

SMBE 2024
PUERTO VALLARTA

Scientific Program

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 Vecchy

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.

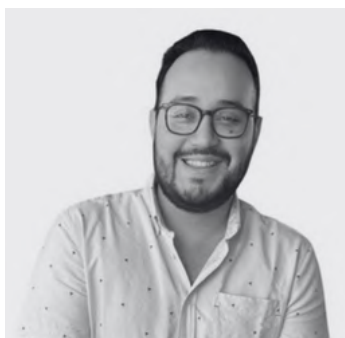
Professional Conference Organizer (PCO) Team



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)

Code of Conduct

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 pbworksolutions@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 pbworksolutions@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.

Guidelines for poster presentations

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

SCIENTIFIC 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 kickoff 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					
HALL NAME	Los Tules (Plenary)	Boca de Tomates	Olas Altas	Las Pilitas	Costa Alegre (upper floor)	
11:30 – 13:20 110 min.	Associate Editors' Symposium	Open Symposium 1	Not just Ne Ne–more: New applications for SMC from ecology to phylogenies	Clustering of human cohorts beyond race and ancestry: Towards relational thinking in genomics	Greener 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					
15:50 – 18:10 140 min.	human evolution in the genomic era	Exploring the Evolutionary Effects of Admixture	Unlocking the hidden dimensions of genomic diversity within species	Structural phylogenetics: investigating deep evolutionary history using protein structure	Progress and challenges for understanding the molecular evolution of sex chromosomes across Eukarya	
20:00–22:00	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					
HALL NAME	Los Tules (Plenary)	Boca de Tomates	Olas Altas	Las Pilitas	Costa Alegre (upper floor)	
10:30 – 12:20 110 min.	Exploring the Frontiers of Single-Cell Biology in Diverse Organisms	IDEA symposium	Aging from a multidisciplinary overview: evolution, longevity and biomedicine	Haplotype-based methods and frameworks for inference of evolutionary history	Everything that is old becomes new: comparative genomics and museum specimens	
12:20–13:20	LUNCH BREAK Boca de Tomates: SMBE Business meeting					
13:20 – 14:50	Poster session 2 Boca de Tomates: GBE editors meeting					
14:50 – 17:10 140 min.	Evolutionary medical genomics	Paleogenomics and human evolutionary history: new insights and novel methods	Pushing the frontiers of conservation genomics	Molecular evolution through metagenomics	Transposable elements in the population genomics era: towards a better understanding of their contribution to evolution	
17:10 – 17:40	COFFEE BREAK					
17:40–19:30 110 min.	One Health and microbial evolution: New ideas and perspectives	Going local: Using engaged research practices to understand regional-scale interactions	Impact of environmental changes on agrobiodiversity and strategies for resilience	Animal paleogenomics beyond higher latitudes	Genetics, 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					
HALL NAME	Los Tules (Plenary)	Boca de Tomates	Olas Altas	Las Pilitas	Costa Alegre (upper floor)	
10:30 – 12:20 110 min.	Novel approaches to study plant domestication: disentangling the complex evolutionary history of crops	Genomes and Generations: Mapping Health and Heritage Through African Genomics	Advances in Machine Learning for Evolutionary Genomics	Unveiling the evolutionary history of pathogens through paleogenomics	Science in the Spotlight: Empowering Education and Public Engagement with Cutting-Edge Science in Molecular Evolution	
12:20–13:20	LUNCH BREAK Boca de Tomates: MBE & GBE 'Q&A session'					
13:20 – 14:50	Poster session 3					
14:50 – 17:10 140 min.	Evolution of microbial communities: 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?	Mitochondria: from powerhouse to processor and from marker to meaning	Deciphering the functional and adaptive effects of genomic structural variation	
19:00–23:00	GALA DINNER at Paradise Village Hotel					
Day 5		Thursday 11 July				
HALL NAME	Los Tules (Plenary)	Boca de Tomates	Olas Altas	Las Pilitas	Costa Alegre (upper floor)	
09:00–10:50 110 min.	New computational approaches to estimate past demographic events and natural selection	Open Symposium 2	Epigenetic inheritance: from molecular mechanisms to evolutionary consequences	Decoding the past to safeguard the future	Human genetic variability in the Pangenomic 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					

Floor Map



CONVENTION CENTER GROUND FLOOR DISTRIBUTION



1. LOBBY
Registration
Front desk

2. FOYER
Sponsors Stands
Coffee break & Lunch
Break

3. POSTER SESSIONS

4. POSTER SESSIONS

5. LOUNGE AREA

6. LOS TULES
Plenary

6. LOS TULES
7. BOCA DE TOMATES
8. OLAS ALTAS
9. LAS PILITAS

Concurrent Symposia

7. BOCA DE TOMATES
Workshops:
Introduction to STDPOPSIM
July 7th 12 - 14 hrs

GENHIST kickoff at SMBE
July 7th 14 - 16 hrs

SMBE Business Meeting.
July 9th 12:20 - 13:20 hrs

MBE & GBE Editors meetings.
July 8th 14:20 - 15:50 hrs
July 9th 13:20 - 14:50 hrs
July 10th 12:20 - 13:20 hrs

