Contents

Welcome Message 2
Local Organizing Committee 4
Delegate Information 6
Social Program 6
Code of Conduct 7
Guidelines for Presenters 8
Oral Presentations 8
Poster Presentations 9
Online Attendees 10
Pre-Meeting Workshops 10
Program Overview 11
Floor Map 12
Keynote Speakers 14
Scientific Program 16
Welcome Message

Dear Delegates ¡Bienvenidos! We warmly welcome you to the 2024 Annual Meeting of the Society for Molecular Biology and Evolution (SMBE 2024) in Puerto Vallarta, Mexico. We are thrilled to have you here in our beautiful country.

It has been a long journey since 2018 when we dreamed of hosting this world-class meeting in Mexico and now it is a reality. This is the first time the Annual SMBE meeting is hosted in mainland Latin America and in a developing/middle-income country. It is a significant gesture from the Society to hold the meeting outside the Global North, highlighting the long-term goal of becoming a more inclusive and global Society. We are honored to have received such trust from the Society and you, our guest, and we hope the meeting meets or even exceeds your scientific and personal expectations.

Mexico is one of the most megadiverse countries in the world and, therefore, has a long history of research in ecology, evolution, molecular biology, and genomics. In the last two decades, Mexico has seen the birth of at least three new research centers with complementary strengths: the National Laboratory of Genomics for Biodiversity (LANGEBIO, Cinvestav), the Center for Genomic Sciences Research (CCG, UNAM), and the International Laboratory for Human Genome Research (LIIGH, UNAM). Our local organizing committee combines members from these different institutions and our joint interests cover a wide range of bleeding-edge topics in Evolutionary Biology which we have reflected in a rich scientific program with an unprecedented number of 39 symposia. This includes Phylogenetics, Evolutionary and Population Genetics, Paleogenomics, Conservation, Crop Evolution, Machine Learning, Education, Medical Genomics, and more. We hope you’ll get to discuss lots of science, interact with as many delegates as possible and strengthen the Society’s mission.
We trust this year’s venue, Puerto Vallarta’s International Convention Center, will be an excellent place for our cherished Annual Meeting and that you’ll get the opportunity to enjoy some of the outstanding natural, entertainment, culinary and cultural experiences Puerto Vallarta has to offer, either the natural charm of its beaches embraced by the Sierra Madre mountain range; the essence of its culture, its gastronomy and traditions; and the warmth of their hospitality of its people. It is a magical destination with an authentic Mexican spirit.

We have strived to provide excellence in your travel and conference experience, including childcare, travel, accommodation and transport to and from the venue from key points across Puerto Vallarta. You can find more about these on the following pages, or you can approach any of us and our staff during the meeting.

We want to thank Artefacto Consultores, our Professional Conference Organizer for embarking in this effort and making this event a success. We also want to thank all the sponsors supporting this meeting. We strongly encourage you to visit their booths, as they are a key part of what has made this meeting possible.

We hope our efforts translate into memorable scientific and personal experiences and connections that will last well beyond the end of this meeting. Thank you for attending SMBE 2024, and we hope you enjoy your stay in Mexico.

On behalf of the Local Organizing Committee - ¡Gracias!
Selene Fernández and Andrés Moreno
Cinvestav
Local Organizing Committee (LOC)

Andrés Moreno Estrada  
Advanced Genomics Unit, Center for Research and Advanced Studies (CINVESTAV), Mexico.

María Avila Arcos  
International Laboratory for Human Genome Research (LIIGH), National Autonomous University of Mexico (UNAM), Mexico.

Valeria Souza  
Institute of Ecology, National Autonomous University of Mexico (UNAM), Mexico.

Diego Ortega Del Vecchyo  
International Laboratory for Human Genome Research (LIIGH), National Autonomous University of Mexico (UNAM), Mexico.

Federico Sánchez Quinto  
International Laboratory for Human Genome Research (LIIGH), National Autonomous University of Mexico (UNAM), Mexico.

Mashaal Sohail  
Center for Genomic Sciences (CCG), National Autonomous University of Mexico (UNAM), Mexico.

Diego Cortez Quezada  
Center for Genomic Sciences (CCG), National Autonomous University of Mexico (UNAM), Mexico.

Selene Fernández Valverde  
Formerly at CINVESTAV, Mexico. Currently: UNSW RNA Institute / School of Biotechnology & Biomolecular Sciences, UNSW Sydney, Australia.

Karla Sandoval Mendoza  
Equity and Gender Office of the Center for Research and Advanced Studies (CODIGO-C), CINVESTAV, Mexico.
LOC Support Team

**Event Planner Coordinator**
Karla Patricia Benítez Castrejón  
Center for Research and Advanced Studies (CINVESTAV), Mexico.

**Scientific Program Copyeditor**
Carmina Barberena Jonas  
Center for Research and Advanced Studies (CINVESTAV), Mexico.

Professional Conference Organizer (PCO) Team

**PCO Director**
Annette Aguilar Bustamante  
ARTEFACTO CONSULTORES, Mexico.

**PCO Staff Manager**
Santiago Iker Aguilar  
ARTEFACTO CONSULTORES, Mexico.

LOC Volunteers

José Antonio Corona  
Laura Carrillo
Viridiana Villa Islas  
Sofía Vieyra
Amara Shaukat  
Daniela Orozco
Walter Nicolás  
Miguel Navarro
Victoria Pastor  
Florencia Alvarez
Fernanda García  
Carmina Barberena
Ram González  
Ernesto Garfias
Delegate Information

1. Registration
   Date: Sunday, 7 July 2024.
   Time: From 14:00 to 18:00
   Venue: Convention Center, Puerto Vallarta, México.

   *SMBE 2024 registration includes: Access to all scientific sessions, Delegate bag, welcome cocktail, lunch breaks, coffee breaks, and poster session refreshments.*

   *SMBE Gala Dinner ticket is NOT included in the registration fee.*

2. Internet Access
   Network: SMBE2024
   Password: holaamigo

Social Program

Welcome Cocktail
   Date: Sunday, 7 July 2024.
   Time: 19:00
   Venue: Convention Center, Puerto Vallarta, México.

Gala Mexican Dinner
   Date: Wednesday, 10 July 2024.
   Time: 19:00
   Venue: Host hotel
   Paradise Village Hotel, Nuevo Nayarit, México.

   - Tickets must be pre-purchased at $85 USD during registration or by emailing attendancesmbe2024@gmail.com.
   - Free transportation will be provided using shuttle route 1 (blue line on the travel guide)
Harassment, Discrimination and Liability

SMBE 2024 attendees are expected to adhere to SMBE’s Code of Conduct. SMBE is dedicated to providing a safe, hospitable, and productive environment for all members. Accordingly, SMBE prohibits all forms of discrimination and harassment (including among members, volunteers, and staff) in all Society activities, including events (online or in person), journal correspondence, social media, etc). Behaviour that undermines the integrity of intellectual discourse is an impediment to scientific progress and will not be tolerated. Unacceptable treatment of others includes (but is not limited to) harassment, stalking, belittling, discrimination, bullying/intimidation, assault, trolling, and retaliation (see above link for descriptions). Any misconduct on the basis of gender, gender identity, sexual orientation, age, disability, physical appearance, race, religion, national origin, ethnicity, or other descriptive categories will not be tolerated. If you need to report an incident, please contact our Safety Officer, Paula Brantner at pbworkolutions@gmail.com

SMBE code of conduct and SMBE Allies

At the next SMBE 2024 meeting in Puerto Vallarta, Mexico, you will notice some attendees wearing a ribbon indicating their status as SMBE Allies. These allies are trained to provide support to those who are victims or witnesses of inappropriate behavior that may violate the SMBE Code of Conduct. Their role is to listen, help affected individuals deal with the situation and provide them with information about their options, including the possibility of filing complaints. However, the allies are not involved in investigations or the imposition of sanctions. In addition, they are committed to creating safe spaces by acting as active observers during the event.

Broadcasting Policy

The SMBE Annual Meeting supports the communication and discussion of science. Information presented at the Meeting (in oral or poster format) may be reported and discussed by attendees and science writers via blogs, social media, or other formats, unless any of the authors requests otherwise. We do request that communications are respectful and do not directly reproduce visual materials (e.g., no posting of photos of slides or posters) unless permission is obtained from the presenter or if they have already made this information freely available in an open-source forum. If a presenter does not want information from his/her presentation to be photographed at all, or broadcast, they should make this clear in their talk/poster and we ask that attendees respect this. If you have questions or concerns about this policy, or would like to report an abuse of it, please contact any member of the Local Organizing Committee or email Paula Brantner at pbworkolutions@gmail.com
Guidelines for oral presentations

Symposia have been allocated various durations depending on the number of presenters. Please check the program to see the allocated time for each talk.

- Allocated time for Invited Speakers: 20 minutes + 5 minutes for Q&A.
- Allocated time for Contributed Talks: 12 minutes + 3 minutes for Q&A.
- Presentation format and submission: Speakers are strongly encouraged to send their presentation in PDF format to avoid potential incompatibilities. Powerpoint is also accepted but the staff cannot ensure proper formatting.
- Presentations must be sent to the following email address before the conference: smbe24speakers@gmail.com.
- If you have any issue providing your presentation please approach the staff at the front desk of the convention center.

