Lieselotte Vermeersch** KU Leuven

195A K29-linked unanchored polyubiquitin chains at crossroads with the functional wiring between ribosome biogenesis and cell division **Harsha Garadi Suresh** Donnelly Centre for Cellular and Biomolecular Research, University of Toronto

196A Regulation of Cdc42 Protein Levels Impacts a Cell Differentiation Program in Yeast **Beatriz Gonzalez** State University of New York at Buffalo

197A PAS kinase controls cellular NADP(H) levels through the phosphorylation and regulation of NAD kinase **Sakhawat Ali** Brigham Young University

198A Identifying the features of highly diverged Wtf proteins to elucidate the mechanism of action **Samuel Campbell** Stowers Institute for Medical Research

199A Exploring alternate start sites for a gene of unknown function in the yeast *Saccharomyces cerevisiae* Jill **Keeney** Juniata College

200A Investigating Kin4-independent functions of Lte1, a Mitotic Exit Network Activator **Anupama Seshan** Emmanuel College

201A Characterizing pathways that regulate prospore membrane morphology in meiosis II **Xheni Mucelli** University of Massachusetts Boston

202A The yeast mitochondrial succinylome: Implications for regulation of mitochondrial nucleoids **Lubomir Tomaska** Comenius University in Bratislava, Faculty of Natural Sciences, Department of Genetics

203A Abstract number not assigned

204A Regulated Secretion Mediates Yeast Cell Fusion **Mark Rose** Georgetown University

205A Cellular protein quality control is sensitive to levels of Caj1; a class II J-domain protein in budding yeast **Preeti** Sagarika Indian Institute of Science Education and Research, Bhopal

206A Re-evaluating the glucose-dependent nuclear localization of hexokinase 2 **Mitchell Lesko** University of Pittsburgh

207A A structural and functional analysis of *Nematostella vectensis* major intrinsic proteins in *Saccharomyces cerevisiae* **James Grissom** University of North Carolina at Charlotte

208A Fission yeast polycystin Pkd2 antagonizes the Hippo pathway Septation Initiation Network in cytokinesis **Debatrayee Sinha** University of Toledo

209A RNA editing by dysregulated Adenosine Deaminase Acting on RNA (ADAR) enzyme induces proteotoxic stress **amit ben david** bar ilan university

210A The sporulation-specific MAPK Smk1 plays a role in prospore membrane development late in meiosis II **Matt Durant** University of Massachusetts Boston

211A Dry3, a novel yeast hydrophilin is required for desiccation tolerance **Hugo Tapia** California State University–Channel Islands

212B Regulation and consequences of SNF1/AMPK complex control across different stress conditions **Karla Zuniga Gonzalez** The University of Manchester

213B Coq11 is an atypical short-chain dehydrogenase/reductase (SDR) that modulates coenzyme Q (CoQ) biosynthesis **Kelsey Feustel** University of California, Los Angeles

214B Integrating multiple single-cell phenotypes in the yeast stress response links activity of the ribosome-gene transcriptional repressor Dot6 to faster acclimation after stress **Rachel Kocik** University of Wisconsin-Madison

215B The regulation of endoplasmic reticulum stress in *Candida albicans* **Samuel Stack-Couture** Western University

216B Respiratory defects caused by mutations affecting the Endoplasmic Reticulum-Mitochondria Encounter Structure (ERMES) can be rescued by deletion of *COQ11* **Noelle Alexa Novales** University of California, Los Angeles

217B Amino acid mimicry: Insights into glyphosate transport and mitochondrial toxicity **Dionysios Patriarcheas** West Virginia University

218B Spo77 acts in a pathway with Cdc15 and Sps1 to regulate exit from meiosis II **Erin Klee** University of Massachusetts Boston

219B Elucidating the uptake of exogenous coenzyme Q and its delivery to mitochondrial respiratory complexes **Michael Guile** University of California, Los Angeles

220B Elucidating the identity and function of mitochondrial membrane contact site tethers in budding yeast gametogenesis **Cyrus Ruediger** University of California Berkeley

221B Meiotic Nuclear Pore Complex Remodeling Provides Key Insights into Nuclear Basket Organization **Grant King** UC Berkeley

222B DNA damage induced SUMOylation regulates nuclear protein quality control in *Saccharomyces cerevisiae* **Arun Kumar** BC Cancer Agency