F FOOD STATION
V VEGAN & VEGETARIAN
FOOD STATION

10. KITCHEN

11. COWORKING AREA
Breastfeeding room
Undergraduate's dinner
July 7th 19 - 21 hrs

12. KIDS CLUB
(0 - 10 years old)

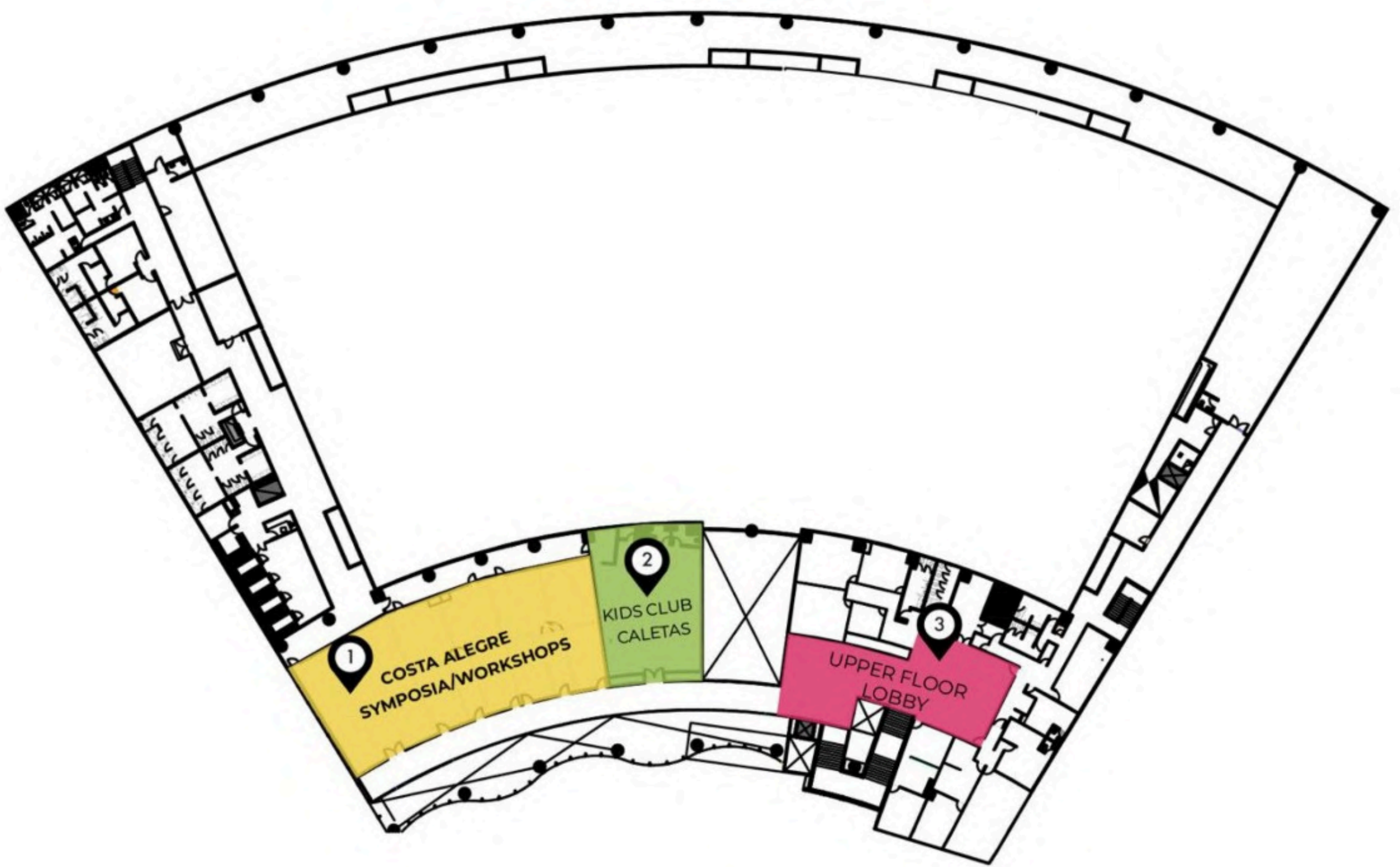
13. DELI & COFFEE

14. MEDICAL SERVICE

Floor Map



CONVENTION CENTER UPPER LEVEL DISTRIBUTION



1. COSTA ALEGRE
Concurrent Symposia

2. CALETAS
Kids Club (11 - 17 years old)

1. COSTA ALEGRE
WORKSHOPS
July 7th 11 - 16 hrs
Introduction to programmatic access to EnsEMBL.

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

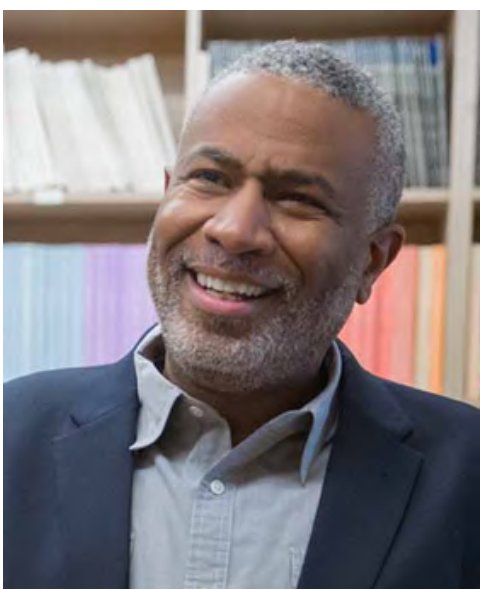
Alicia is a biologist from the National Autonomous University of Mexico (UNAM), and holds a PhD from the University of East Anglia, England. She currently works as a CONAHCYT Research Fellow at Instituto de Ecología - UNAM. Her research focuses on incorporating genetic diversity into conservation using 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.

Keynote Speakers



Aida Andrés
University College London, UK

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 V. Edwards
Harvard University, USA

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)

14:00-18:00

Registration

12:00-14:00

Workshop On site “Introduction to STDPOPSIM workshop” (Popgen)

Boca de Tomates

14:00-16:00

Workshop On site “GENHIST kickoff at SMBE” (Popgen)

Boca de Tomates

11:00-16:00

Workshop Online “Introduction to programmatic access to EnSEMBL”

Costa Alegre

18:00-19:00

Opening Keynote Speaker

Los Tules

Stephen Wright

Adaptation and maladaptation in plant genomes.

19:00-20:00

Welcome Cocktail

Day 2 (8 July)

9:00-11:00

Graduate Student Excellence Awards

Los Tules

9:00-9:13

Bárbara Sousa da Mota

Investigating the ecological suicide (“ecocide”) theory in Rapa Nui with ancient DNA data

9:13-9:26