Please arrive to your presentation room at least 15 minutes before your presentation so you can get prepared and meet the session chair.

Remote Speakers

Remote speakers have been requested to send a pre-recorded video of their presentation, which will be played on site during their respective symposium. However, remote speakers will be online during the Q&A session following their talk to be able to answer questions from the public. Remote speakers will receive a URL link via email with their credentials to connect live during their Q&A session.
Poster sessions will be in-person only.

Poster presentations have been distributed across 3 sessions according to the topics of symposia presented each day. Numbered boards will be used to exhibit posters in three groups colored by date:

- **Orange numbers: Monday 8 July**
- **Blue numbers: Tuesday 9 July**
- **Green numbers: Wednesday 10 July**

- Posters assigned to **Session 1** (Monday 8 July, 14:20-15:50), must be on display from 9:00-15:50 in the poster exhibition hall using the board marked with your poster number (e.g., **100-Mon**). Posters assigned to **Session 1** should be removed by 18:30 on Monday, July 8.

- Posters assigned to **Session 2** (Tuesday 9 July, 13:20-14:50), must be on display from 9:00-14:50 in the poster exhibition hall using the board marked with your poster number (e.g., **100-Tue**). Posters assigned to **Session 2** should be removed by 20:00 on Tuesday, July 9.

- Posters assigned to **Session 3** (Wednesday 10 July, 13:20-14:50), must be on display from 9:00-14:50 in the poster exhibition hall using the board marked with your poster number (e.g., **100-Wed**). Posters assigned to **Session 3** should be removed by 17:30 on Wednesday, July 10.

**Check your poster number!**

Follow the QR code to download the poster presentations schedule

**Upon Arrival**

- Posters must be brought to the meeting by the presenter.
  - Recommended poster size: 0.70 x 1 m (width x height)
  - Dimension limits: 0.80 x 1.20 m (width x height)
- Pushpins will be provided by the conference staff for presenters to put up their posters.
- Set-up, removal, and storage of posters are the responsibility of presenters. Any posters remaining on the boards after each poster session will be disposed of by the conference staff.
- Poster presenters are requested to stand-by their posters during the allocated time to make the brief introductory presentation and to take part in the poster discussion.
Guidelines for Online attendees

Live broadcasting

- SMBE 2024 will host five parallel sessions throughout most of the event. Broadcasting of oral presentations will be exclusively available to SMBE 2024 delegates who registered to attend the conference online. Access will be provided through the SMBE 2024 website (https://smbe2024.org) using a password protected link per user.
- Online attendees will receive an email from the conference staff prior to the event with their access credentials. Live broadcasting will take place throughout the event under UTC -6 time zone according to the schedule of the scientific program.

On-demand streaming

- Talks will be recorded and accessible upon completion of each symposium in order to give the opportunity to delegates to virtually attend symposia they may have missed.
- Recorded talks will be available for on-demand streaming for 4 weeks after the end of the event. An email will be sent to both onsite and online attendees with credentials to access recorded talks.
- This will be limited to those talks with prior authorization by the speaker to be recorded and will be available by user/password access through the SMBE 2024 website for on-demand streaming.

Guidelines for Workshops

Pre-congress Workshops

On Sunday July 7th, there will be three training workshops that will take place before the main SMBE 2024 conference starts. Specific times and locations are as follows:

- **Introduction to programmatic access to EnsEMBL.**
  - Costa Alegre Hall (upper floor) from 11:00 to 16:00
- **Introduction to STDPOPSIM workshop (Popgen).**
  - Boca de Tomates Hall from 12:00 to 14:00
- **GENHIST Competition kickoff at SMBE (Popgen).**
  - Boca de Tomates Hall from 14:00 to 16:00

*Please note that these workshops have limited capacity and access is restricted to pre-registered participants only.*
# Program Overview

## Day 1
- **Sunday 7 July**
- **8:00-19:00**: SMBE Council Meeting (Council members only)
- **11:00-16:00**: Workshop On site “Introduction to programmatic access to EnSeMBL” (Hall: Costa Alegre)
- **12:00-14:00**: Workshop On site “Introduction to STDPopsim workshop” (Hall: Boca de Tomates)
- **14:00-16:00**: Workshop On site “GENHIST kick-off at SMBE” (Hall: Boca de Tomates)
- **14:00-18:00**: Registration
- **18:00-19:00**: Plenary Hall (Los Tules) – Opening Keynote Speaker: Stephen Wright
- **19:00-20:00**: Welcome Cocktail

## Day 2
- **Monday 8 July**
- **9:00-11:00**: Plenary Hall (Los Tules) – Graduate Student Excellence Awards
- **11:00-11:30**: COFFEE BREAK
- **11:30-13:30**: HALL NAME
  - Los Tules (Plenary)
  - Open Symposium I
  - Associate Editors’ Symposium
  - Not just No, but...: New applications for QHC from ecology to phylogenomics
  - Clustering of human cohorts beyond race and ancestry: Towards redefined thinking in biogeography
  - Greater and Sustainable Computing in Molecular Evolution: Methods, Algorithms, Tools, and Protocols
- **13:20-14:20**: LUNCH BREAK
- **14:20-15:50**: Poster session 1
  - Boca de Tomates: MBE editors meeting
  - Human evolution in the genomic era
  - Exploring the evolutionary impacts of extreme habitats
  - Unlocking the hidden dimensions of genomic diversity within species
  - Structural/phylogenetic investigating deep evolutionary history using protein structure
  - Progress and challenges for understanding the molecular evolution of organisms across Eukarya
- **16:00-22:00**: Paradise Village Hotel: MBE Editors dinner

## Day 3
- **Tuesday 9 July**
- **9:00-10:00**: Plenary Hall (Los Tules) – Keynote Speaker: Alicia Mastretta-Yanes
- **10:00-10:30**: COFFEE BREAK
- **10:30-12:20**: HALL NAME
  - Los Tules (Plenary)
  - Open Symposium II
  - Exploring the Frontiers of Single-Cell Biology in Diverse Organisms
  - IDEA symposium
  - Aging from a multi-disciplinary overview: evolution, longevity and biomedicine
  - Haptotaxis-based methods and frameworks for inference of evolutionary history
  - Everything that has to become new: comparative genomics and museum specimens
- **12:20-13:20**: LUNCH BREAK
- **13:20-14:50**: Poster session 2
  - Boca de Tomates: SMBE Business meeting
- **14:50-17:10**: COFFEE BREAK
- **17:10-17:40**: Poster session 3
  - Boca de Tomates: GBE editors meeting
  - Evolutionary medical genetics
  - Palaeogenomics and human evolutionary history: new insights and novel methods
  - Pushing the boundaries of conservation genetics
  - Molecular evolution through metagenomics
  - Transportable elements in the population genomics era: Toward a new understanding of their contribution to evolution
  - They work by sharing their experience with others
  - Oceans, Molecular Biology, and the Future of Forensic Science
- **17:40-19:30**: Poster session 4
  - One Health and microbial evolution: New ideas and perspectives
  - Doing local: Using engaged research practices to understand regional-scale interactions
  - Impact of environmental changes on primate diversity and strategies for resilience
  - Animal palaeogenomics beyond higher taxonomies
  - Oceans, Molecular Biology, and the Future of Forensic Science
- **20:00-22:00**: Paradise Village Hotel: GBE Editors dinner

## Day 4
- **Wednesday 10 July**
- **9:00-10:00**: Plenary Hall (Los Tules) – Keynote Speaker: Aida Andrés
- **10:00-10:30**: COFFEE BREAK
- **10:30-12:20**: HALL NAME
  - Los Tules (Plenary)
  - Open Symposium III
  - Novel approaches to study plant domestication: disentangling the complex evolutionary history of crops
  - Advances in Machine Learning for Evolutionary Dynamics
  - Unveiling the evolutionary history of pathogens through palaeogenomics
  - Science in the Spotlight: Empowering Education and Public Engagement with Experimental Molecule Evolution
- **12:20-13:20**: LUNCH BREAK
- **13:20-14:50**: Poster session 5
  - Boca de Tomates: MBE & GBE ‘Q&A session’
  - Evolution of microbial co-metabolism: Is the sum of parts greater than the whole?
  - Human population demography and adaptation signals in the Americas
  - Spatial population genetics: where are we now?
  - Hoxdomestic: from powerhouses to processors and from marker to meaning
  - Depicting the functional and adaptive effects of genomic structural variation
- **19:00-23:00**: GALA DINNER at Paradise Village Hotel

## Day 5
- **Thursday 11 July**
- **9:00-10:50**: HALL NAME
  - Los Tules (Plenary)
  - Open Symposium 2
  - New computational approaches to estimate past demographic events and natural selection
  - Epigenetic inheritance: From molecular mechanisms to evolutionary consequences
  - Decoding the part to safeguard the future
  - Human genetic variability in the Fargenomic era
- **10:50-11:20**: COFFEE BREAK
- **11:20-12:20**: Plenary Hall (Los Tules) – Closing Keynote Speaker: Scott Edwards
- **12:20-14:20**: Awards Ceremony and Introduction to SMBE 2025
Keynote Speakers

Stephen Wright
SMBE President
University of Toronto, Canada

Stephen is the current President of the Society for Molecular Biology and Evolution (SMBE). His research focuses on understanding nucleotide polymorphism and genome evolution in natural plant populations. He explores questions such as the role of mutation vs. natural selection in genome structure evolution, how population history and mating systems affect genetic variability, and the rate and genetic basis of adaptive evolution and deleterious mutation. He uses DNA sequence polymorphism and molecular evolution analysis, large-scale genome sequence data analysis, and population genetic theory to investigate these questions. He applies these approaches in a comparative context, studying both model and non-model organisms, to understand genome diversity and structure patterns. His current projects include studying transposable element evolution, the impact of recombination and mating systems on genome evolution, the effects of demographic history and natural selection on genetic diversity, and the role of gene and genome duplication in species diversification and genome evolution.