223B Phosphoregulation of the yeast Pma1 H⁺-ATPase autoinhibitory domain is mediated by Ptk1/2 kinases and Glc7 PP1 phosphatase and is under TORC1 control Nadia Pia Guarini ULB

224B Mechanisms and functions of Whi5 phosphorylation at the Start transition of the budding yeast cell cycle **Jordan Xiao** Stanford University

225B Cbf1 as a pivotal point in the partitioning of glucose to respiration and lipid biogenesis through differential function of its phosphorylated forms. **Spencer Ellsworth** Brigham Young University

226B Differential regulation of Yeast Osh and ORP genes, supporting the evolution of genes for different functions and pathways **Kenneth Ewool** Brigham Young University

227B Adopting an ORFan and *AIM*(*33*)ing for a function. **Julia Iacovella** Saint Joseph's University

228B TORC1 Signaling Controls the Stability and Function of α -Arrestins Aly1 and Aly2 **Eric Jordahl** University of Pittsburgh

229B Cadmium Quantum Dots Affect Receptor Mediated Endocytosis and Cell Polarity **Nhi Le** Missouri State University

230B Stress-related localization of RNA processing proteins to the mitochondria **Sarah Sherts** Scripps College

231B Whi2 beyond TorC1 regulation **Terrance Cooper** University of Tennessee Health Science Center

232B Studying the Mechanism for Ricin-Induced Apoptosis **Daniel Judge** West Virginia University

233V Strain dependent insulation of the HOG and mating pathways **Taylor Scott** University of Wisconsin-Madison

234V Analysis of cell elongation phenomena caused by Massive expression of EGFP **shotaro namba** Okayama University

235V Candida albicans cells without Tor1 kinase N-terminal HEAT repeats are hypersensitive to cell wall stress and defective in mitochondrial function **Wanjun Qi** Boston Children's Hospital / Harvard Medical School

236V Checks and balances of the RTG pathway under arginine deprivation and canavanine exposure in *Saccharomyces cerevisiae* **Marina Druseikis** Hebrew University of Jerusalem

237V Met15 is not required for sulfur assimilation in Saccharomyces cerevisiae **Anne-Ruxandra Carvunis** University of Pittsburgh

238V The transmembrane domain of fission yeast polycystin Pkd2 is essential for both its localization and function **Mamata Malla** The University of Toledo

239V Gene by Environment Interactions reveal new regulatory aspects of signaling network plasticity Matthew Vandermeulen University at Buffalo

New Technology and Resources

240A Stringent genetic biocontainment in *Saccharomyces cerevisiae* by conditional stability of essential proteins **Stefan Hoffmann** University of Manchester

241A Efficient Information Coding Over Living Organisms **Rachel Cohen-Kupiec** Tel Aviv University

242A Application of CRI-SPA as a tool for identifying genes affecting the biosynthesis of polyketides and non-ribosomal peptides in *S. cerevisiae* **Andreas Vestergaard** Technical University of Denmark

243A Population genomic analysis reveals a large genomic and phenotypic diversity across South American *Lachancea cidri* strains **Pablo Villarreal** Universidad de Santiago de Chile

244A Protein Structural Orthologs and more using Predicted Protein Structures **Fred Dietrich** Duke University

245A Rapid, scalable, combinatorial genome engineering by Marker-less Enrichment and Recombination of Genetically Engineered loci (MERGE) **Mudabir Abdullah** Concordia University

246A PET plastic degradation using yeast: development of a whole-cell catalyst for MHET conversion into ethylene glycol and TPA **Raphael Loll-Krippleber** University of Toronto

247A Development of a high-throughput framework to improve the replicability of molecular biology experiments **Molly Monge** National Human Genome Research Institute, National Institutes of Health

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Yeast as a Teaching Tool

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263A Teaching genetics with yeast domestication case studies **Bryce Taylor** Loras College

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267B yEvo Lab: A University-High School Collaboration to Evolve Caffeine Tolerance in Yeast **Naomi Moresi** University of Washington

268B Investigating Genes of Unknown Function: Student Experience **Claire Magill** Juniata College

269B A Yeast CRISPR Course-Based Undergraduate Research Experience (CURE) **Brian Wasko** Western University of Health Sciences

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