Benjamin Moran

A lethal mitonuclear incompatibility in complex I of natural hybrids

9:26-9:39

Christopher Blake

Evolutionary shift of a tipping point forestalls collapse in a microbial community.

9:39-9:52

Jaison Jeevan Sequeira

The provenance of Proto-North Dravidian ancestry in the Indus valley

9:52-10:05

María José Palma Martínez

Beyond Continental Groups: Unveiling Dynamic Human Genetic Communities with a Novel Network Analysis Pipeline

10:05-10:18

Mariela Tenorio

MAYEX is an ancient long non-coding RNA recruited for X chromosome dosage compensation in lizards

10:18-10:31

Meaghan Marohn

Revisiting the evolution of lactase persistence: insights from South Asian genomes

10:31-10:44

Siliang Song

Human sex ratio at birth has virtually no detectable genetic variation: Was Fisher wrong about the evolution of sex ratio?

10:44-10:57

Sung-Ya Lin

Rapid coevolution preserves the epigenetic establishment of telomere protection

11:00- 11:30

COFFEE BREAK

11:30 - 13:20

S39-Associate Editors’ Symposium

Los Tules

11:30-11:45

Aida Ouangraoua

Transcript Homology Relationships and Phylogeny Reconstruction

11:45-12:00

Carolin Kosiol

PoMo via RevBayes: Inferring Phylogenies, Disentangling GC-bias and Balancing Selection

12:00-12:15

Jianzhi Zhang

Evidence for the role of selection for reproductively advantageous alleles in human aging

12:15-12:30

Joanna Kelley

The evolution of hibernation-related shifts in gene expression across hibernating mammals

12:30-12:45

Kirk Lohmueller

The distribution of fitness effects varies with phylogeny across animals

12:45-13:00

Maud Tenailon

Detecting barriers to gene flow from genomic patterns: application to maize and teosintes

13:00-13:15

Adam Eyre-Walker

Is there nepotism in the allocation of research grants?