Alicia Mastretta-Yanes
CONAHCYT - UNAM, Mexico

Alicia is a biologist from the National Autonomous University of Mexico (UNAM), and holds a PhD from the University of East Anglia, England. She currently Works as a CONAHCYT Research Fellow at Instituto de Ecología - UNAM. Her research focuses on incorporating genetic diversity into conservation using evolutionary approaches, spanning diverse ecosystems such as the Lacandona jungle, sky-islands, polluted forests, and Mexican agroecosystems. She contributed to the development of genetic diversity indicators, now adopted by the Global Biodiversity Framework, and she is actively involved in co-formulating approaches for nations to monitor and safeguard genetic diversity on a global scale.
Aida is Professor of Population and Evolutionary Genomics at University College London (UK). She is interested in how organisms adapt to their environment. In her work, this means analysing genomes, both modern and ancient, to infer how natural selection mediates genetic adaptations. Her group works mostly on humans, as they have an interesting history of fast colonisation of diverse habitats, and in endangered primates, where the ability to adapt to quickly changing environments is crucial for survival. Her group tackles these questions using genomic approaches to study the processes of adaptation, population genetic techniques to make inferences on the history of selected alleles, and functional information to infer the consequences in present-day phenotypes of previously adaptive alleles. The group is particularly interested in the types of natural selection that maintain diversity within populations (e.g. balancing selection) or that create differences among populations (e.g. local adaptation), as well as adaptive introgression.

Scott holds a B.A. from Harvard University (1986) and a PhD from the University of California, Berkeley (1992). Following his doctoral studies, he served as an Alfred P. Sloan Postdoctoral Fellow in Molecular Evolution at the University of Florida, Gainesville (1992-94). As a scientist, he has broad interests in the evolution of life on earth and the processes that have generated biodiversity. His research primarily utilizes birds as models to study patterns of speciation, biogeography, evolution of the genome, and the process of adaptation. This work has exposed his lab to a wide range of questions, from the evolution of immune genes and disease resistance to how best to reconstruct the tree of life.
## Scientific Program

### Day 1 (7 July)

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<thead>
<tr>
<th>Time</th>
<th>Event</th>
<th>Location</th>
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<tbody>
<tr>
<td>14:00-18:00</td>
<td>Registration</td>
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<tr>
<td>12:00-14:00</td>
<td>Workshop On site “Introduction to STDPOPSIM workshop” (Popgen)</td>
<td>Boca de Tomates</td>
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<td>14:00-16:00</td>
<td>Workshop On site “GENHIST kickoff at SMBE” (Popgen)</td>
<td>Boca de Tomates</td>
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<tr>
<td>11:00-16:00</td>
<td>Workshop Online “Introduction to programmatic access to EnsEMBL”</td>
<td>Costa Alegre</td>
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<td>18:00-19:00</td>
<td>Opening Keynote Speaker</td>
<td>Los Tules</td>
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<td>19:00-20:00</td>
<td>Welcome Cocktail</td>
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### Day 2 (8 July)

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<th>Event</th>
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<tr>
<td>9:00-11:00</td>
<td>Graduate Student Excellence Awards</td>
<td>Los Tules</td>
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<tr>
<td>9:00-9:13</td>
<td>Bárbara Sousa da Mota</td>
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<td>9:13-9:26</td>
<td>Benjamin Moran</td>
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<td>9:26-9:39</td>
<td>Christopher Blake</td>
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<td>9:39-9:52</td>
<td>Jaison Jeevan Sequeira</td>
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<td>9:52-10:05</td>
<td>Maria José Palma Martinez</td>
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<td>10:05-10:18</td>
<td>Mariela Tenorio</td>
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<td>10:18-10:31</td>
<td>Meaghan Marohn</td>
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<td>10:31-10:44</td>
<td>Siliang Song</td>
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<td>10:44-10:57</td>
<td>Sung-Ya Lin</td>
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<tr>
<td>11:00-11:30</td>
<td>COFFEE BREAK</td>
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<tr>
<td>11:30-13:20</td>
<td>S39-Associate Editors’ Symposium</td>
<td>Los Tules</td>
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<tr>
<td>11:30-11:45</td>
<td>Aida Ouangraoua</td>
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<td>11:45-12:00</td>
<td>Carolin Kosiol</td>
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<td>12:00-12:15</td>
<td>Jianzhi Zhang</td>
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<td>12:15-12:30</td>
<td>Joanna Kelley</td>
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<td>12:30-12:45</td>
<td>Kirk Lohmueller</td>
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<td>12:45-13:00</td>
<td>Maud Tenaillon</td>
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<tr>
<td>13:00-13:15</td>
<td>Adam Eyre-Walker</td>
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</tbody>
</table>
Scientific Program

Day 2 (8 July)

S38-Open Symposium 1

11:30 - 13:20

Boca de Tomates

11:30-11:45
Ulises Rosas
Size matters: revealing the genes controlling shot apical meristem gigantism in cacti

11:45-12:00
Navya Shukla
Investigating Functional Convergence Across Millions Of Years Of Evolution

12:00-12:15
Christian Landry
Compensatory mutations potentiate constructive neutral evolution by gene duplication

12:15-12:30
Dulce Valdivia Martínez
Exploring the role of tRNA regulation in the transition to multicellularity of the amoeba Dictyostelium discoideum.

12:30-12:45
Landen Gozashti
How repeats rearrange chromosomes in deer mice

12:45-13:00
Ying Zhen
Firefly toxin lucibufagins evolved after the origin of bioluminescence

13:00-13:15
Leon Hilgers
Seven new reference-quality genomes illuminate the genomic evolution of genetic sex determination in turtles

13:15-13:20
Paul Taylor
Insights into Human Neurotransmission through Molecular Evolution Studies in Bacteria

S32-Not just Ne Ne-more: New applications for SMC from ecology to phylogenies.

11:30 - 13:20

Olas Altas

11:30-11:55
Noah Rose
Mosquito evolution and the emergence of mosquito-borne disease in the human era

11:55-12:10
Anastasia Ignatieva
Detecting structural variation in reconstructed genealogies

12:10-12:25
Toby Kovacs
Drivers of historical population declines in Australian Marsupials: are humans behind the wheel?

12:25-12:40
Alba Nieto Heredia
AI and demographic inference in structured populations

12:40-12:55
Arun Durvasula
Accurate inference of population history in the presence of background selection

12:55-13:20
Stefan Strütt
Joint inference of evolutionary transitions to self-fertilization and demographic history using whole-genome sequences

S8- Clustering of human cohorts beyond race and ancestry: Towards relational thinking in genomics

11:30 - 13:20

Las Pilitas

11:30-11:45
Hussein Mohsen
What is in a discrete category? Clustering genomics cohorts beyond race, ethnicity—and ancestry

11:45-12:00
Simon Gravel
Genetically informed representations of ancestry and ethnicity

12:00-12:15
Luke Anderson-Trocmé
Breaking Boundaries: Leveraging Continuous Models for Improved Population Genetics Analyses

12:15-12:30
Benjamin Peter
Quantitative Interpretations of Principal Component Analysis

12:30-12:45
John Novembre
Non-parametric representations of structure in genetic ancestry through time

12:45-13:00
Landen Gozashti
Joint inference of evolutionary transitions to self-fertilization and demographic history using whole-genome sequences

13:00-13:15
Simon Gravel
Genetically informed representations of ancestry and ethnicity

13:15-13:20
Luke Anderson-Trocmé
Breaking Boundaries: Leveraging Continuous Models for Improved Population Genetics Analyses

S36- Greener and Sustainable Computing in Molecular Evolution: Methods, Algorithms, Tools, and Protocols

11:30 - 13:20

Costa Alegre

11:30-11:45
Beatriz Mello
Green Computing in Molecular Evolution and Phylogenetics for the Global South

11:45-12:00
Bui Minh
CMAPLE: efficient phylogenetic inference in the pandemic era

12:00-12:15
Sudhir Kumar
MEGA 12: Advancing Green Computing and Phylogenomics
### Scientific Program

#### Day 2 (8 July)

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>11:30 - 13:20</td>
<td>S36- Greener and Sustainable Computing in Molecular Evolution: Methods, Algorithms, Tools, and Protocols</td>
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<tr>
<td>12:35-12:50</td>
<td>Gavin Huttley</td>
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<td>12:50-13:05</td>
<td>Jians Gao</td>
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<tr>
<td>13:05-13:20</td>
<td>Li Liu</td>
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<tr>
<td>13:20 - 14:20</td>
<td>LUNCH BREAK</td>
</tr>
<tr>
<td>14:20 - 15:50</td>
<td>Event: MBE Editors Meeting</td>
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<tr>
<td>15:50 - 18:30</td>
<td>S5- Human evolution in the genomic era.</td>
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<tr>
<td>15:50 - 16:15</td>
<td>Katherine Pollard</td>
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<td>16:15 - 16:30</td>
<td>Erin Gilbertson</td>
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<tr>
<td>16:30 - 16:45</td>
<td>Ryder Easterlin</td>
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<tr>
<td>16:45 - 17:00</td>
<td>Maddy Comerford</td>
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<td>17:00 - 17:15</td>
<td>Samvardhini Sridharan</td>
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<td>17:15 - 17:30</td>
<td>Eva Briggs Barril</td>
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<td>17:30 - 17:45</td>
<td>Moises Coll Macia</td>
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<tr>
<td>17:45 - 18:10</td>
<td>Bo Xia</td>
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<tr>
<td>15:50 - 18:30</td>
<td>S12-Exploring the Evolutionary Effects of Admixture</td>
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<tr>
<td>15:50 - 16:15</td>
<td>Alexander Ioannidis</td>
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<td>16:15 - 16:30</td>
<td>Alexander Kirschel</td>
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<td>16:30 - 16:45</td>
<td>Daniel Powell</td>
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<td>16:45 - 17:00</td>
<td>Lucia Morales Reyes</td>
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<tr>
<td>17:00 - 17:15</td>
<td>Maria Fariello Rico</td>
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<tr>
<td>17:15 - 17:30</td>
<td>Andrew Vaughn</td>
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<tr>
<td>15:50-18:30</td>
<td><strong>Scientific Program</strong></td>
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<tr>
<td>17:30-17:45</td>
<td><strong>S12-Exploring the Evolutionary Effects of Admixture</strong></td>
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<tr>
<td></td>
<td>Aaron Pfennig</td>
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<td></td>
<td>Complex neutral processes drive the evolutionary fate of Neanderthal alleles in 30,780 admixed genomes with African-like and European-like ancestry</td>
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<tr>
<td>17:45-18:10</td>
<td>Emilia Huerta Sanchez</td>
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<tr>
<td></td>
<td>Evolutionary insights from admixed genomes</td>
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<tr>
<td>15:50-18:30</td>
<td><strong>S24- Unlocking the hidden dimensions of genomic diversity within species.</strong></td>
</tr>
<tr>
<td>15:50-16:15</td>
<td>Mayra Furlan-Magaril</td>
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<td>Chromatin 3D conformation of a silent genome: the case of nucleated erythrocytes</td>
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<td>16:15-16:30</td>
<td>Paco Majic Bergara</td>
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<td>On mutational neighbourhoods and their influence on evolutionary processes</td>
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<tr>
<td>16:30-16:45</td>
<td>James Phipps-Tan Sheng Yi</td>
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<td></td>
<td>Beyond averages: transcriptional variability in outbred Drosophila melanogaster and its environmental and genetic dependence</td>
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<tr>
<td>16:45-17:00</td>
<td>Thea Rogers</td>
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<td>Novel topological units characterise a distinct regulatory architecture underlying the evolution of complex traits in coleoid cephalopods</td>
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<tr>
<td>17:00-17:15</td>
<td>Christabel-Fló Bucao</td>
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<td></td>
<td>Gene expression variability implies stable cis-regulation of brain genes across non-nervous organs</td>
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<td>17:15-17:30</td>
<td>Justin Wilcox</td>
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<td>Population genomics of wild avian embryos uncovers hidden genetic diversity</td>
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<tr>
<td>17:30-17:45</td>
<td>Gabriela Santos Rodríguez</td>
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<td></td>
<td>The evolution of transcriptome complexity using Oxford Nanopore long-read sequencing technology.</td>
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<tr>
<td>17:45-18:10</td>
<td>Aurora Ruiz-Herrera</td>
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<td>Plasticity of 3D chromatin folding across timescales</td>
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<tr>
<td>15:50-18:30</td>
<td><strong>S1- Structural phylogenetics: investigating deep evolutionary history using protein structure</strong></td>
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<tr>
<td>15:50-16:15</td>
<td>Martin Steinegger</td>
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<td>Supercharged Protein Analysis in the era of AI</td>
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<tr>
<td>16:15-16:30</td>
<td>Hector Romero</td>
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<td>Exploring protein evolution through natural and simulated sequences using experimental and modeled 3D structures</td>
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<tr>
<td>16:30-16:45</td>
<td>Stefano Pascarelli</td>
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<td>AlphaHOG, a protein structure-based reference classification to improve orthology inference</td>
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<td>16:45-17:00</td>
<td>David Moi</td>
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<tr>
<td></td>
<td>Foldtree. Empirical benchmarking of structural phylogenetics methods</td>
</tr>
<tr>
<td>17:00-17:25</td>
<td>Betul Kaçar</td>
</tr>
<tr>
<td></td>
<td>Early protein evolution using deep time sequence and structure reconstructions</td>
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<tr>
<td>17:25-17:40</td>
<td>Desiree Langer</td>
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<td></td>
<td>Structural phylogenetics of the jelly roll fold sheds light on viral evolution</td>
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<tr>
<td>17:40-17:55</td>
<td>Claudia Álvarez Carreno</td>
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<td>Polyphyletic insertions in the bacterial DNA-directed RNA polymerase</td>
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<td>17:55-18:10</td>
<td>Charles Carter, Jr</td>
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<td></td>
<td>Structural Enzymology, Phylogenetics, Differentiation and Symbolic Reflexivity at the Dawn of Biology</td>
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<tr>
<td>15:50-18:30</td>
<td><strong>S3- Progress and challenges for understanding the molecular evolution of sex chromosomes across Eukarya</strong></td>
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<tr>
<td>15:50-16:15</td>
<td>Gabriel Marais</td>
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<tr>
<td></td>
<td>The Silene latifolia genome and its giant Y chromosome</td>
</tr>
<tr>
<td>16:15-16:30</td>
<td>Erik Fogh Sorensen</td>
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<tr>
<td></td>
<td>The struggle of being a sex chromosome: Why X has a lower diversity than expected in primates</td>
</tr>
<tr>
<td>16:30-16:45</td>
<td>Claudia C Weber</td>
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<td></td>
<td>Do Z chromosomes in Butterflies and Moths Show Evidence of Increased Rates of Adaptation?</td>
</tr>
<tr>
<td>16:45-17:00</td>
<td>Josué Barrera-Redondo</td>
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<tr>
<td></td>
<td>The UV sex chromosomes of brown algae act as genomic cradles for new genes that evolve de novo</td>
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</tbody>
</table>
## Scientific Program

### Day 2 (8 July)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
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</thead>
<tbody>
<tr>
<td>15:50-18:10</td>
<td><strong>S3- Progress and challenges for understanding the molecular evolution of sex chromosomes across Eukarya</strong></td>
<td>Costa Alegre</td>
</tr>
<tr>
<td>17:00-17:15</td>
<td>Sophia Catherine MacRae Orzechowski</td>
<td></td>
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<tr>
<td></td>
<td>Shining a light on early stages of neo-sex chromosome evolution in Australian honeyeaters (Aves: Meliphagidae)</td>
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<tr>
<td>17:15-17:30</td>
<td>Gabrielle Coffing</td>
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<td></td>
<td>Cephalopod sex determination and its ancient evolutionary origin revealed by chromosome-level assembly of the California two-spot octopus</td>
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<tr>
<td>17:30-17:45</td>
<td>Sarah Carey</td>
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<td></td>
<td>Using phased genome assemblies to examine the evolution of heteromorphic sex chromosomes in Cannabaceae</td>
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<tr>
<td>17:45-18:10</td>
<td>Melissa Wilson</td>
<td></td>
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<tr>
<td></td>
<td>Alignment and Variant Calling in Reference Genomes to Improve Sex Chromosome Comparative Genomics</td>
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### Day 3 (9 July)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
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<tbody>
<tr>
<td>9:00-10:00</td>
<td><strong>Keynote Speaker</strong></td>
<td>Los Tules</td>
</tr>
<tr>
<td></td>
<td>Alicia Mastretta-Yanes</td>
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<tr>
<td></td>
<td>Genetic diversity in the Anthropocene and the role of molecular studies for the future of biodiversity</td>
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<tr>
<td>10:00-10:30</td>
<td><strong>COFFEE BREAK</strong></td>
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<tr>
<td>10:30-12:20</td>
<td><strong>S23- Exploring the Frontiers of Single-Cell Biology in Diverse Organisms</strong></td>
<td>Los Tules</td>
</tr>
<tr>
<td>10:30-10:55</td>
<td>Carlos Ortiz Ramirez</td>
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<td></td>
<td>Single-cell genomics for understanding trait evolution and rapid adaptation</td>
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<tr>
<td>10:55-11:10</td>
<td>Jesús Murga-Moreno</td>
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<td></td>
<td>Quantifying adaptive evolution of the human immune cell landscape</td>
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<tr>
<td>11:10-11:25</td>
<td>Roberto Arbore</td>
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<td></td>
<td>The molecular bases of red-to-yellow color variation in parrots</td>
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<td>11:25-11:40</td>
<td>Meritxell Riera</td>
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<td></td>
<td>Evolutionary impact of transcriptomic variation in X and Y carrying gametes</td>
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<tr>
<td>11:40-11:55</td>
<td>Taylor Cooper</td>
<td></td>
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<td>Characterizing neuronal evolution between recently diverged species at single-cell resolution</td>
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<tr>
<td>11:55-12:10</td>
<td>Ines Hellmann</td>
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<td></td>
<td>Cross-species comparison of gene regulatory networks using single cell sequencing</td>
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<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
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<tbody>
<tr>
<td>10:30-12:20</td>
<td><strong>S37- IDEA Symposium</strong></td>
<td>Boca de Tomates</td>
</tr>
<tr>
<td>10:30-11:00</td>
<td>Miriam Miyagi</td>
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<td></td>
<td>Contextual Analysis of Genetic Studies of Gender, Sex, and Sexuality</td>
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<tr>
<td>11:00-11:30</td>
<td>Rori RohlfS</td>
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<td>Science Wise: From ‘hidden figures’ to scientific foremothers getting their flowers</td>
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<td>11:30-11:45</td>
<td>Joanna Kelley</td>
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<tr>
<td>11:45-12:00</td>
<td>Samantha López Clinton</td>
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<tr>
<td>12:00-12:20</td>
<td>Discussion</td>
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<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
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<tbody>
<tr>
<td>10:30-12:20</td>
<td><strong>S17-Aging from a multidisciplinary overview: evolution, longevity and biomedicine.</strong></td>
<td>Olas Altas</td>
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<tr>
<td>10:30-10:55</td>
<td>Luis Gutierrez Robledo</td>
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<tr>
<td></td>
<td>Evolutionary medicine, aging and longevity</td>
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<tr>
<td>10:55-11:20</td>
<td>Tamas Szekely</td>
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<td></td>
<td>Sex difference in longevity: causes and implications</td>
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<tr>
<td>11:20-11:35</td>
<td>Mariangela Iannello</td>
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<td></td>
<td>Signatures of extreme longevity: a perspective from bivalve molecular evolution</td>
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<tr>
<td>11:35-11:50</td>
<td>Miriam Merenciano</td>
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<td></td>
<td>Contribution of transposable elements in the sex gap longevity of different Drosophila species</td>
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</table>
### Scientific Program

**Day 3 (9 July)**

#### 10:30 - 12:20

**S17-Aging from a multidisciplinary overview: evolution, longevity and biomedicine.**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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</thead>
<tbody>
<tr>
<td>10:30-10:55</td>
<td>Gillian Meeks</td>
<td>Accounting for common genetic variation improves chronological age prediction in African populations</td>
</tr>
<tr>
<td>10:55-11:10</td>
<td>Eugenio Mancera</td>
<td>Exploring the chronological lifespan spectrum of Candida species</td>
</tr>
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</table>

#### 10:30 - 12:20

**S31- Haplotype-based methods and frameworks for inference of evolutionary history**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30-10:55</td>
<td>Pier Palamara</td>
<td>Inference of recent effective population size from high and low coverage DNA data</td>
</tr>
<tr>
<td>10:55-11:10</td>
<td>Katia Bougiouri</td>
<td>How to paint a dog: limits of local ancestry inference in ancient genomes</td>
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<tr>
<td>11:10-11:25</td>
<td>Eduardo Gonzalez Orozco</td>
<td>Archaic ancestry fragment calling using wavelet decomposition</td>
</tr>
<tr>
<td>11:25-11:40</td>
<td>Amy Williams</td>
<td>Reconstructing parent genotypes at genotyping array accuracy using siblings and other relatives</td>
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<tr>
<td>11:40-11:55</td>
<td>Jazeps Medina Tretmanis</td>
<td>Improving Local Ancestry Inference through Neural Networks</td>
</tr>
<tr>
<td>11:55-12:20</td>
<td>Amy Goldberg</td>
<td>Ancestry-based approaches for inference of evolutionary history on short timescales</td>
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</table>

#### 10:30 - 12:20

**S4- Everything that is old becomes new: comparative genomics and museum specimens.**

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<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
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<tbody>
<tr>
<td>10:30-10:55</td>
<td>Elinor Karlsson</td>
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<tr>
<td>10:55-11:10</td>
<td>Alexandra Keene</td>
<td>Viral and host metagenomics of 100-year-old insect museum specimens</td>
</tr>
<tr>
<td>11:10-11:25</td>
<td>Eucharist Kun</td>
<td>The trait specific timing of accelerated genomic change in the human lineage.</td>
</tr>
<tr>
<td>11:25-11:40</td>
<td>Lucas Rocha Moreira</td>
<td>Evolutionary paths to thermal resilience in placental mammals: functional genomics insights from the Frozen Zoo Biobank</td>
</tr>
<tr>
<td>11:40-11:55</td>
<td>Michelle Stitze</td>
<td>From swampy ancestors to modern maze: tracing the allopolyploid origins of Zea</td>
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<tr>
<td>11:55-12:20</td>
<td>Nico Franz</td>
<td>Title to be confirmed</td>
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#### 12:20 - 13:20

**LUNCH BREAK**

#### 12:20 - 13:20

**Event: SMBE Business Meeting**

#### 13:20 - 14:50

**Poster session 2**

- Aging from a multidisciplinary overview: evolution, longevity and biomedicine.
- Animal paleogenomics beyond higher latitudes.
- Everything that is old becomes new: comparative genomics and museum specimens.
- Evolutionary medical genomics.
- Exploring the Frontiers of Single-Cell Biology in Diverse Organisms.
- Genetics, Molecular Biology, and the Future of Forensic Science.
- Going local: Using engaged research practices to understand regional-scale interactions.
- Haplotype-based methods and frameworks for inference of evolutionary history.
- Impact of environmental changes on agrobiodiversity and strategies for resilience.
- Molecular evolution through metagenomics.
- One Health and microbial evolution: New ideas and perspectives.
- Paleogenomics and human evolutionary history: new insights and novel methods.
- Pushing the frontiers of conservation genomics.
- Transposable elements in the population genomics era: towards a better understanding of their contribution to evolution.

#### 13:20 - 14:50

**Event: GBE Editors Meeting**
Day 3 (9 July)

**S16- Evolutionary Medical Genomics**

Los Tules

- **14:50-15:15**
  - Pleuni Pennings: Why aren’t all E. coli resistant to antibiotics?
  - Imroze Khan: Rapid evolution of mutation rate and germline maintenance under strong pathogen selection: new insights from experimental evolution experiments
  - Cara Love: Radiation-induced stress and signatures of selection on anti-tumor immunity in Chernobyl wolves
  - Daniel Jordan: Deep learning phenotype imputation to measure dominance of rare variant effects on rare disease in UK Biobank
  - Aliêf Mouliana: Epistasis and pleiotropy constrain and expand the evolution of SARS-CoV-2 Omicron lineage

- **15:15-15:30**
  - Helen Hopson: Interactions between sickle cell and Plasmodium falciparum genotypes in asymptomatic malaria
  - Evan Irving-Pease: The evolutionary origins of autoimmune and infectious disease risks
  - Shamil Sunyaev: Evolutionary perspective on human polygenic traits

- **15:30-15:45**
  - Maanasa Raghavan: Human genetic histories at the Himalayan frontiers
  - Dilek Koptekin: Overcoming bias and postmortem damage to improve the accuracy of ancient genome analysis

- **15:45-16:00**
  - Hugh McColl: Steppe Ancestry in Western Eurasia and the spread of the Germanic Languages

- **16:00-16:15**
  - Stéphane Peyrégne: A high-quality genome from a 200,000-year-old Denisovan

- **16:15-16:30**
  - Yulin Zhang: Reconstructing mutation patterns over the course of human evolution

- **16:30-16:45**
  - Yulin Zhang: Reconstructing mutation patterns over the course of human evolution

- **16:45-17:10**
  - Archivo Rosario Capodiferro: Archaic ancestry inference in imputed ancient human genomes

**S15- Paleogenomics and human evolutionary history: new insights and novel methods.**

Boca de Tomates

- **14:50-15:15**
  - Kay Prüfer: Ancient Genomes of Neandertals and Modern Humans from Europe
  - Marco Rosario Capodiferro: Archaic ancestry inference in imputed ancient human genomes

- **15:15-15:30**
  - Yulin Zhang: Reconstructing mutation patterns over the course of human evolution

- **15:30-15:45**
  - Stéphane Peyrégne: A high-quality genome from a 200,000-year-old Denisovan

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- **16:15-16:30**
  - Sandra Oliveira: Tracing admixture in European early farmers using local ancestry inference

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- **17:10-17:20**
  - Hugh McColl: Steppe Ancestry in Western Eurasia and the spread of the Germanic Languages

**S20- Pushing the frontiers of conservation genomics.**

Olas Altas

- **14:50-15:15**
  - Carolyn Hogg: Conservation Genomics: innovations, applications & where to next?

- **15:15-15:30**
  - Genís Garcia-Erill: The genetic architecture of an adaptive phenotype conditions vulnerability and populations evolutionary response to climate change

- **15:30-15:45**
  - Jonas Aguirre Liguori: The evolutionary genomics of population’s responses to climate change

- **15:45-16:00**
  - Paulina Nuñez-Valencia: Predicting Pathogenic Variation for conservation: a deep learning approach

- **16:00-16:15**
  - Rebekah Rogers: Low Rates of Gene Duplication in an Endangered Freshwater Mussel

- **16:15-16:30**
  - Eugenie Charley Yen: Epigenome-wide scans identify DNA methylation markers for monitoring sublethal thermal stress in endangered sea turtles

- **16:30-16:45**
  - Theo Phanu Serivichyaswat: Towards genome-wide data of Arctic species obtained from snow footprints

- **16:45-17:10**
  - Eduardo Eizirik: Conservation Genomics of Neotropical Wild Cats
**Scientific Program**

**Day 3 (9 July)**

**14:50 - 17:30**

**Las Pilitas**

**S6- Molecular evolution through metagenomics**

14:50 - 15:15

**Gabriela Olmedo Álvarez**

Clues to the Evolution of Antibiotic resistance from bacteria and ancient communities from pristine sites in Cuatrocienegas, Coahuila, Mexico.

15:15 - 15:30

**Abigail Lind**

Host adaptation and genomic change in intestinal eukaryotes revealed from sequencing microbial mixtures.

15:30 - 15:45

**Maya Lemmon-Kishi**

What’s the Rate: Molecular Clock Calibration Using Sedimentary Ancient DNA.

15:45 - 16:00

**Edder Daniel Bustos-Díaz**

Nitrogen cycling in symbiotic bacterial communities associated with ancient American plants.

16:00 - 16:15

**Irina Velsko**

De novo assembly of ancient human metagenomes improves community diversity estimates and reveals varied microbial taxon-specific evolutionary trajectories.

16:15 - 16:30

**Mariana Guerrero-Osornio**

Time-lapse of the microbial composition during agave fermentation using Meta-HiC.

16:30 - 16:45

**Davide Bozzi**

Genomic characterization of novel Treponema species from the oral microbiome of Aboriginal Australians.

16:45 - 17:10

**Nandita Garud**

Pervasive selective sweeps within and across human gut microbiomes.

**14:50 - 17:30**

**Costa Alegre**

**S27- Transposable elements in the population genomics era: towards a better understanding of their contribution to evolution.**

14:50 - 15:15

**Grace Yuh Chwen Lee**

How transposable element shapes genome evolution through epigenetic mechanisms?

15:15 - 15:40

**Leandro Quadrana**

Transposon-Mediated Environmental Regulation: Catalyst for Adaptive Responses?

15:40 - 15:55

**Marie Lebherz**

DNA Transposons favour de novo transcript emergence through enrichment of transcription factor binding motifs.

15:55 - 16:10

**Riccardo Pianezza**

Double trouble: two retrotransposons triggered a cascade of horizontal transfers in Drosophila species within the last 50 years.

16:10 - 16:25

**Jilong Ma**

Independent transitions to sociality in Stegodyphus spiders are associated with transposable element expansions.

16:25 - 16:40

**Austin Daigle**

TEforest: Enhancing short-read transposable element detection with machine learning.

16:40 - 16:55

**Cei Abreu-Goodger**

Evolution of transposable elements as the source of extracellular RNA.

16:55 - 17:10

**Jordana Oliveira**

Evolution of transposable elements in arbuscular mycorrhizal fungi: insights into genome variability and gene regulation.

**17:10 - 17:40**

**COFFEE BREAK**

**17:40 - 19:30**

**Los Tules**

**S18- One Health and microbial evolution: New ideas and perspectives**

17:40 - 17:55

**Mirna Vázquez-Rosas-Landa**

Microbial dynamics in mangrove sediments during the anthropogenic era.

17:55 - 18:10

**Matthew Shepherd**

Within-patient evolution of ciprofloxacin resistance in Pseudomonas aeruginosa across a large-scale clinical trial.

18:10 - 18:25

**Rahgavi Poopalarajah**

Evolution of the human gut resistome across diverse lifestyles and environments.

18:25 - 18:40

**Manuel Ochoa-Sánchez**

Feather microbiota compositional and functional landscapes across phenology and biogeography in Magellanic penguins in the Magellan Strait, Chile.
S18- One Health and microbial evolution: New ideas and perspectives
Santiago Elena
An evolving world for evolving pathogens: ecological drivers of virus diversification and adaptation
Fernando González Candelas
Evolutionary genomics and the one health approach to AMR

S34- Going local: Using engaged research practices to understand regional-scale interactions.
Maria Ávila-Arcos
Community engagement experiences of the Afromexico Genomics Project
Eleni Seferidou
An ancient genetic insight into pre-colonial Trinidad
Daniela Orozco-Perez
Paleogenomic analyses of archaeological remains reveal sex roles and mobility of ancient families in central Mexico
Esha Bandypadhyay
Distinct positions of genetic and oral histories: Perspectives from India
Constanza de la Fuente Castro
Conversations in community-based genomic research: Showcasing a platform from Chile to integrate Indigenous engagement and representation
Laura Weyrich
Uncovering the global origins of an industrialized microbiome using regionally focused studies

S22- Impact of environmental changes on agrobiodiversity and strategies for resilience.
Brandon Gaut
Crop wild relatives, climate change and genomic diversity
Luis Eguiarte
Population genomics of tequila and mezcal (Agave spp.): Unexpected findings and lessons for these Mexican industries in the face of climate change
Mirte Bosse
A boaring story of hybridization and adaptation in wild boars, domestic pigs and feral swine
Alejandra Hernandez-Teran
Disentangling microbiome effects on plant adaptation
Ayelet Salman-Minkov
Strategies for mining useful alleles for climate change adaptation
Azalea Guerra-García
Building agroecosystems resilience by fostering native crops and their wild relatives

S13- Animal paleogenomics beyond higher latitudes.
Selina Brace
Museomics and the Tropics: occasionally vexing, but a rewarding partnership
Alida de Flamingh
Compacted hair in broken carnivore teeth reveal dietary prey of historic lions
Gloria Gonzalez Fortes
The last specimen of Eurasian lynx (Lynx lynx) from the Iberian Peninsula: new genetic data leads to review the biogeographic history of lynx matrilineal lineages in western Europe
David Ledesma
Small but mighty: ancient DNA analyses of late Pleistocene and Holocene microvertebrates from Central Texas
Federico Sánchez Quinto
The evolutionary origin of the Columbian mammoths from the Basin of Mexico and its implications for the Mammuthus genus
Viviane Slon
Sedimentary ancient DNA studies in challenging preservation contexts: Insights from the southern Levant
### Day 3 (9 July)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>17:40</td>
<td><strong>S35-Genetics, Molecular Biology, and the Future of Forensic Science</strong></td>
<td>Costa Alegre</td>
</tr>
<tr>
<td>18:05</td>
<td>Rori Rohlfs: Quantifying the accuracy of forensic genetic technologies</td>
<td></td>
</tr>
<tr>
<td>18:20</td>
<td>Anne Stone: The recovery of DNA from burned forensic contexts.</td>
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<tr>
<td>18:35</td>
<td>Feriel Ouerghi: How should we report genetic matches following an Investigative Genetic Genealogy search?</td>
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</tr>
<tr>
<td>18:50</td>
<td>Meghna Swayambhu: Highly accurate predictions indicating sexual activity using microbiome-based analyses in forensic settings</td>
<td></td>
</tr>
<tr>
<td>19:05</td>
<td>Maria Flores: Construction of Epigenetic Clock using Cell-Free DNA</td>
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</tr>
<tr>
<td>19:30</td>
<td>Jaehee Kim: Population genetics approaches for forensic genetic record-matching</td>
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<tr>
<td>20:00</td>
<td><strong>Event: GBE Editors Dinner</strong></td>
<td>Mayapán</td>
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<td></td>
<td></td>
<td>Restaurant at</td>
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<td></td>
<td></td>
<td>Paradise Village Resort</td>
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### Day 4 (10 July)

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Location</th>
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</thead>
<tbody>
<tr>
<td>9:00</td>
<td><strong>Keynote Speaker</strong></td>
<td>Los Tules</td>
</tr>
<tr>
<td>10:00</td>
<td><strong>COFFEE BREAK</strong></td>
<td></td>
</tr>
<tr>
<td>10:30</td>
<td><strong>S2- Novel approaches to study plant domestication: disentangling the complex evolutionary history of crops</strong></td>
<td>Los Tules</td>
</tr>
<tr>
<td>10:55</td>
<td>June Simpson: Exploring the fructan syndrome in Agave tequilana-a non-typical crop plant</td>
<td></td>
</tr>
<tr>
<td>11:10</td>
<td>Xiranran Li: Deciphering Sorghum Domestication: The Pivotal Role of Condensed Tannins in Co-evolution Among Plants, Humans, and Birds</td>
<td></td>
</tr>
<tr>
<td>11:25</td>
<td>Arthur Wojcik: Meta-analysis of wild and domesticated crop phenotypic spaces</td>
<td></td>
</tr>
<tr>
<td>11:40</td>
<td>Laura Botigué: Wheat domestication and adaptation to new environments: the role of wild emmer.</td>
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<tr>
<td>11:55</td>
<td>Miriam Ferrer: Multi-purpose species domestication in Mayan homegardens</td>
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<tr>
<td>12:05</td>
<td>Alejandro Quintero: Exploring the patterns of microbiota recruitment and inheritance on the chocolate tree, Theobroma cacao L</td>
<td></td>
</tr>
<tr>
<td>10:30</td>
<td><strong>S10- Genomes and Generations: Mapping Health and Heritage Through African Genomics.</strong></td>
<td>Boca de Tomates</td>
</tr>
<tr>
<td>10:55</td>
<td>Brenna Henn: A Rich Resource of African-Descent Genomes (CAAPA2)</td>
<td></td>
</tr>
<tr>
<td>11:20</td>
<td>Dhriti Sengupta: Impact of Khoe-San gene flow in phenotypic variation of anthropometric and cardiometabolic traits</td>
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<tr>
<td>11:35</td>
<td>Jeremy Choin: Genomic Insights into the population history of southern-central Africa</td>
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<tr>
<td>11:50</td>
<td>Rohini Janivara: Heterogeneous genetic architectures and evolutionary genomics of prostate cancer in Sub-Saharan Africa</td>
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</tr>
<tr>
<td>12:05</td>
<td>Esther Brielle: Sudanic, Central, and Western African ancestry contributions to ancient Ugandan Populations</td>
<td></td>
</tr>
<tr>
<td>12:20</td>
<td>Jasmin Rees: Evolutionary History of Transient Receptor Proteins in Sub-Saharan Africa</td>
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</tbody>
</table>
### S29- Advances in Machine Learning for Evolutionary Genomics.

**Talks**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30</td>
<td>Sara Mathieson</td>
<td>Interpreting deep learning methods for population genetic inference</td>
</tr>
<tr>
<td>10:55</td>
<td>Siavash Mirarab</td>
<td>Metric learning for phylogenetic placement</td>
</tr>
<tr>
<td>11:20</td>
<td>Carina Cornejo Paramo</td>
<td>A Bag-Of-Motif Model Captures Context-Specific Distal Regulatory Elements</td>
</tr>
<tr>
<td>11:35</td>
<td>Steven Reilly</td>
<td>Interrogating the relationship between conservation and regulatory function across all human promoters using machine-learning variant effect predictions</td>
</tr>
<tr>
<td>11:50</td>
<td>Murillo Rodrigues</td>
<td>A deep learning framework for evolutionary inference using ancestral recombination graphs</td>
</tr>
<tr>
<td>12:05</td>
<td>Zhengting Zou</td>
<td>Sequence embeddings by pretrained language model indicate adaptive convergence of high-order protein features.</td>
</tr>
</tbody>
</table>

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### S14- Unveiling the evolutionary history of pathogens through paleogenomics

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30</td>
<td>Tanvi Honap</td>
<td>Exploring oral microbial evolution in the context of European colonization of the Americas</td>
</tr>
<tr>
<td>10:55</td>
<td>Laura Carrillo-Olivas</td>
<td>Exploring Pathogens and Demographic Dynamics in Colonial Mexico City through Paleogenomics</td>
</tr>
<tr>
<td>11:20</td>
<td>Paola Campos</td>
<td>Deciphering the emergence and evolutionary history of a bacterial crop pathogen: insights from historical herbarium specimens</td>
</tr>
<tr>
<td>11:35</td>
<td>Sojung Han</td>
<td>DNA virus genomes from historical specimens of great apes</td>
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<tr>
<td>11:50</td>
<td>Nasreen Broomandkhoshbacht</td>
<td>Characteristics of a 5,500-year-old Treponema pathogen from Colombia</td>
</tr>
<tr>
<td>12:05</td>
<td>Elizabeth Nelson</td>
<td>Tuberculosis and Sociocultural Dynamics: Critical Insights from Paleogenomics in South America and Beyond</td>
</tr>
</tbody>
</table>

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### S33- Science in the Spotlight: Empowering Education and Public Engagement with Cutting-Edge Science in Molecular Evolution.

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>10:30</td>
<td>Roberto Torres</td>
<td>Melanogaster Catch The Fly! Rural high schools committed to frontier research on genomics and evolution through citizen science</td>
</tr>
<tr>
<td>10:55</td>
<td>Sarah Schaack</td>
<td>TE Hub: A Community for Developing Tools, Trainings, and Resources to Analyze DNA Repeats</td>
</tr>
<tr>
<td>11:20</td>
<td>Kate Duggan</td>
<td>Disease Detectives: Using Minecraft to explore virus evolution and epidemiology</td>
</tr>
<tr>
<td>11:35</td>
<td>Sònia Casillas</td>
<td>Adopting ESG principles in PopLife, the population genomics browser across the tree of life</td>
</tr>
<tr>
<td>11:50</td>
<td>Rebecca Siford</td>
<td>Evaluating community perceptions and ethical considerations in genetics research in small scale northern Kenyan populations</td>
</tr>
<tr>
<td>12:05</td>
<td>Nicolette Caperello</td>
<td>Engaging the Public on Biology's Moonshot: The Earth BioGenome Project</td>
</tr>
</tbody>
</table>

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**LUNCH BREAK**

**Event:** MBE & GBE Editors ‘Q&A session’
### Scientific Program

**Day 4 (10 July)**

### Poster session 3

**14:50 - 17:10**

**S19- Evolution of microbial communities: is the sum of parts greater than the whole?**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>14:50</td>
<td>Paul Rainey</td>
<td>Communities, lineages, and the evolution of evolvability</td>
</tr>
<tr>
<td>15:15</td>
<td>José Flores-Uribe</td>
<td>Experimental evolution of synthetic phototrophic communities</td>
</tr>
<tr>
<td>15:30</td>
<td>Mike McDonald</td>
<td>A new genome from the pan-genome - experimental evolution with horizontal gene transfer.</td>
</tr>
<tr>
<td>15:45</td>
<td>Pu Wang</td>
<td>Eco-evolutionary feedbacks promoted by hypermutation rate in a predator-prey microcosm.</td>
</tr>
<tr>
<td>15:45</td>
<td>Edmund Moody</td>
<td>The nature of the Last Universal Common Ancestor and its impact on the early Earth system.</td>
</tr>
<tr>
<td>15:45</td>
<td>Autumn Peterson</td>
<td>Disentangling the evolutionary impacts of relatedness and facultative obligate life cycles during the transition to multicellularity</td>
</tr>
<tr>
<td>16:15</td>
<td>Sarit Avrani</td>
<td>Tradeoffs between phage resistance and nitrogen fixation drive the evolution of multicellular cyanobacteria</td>
</tr>
</tbody>
</table>

### S9- Human population demography and adaptation signals in the Americas

**14:50 - 17:10**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>14:50</td>
<td>Cosimo Posth</td>
<td>The genetic history of early Americans</td>
</tr>
<tr>
<td>15:15</td>
<td>Santiago Medina-Muñoz</td>
<td>Inferring fine-scale demography of indigenous lineages from 500 whole genomes across Mexico</td>
</tr>
<tr>
<td>15:15</td>
<td>Valeria Anorve-Garibay</td>
<td>The contribution of Neanderthal introgression to the heritability of human complex traits in Mexico</td>
</tr>
<tr>
<td>15:30</td>
<td>Esther Brielle</td>
<td>Adaptation in Ancient Maya</td>
</tr>
<tr>
<td>15:45</td>
<td>Tábita Hünemeier</td>
<td>Evolutionary Changes Throughout Human History in America</td>
</tr>
<tr>
<td>15:45</td>
<td>Epifanía Arango Isaza</td>
<td>Uncovering South American genomic diversity in the Southern Cone</td>
</tr>
<tr>
<td>15:45</td>
<td>Marisol Espitia Fajardo</td>
<td>Colombian Arawak genomes shed light on population demography of South America</td>
</tr>
<tr>
<td>16:00</td>
<td>Thomas Pinotti</td>
<td>Picuris Pueblo oral history and genomics reveal genetic continuity in North American Southwest</td>
</tr>
</tbody>
</table>

### S11- Spatial population genetics: where are we now?  

**14:50 - 17:10**

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Title</th>
</tr>
</thead>
<tbody>
<tr>
<td>14:50</td>
<td>Alison Feder</td>
<td>Spatial drivers of disease progression in bacteria and viruses</td>
</tr>
<tr>
<td>15:15</td>
<td>Alessandro Lopez-Hernandez</td>
<td>A space-time model for jointly inferring gene flow and natural selection</td>
</tr>
<tr>
<td>15:45</td>
<td>Clara Rehmann</td>
<td>In space no one can hear you sweep: a novel signal of selective sweeps in continuous geographic space</td>
</tr>
</tbody>
</table>
**S11- Spatial population genetics: where are we now?**

**14:50 - 15:00**
- Jack Harper
  - Using biological invasions to understand rapid adaptation to new environments: a genomic reconstruction of the house sparrow global spread

**15:00 - 15:15**
- Andy Kern
  - Deep Space- supervised machine learning methods for spatial population genetics

**15:15 - 15:30**
- Gillia Patterson
  - A spatially explicit close kin mark recapture method for estimating census size from genetic data

**15:30 - 15:45**
- Vivaswat Shastry
  - Inference of long-range gene-flow events in a background of spatially heterogeneous isolation-by-distance

**15:45 - 16:00**
- Michael Grundler
  - Spatial ancestry reconstruction using parsimony on tree sequences

---

**S25- Mitochondria: from powerhouse to processor and from marker to meaning**

**14:50 - 15:00**
- Dennis Lavrov
  - Evolution of mitochondrial mRNA editing and linear multipartite mt-genome architecture in calcareous sponges

**15:00 - 15:15**
- Vaishali Katju
  - No passive sidekick: a substantial role for mitochondrial compensatory evolution during adaptation of ETC-deficient strains of Caenorhabditis elegans

**15:15 - 15:30**
- Toni Gossmann
  - Phyloinformatics uncovers diverse evolutionary trajectories of mitogenomic fossils buried in mammalian and avian genomes

**15:30 - 15:45**
- Dennis Lavrov
  - Evolution of mitochondrial mRNA editing and linear multipartite mt-genome architecture in calcareous sponges (invited talk)

**15:45 - 16:00**
- Konstantin Popadin
  - Decoding the Puzzle of Human Somatic mtDNA Mutagenesis: Bridging Species Life-History Traits and Organ-Specific Cellular Properties

**16:00 - 16:15**
- Leah Darwin
  - The contribution of within- and between-species mitochondrial variation to adaptation in experimental Drosophila populations

**16:15 - 16:30**
- Wei-Chin Ho
  - Population-Genetic Environment of Genome Retention and Reduction in Mitochondria

**16:30 - 16:45**
- Michael Garvin
  - The Importance of Mito-nuclear Epistasis in Evolutionary Genetics

---

**S26- Deciphering the functional and adaptive effects of genomic structural variation**

**14:50 - 15:00**
- Mia Levine
  - DNA satellite evolution triggers a cross-species incompatibility

**15:00 - 15:15**
- Julie Chuong
  - DNA replication errors are a major source of gene amplification in adaptive evolution

**15:15 - 15:30**
- Elli Cryan
  - Molecular evolution of a maize hybrid barrier over 12 million years suggests epistatic silencing

**15:30 - 15:45**
- Samuel Bogan
  - Convergent Structural Variation of Antifreeze Proteins in Polar and Deep Sea Fishes

**15:45 - 16:00**
- Tristram Dodge
  - Intergenic structural variation and ancient gene duplication underpin pigmentation diversification in swordtail fish

**16:00 - 16:15**
- Diego Hartasánchez
  - The role of structural variation in clownfish adaptive radiations

**16:15 - 16:30**
- Megan Dennis
  - Gene expansions contributing to human brain evolution

**16:30 - 16:45**
- Christine Beck
  - Repetitive sequences drive genomic variation and vary regulatory landscapes

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**GALA DINNER**

**19:00-23:00**

**Host Hotel Paradise Village**
Day 5 (11 July)

09:00-10:50  S30- New computational approaches to estimate past demographic events and natural selection.  Los Tules

09:00:09:25  Jazlyn Mooney  Considerations for Inferring Demography and Detecting Selection in Understudied Species
09:25-09:40  Charleston Chiang  A genealogy-based framework to estimate population structure and demographic history
09:40-09:55  Ekaterina Noskova  Hidden Diffusion: Accurate Joint Inference of Selection and Demographic History from Time-series Data for Multiple Populations
09:55-10:10  Yun Deng  Understanding the interactions between demography and selection landscapes in human populations: insights from Ancestral Recombination Graphs (ARGs)
10:10-10:25  Anastasia Lyulina  Linkage equilibrium between rare alleles
10:25-10:40  Joshua Schraiber  Inference of ultra recent demography, recurrent mutation, and natural selection from biobank-scale site frequency spectra
10:40-10:55  M. Elise Lauterbur  Bayesian mediation models reveal patterns of host genomic disease adaptation driven by environment

09:00-10:50  S38- Open Symposium 2  Boca de Tomates

9:00-9:15  Nadia Haghani  The genetic and structural basis of a novel iridescence phenotype in the platyfish, Xiphophorus variatus
9:15-9:30  Tamsen Dunn  Inferring the characteristics of ancient polyploidization events from modern plant genomes
9:30-9:45  Sara Miller  Genomic architecture in social insects is more strongly associated with phylogeny than social behavior
9:45-10:00  Hélêna Vassilieff  A new scenario for the macroevolution of the Caulimoviridae based on the analysis of endogenous caulimovirids using CAULIFINDER
10:00-10:15  Maëlle Daunesse  Phylogenetic modeling of gene expression shifts in the mole-rat clade
10:15-10:30  Jay Storz  Life at extreme elevations: genomic and physiological insights into mechanisms of hypoxia adaptation in Andean mice
10:30-10:45  Angel Rivera-Colón  Population genetics of the Pacific acorn barnacle and insights into evolution in large populations

09:00-10:50  S7- Epigenetic inheritance: from molecular mechanisms to evolutionary consequences.  Olas Altas

9:00-9:25  Peter Sarkies  Contribution of epimutation to evolution in C. elegans and beyond
9:25-9:40  Elisa Israel  MiB2/3 lost its methyl-CpG binding ability in multiple families of Holometabola
9:40-9:55  Pierre Baduel  Molecular determinants of transgenerational epigenetic variation at transposable element sequences in plants and its impact in nature
9:55-10:10  Mariana Gómez-Schiavon  Exploring the evolutionary dynamics of epigenetic switches and beyond: Insights from gene regulatory circuit models
10:10-10:25  Gustavo Tapia  The role of CTCF in the transcriptional activation of the hematopoietic-specific gene HBA2 is evolutionary conserved
10:25-10:50  Sito Torres-García  Exploring the potential for epimutations to drive cancer cell adaptation

09:00-10:50  S21- Decoding the past to safeguard the future.  Las Pilitas

9:00-9:25  Mafalda Sousa Ferreira  Harnessing the past to predict the future: the evolution and future adaptive potential of seasonal camouflage in white-tailed jackrabbits
9:25-9:50  Laurent Frantz  Tracking human-mediated animal translocation in Island Southeast Asia using ancient DNA
### Scientific Program

#### Day 5 (11 July)

<table>
<thead>
<tr>
<th>Time</th>
<th>Location</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>09:00-10:50</td>
<td>Las Pilitas</td>
<td><strong>S21- Decoding the past to safeguard the future.</strong></td>
</tr>
<tr>
<td>09:00-10:50</td>
<td></td>
<td>Germán Hernández-Alonso</td>
</tr>
<tr>
<td>09:00-10:50</td>
<td></td>
<td>Exploring the Rock Dove’s (Columba livia) Genetic Diversity: Insights into the Species’ Evolutionary History and Conservation Challenges</td>
</tr>
<tr>
<td>09:50-10:05</td>
<td></td>
<td>Chenyu Jin</td>
</tr>
<tr>
<td>09:50-10:05</td>
<td></td>
<td>Metagenomic reconstruction of the plant community in the stomach content of a steppe bison living over 48,000 C14 years ago</td>
</tr>
<tr>
<td>10:05-10:20</td>
<td></td>
<td>Maria Zicos</td>
</tr>
<tr>
<td>10:05-10:20</td>
<td></td>
<td>Reconstructing the population history of the endangered Hispaniolan solenodon, one of the most evolutionary distinct mammals on earth</td>
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<tr>
<td>10:20-10:35</td>
<td></td>
<td>Xuejing Wang</td>
</tr>
<tr>
<td>10:20-10:35</td>
<td></td>
<td>Reviving from four birds: post-bottleneck overview of temporal genomics of Mauritius kestrel</td>
</tr>
<tr>
<td>09:00-10:50</td>
<td>Costa Alegre</td>
<td><strong>S28- Human genetic variability in the Pangenomic era..</strong></td>
</tr>
<tr>
<td>09:00-9:25</td>
<td></td>
<td>Erik Garrison</td>
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<tr>
<td>09:25-9:40</td>
<td></td>
<td>Implicit pangenomics</td>
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<tr>
<td>09:40-9:55</td>
<td></td>
<td>Gabriel Renaud</td>
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<tr>
<td>09:40-9:55</td>
<td></td>
<td>Maximum-likelihood inferences from ancient environmental DNA using panmitogenomes</td>
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<tr>
<td>09:55-10:10</td>
<td></td>
<td>Runyang Nicolas Lou</td>
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<tr>
<td>09:55-10:10</td>
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<td>Global diversity, recurrent evolution, and recent selection on amylase structural haplotypes in humans</td>
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<td>10:10-10:25</td>
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<td>Joana Rocha</td>
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<td>10:10-10:25</td>
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<td>A Pan-pangenome captures the full spectrum of genetic variation in humans, chimpanzees and bonobos</td>
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<td>10:25-10:50</td>
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<td>Rick McLaughlin</td>
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<td>Pangenome assemblies reveal the evolution and recent in vivo activity of human LINE-1 retrotransposons</td>
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<td>10:50-11:20</td>
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<td>10:50-11:20</td>
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<td>Living with your dynamic genome: lessons learned from T2T genomes</td>
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<td>11:20-12:20</td>
<td>Los Tules</td>
<td><strong>Closing Keynote Speaker</strong></td>
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<td>11:20-12:20</td>
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<td>Scott Edwards</td>
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<td>PhyloG2P: the new science of connecting genomes to phenotypes via phylogenies</td>
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<td>12:20-14:20</td>
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<td><strong>Awards Ceremony and Introduction to SMBE 2025</strong></td>
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