Scientific Program

Day 2 (8 July)

11:30 - 13:20

S38-Open Symposium 1

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

13:15-13:25

Paul Taylor

Insights into Human Neurotransmission through Molecular Evolution Studies in Bacteria

11:30 - 13:20

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

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

11:30 - 13:20

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

Las Pilitas

11:30-11:55

Hussein Mohsen

What is in a discrete category? Clustering genomics cohorts beyond race, ethnicity—and ancestry

11:55-12:20

Simon Gravel

Genetically informed representations of ancestry and ethnicity

12:20-12:35

Luke Anderson-Trocme

Breaking Boundaries: Leveraging Continuous Models for Improved Population Genetics Analyses

12:35-12:50

Benjamin Peter

Quantitative Interpretations of Principal Component Analysis

12:50-13:05

John Novembre

Non-parametric representations of structure in genetic ancestry through time

13:05-13:20

Marta Ciccarella

Multiple periods of admixture and isolation during and after the Transatlantic Slave Trade on the island of São Tomé.

11:30 - 13:20

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

Costa Alegre

11:30-11:55

Beatriz Mello

Green Computing in Molecular Evolution and Phylogenetics for the Global South

11:55-12:20

Bui Minh

CMAPLE: efficient phylogenetic inference in the pandemic era

12:20-12:35

Sudhir Kumar

MEGA 12: Advancing Green Computing and Phylogenomics

Scientific Program

Day 2 (8 July)

11:30 - 13:20

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

Costa Alegre

12:35-12:50

Gavin Huttley

A spectral step on the divide and conquer path to energy efficient phylogenetic reconstruction

12:50-13:05

Jiansi Gao

Causes and impacts of the widespread lack of topological convergence in Bayesian phylodynamic inference on large viral datasets

13:05-13:20

Li Liu

Shifting Focus from Gene-centric to Evolution-centric Analyses in Cancer Genomics

13:20- 14:20

LUNCH BREAK

14:20 - 15:50

Poster session 1

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

Exploring the Evolutionary Effects of Admixture.

Human evolution in the genomic era.

Human genetic variability in the Pangenomic era.

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

Open Symposium 1

Progress and challenges for understanding the molecular evolution of sex chromosomes across Eukarya

Structural phylogenetics: investigating deep evolutionary history using protein structure.

Unlocking the hidden dimensions of genomic diversity within species.

14:20 - 15:50

Event: MBE Editors Meeting

Boca de Tomates

15:50 -18:10

S5- Human evolution in the genomic era.

Los Tules

15:50-16:15

Katherine Pollard

Decoding the evolution and functions of Human Accelerated Regions with deep learning

16:15-16:30

Erin Gilbertson

Machine learning reveals the diversity of human 3D chromatin contact patterns

16:30-16:45

Ryder Easterlin

Discovering the cis-regulatory basis of archaic human-derived phenotypes

16:45-17:00

Maddy Comerford

Functional characterisation of the regulatory activity of archaic DNA in Island Southeast Asia

17:00-17:15

Samvardhini Sridharan

Worldwide patterns of diversity at the 17q21.31 locus in modern human genomes

17:15-17:30

Eva Brigos Barril

Why do we get sick? Unraveling Genetic Trade-offs between Fertility, Longevity, and Complex Diseases

17:30-17:45

Moisès Coll Macià

Archaic introgression in modern humans modelled by ancestral components

17:45-18:10

Bo Xia

On the genetic basis of tail loss evolution in humans and apes

15:50 -18:10

S12-Exploring the Evolutionary Effects of Admixture

Boca de Tomates

15:50-16:15

Alexander Ioannidis

Disentangling the effects and history of human admixture from the Americas to Oceania

16:15-16:30

Alexander Kirschel

Alternative genomic and biochemical pathways to red carotenoid pigments in birds

16:30-16:45

Daniel Powell

Pervasive gene flow despite strong and varied reproductive barriers in swordtails

16:45-17:00

Lucia Morales Reyes

Genomic Insights into the Recurrent Interspecific Hybridizations of Agave-Associated Saccharomyces Yeasts

17:00-17:15

Maria Fariello Rico

Detecting selection in admixed populations using haplotypic information

17:15-17:30

Andrew Vaughn

Bayesian Inference of Admixture Graphs on Native American and Arctic Populations

Scientific Program

Day 2 (8 July)

15:50 -18:10

S12-Exploring the Evolutionary Effects of Admixture

Boca de Tomates

17:30-17:45

Aaron Pfennig

Complex neutral processes drive the evolutionary fate of Neanderthal alleles in 30,780 admixed genomes with African-like and European-like ancestry

17:45-18:10

Emilia Huerta Sanchez

Evolutionary insights from admixed genomes

15:50 -18:10

S24- Unlocking the hidden dimensions of genomic diversity within species.

Olas Altas

15:50-16:15

Mayra Furlan-Magaril

Chromatin 3D conformation of a silent genome: the case of nucleated erythrocytes

16:15-16:30

Paco Majic Bergara

On mutational neighbourhoods and their influence on evolutionary processes

16:30-16:45

James Phipps-Tan Sheng Yi

Beyond averages: transcriptional variability in outbred *Drosophila melanogaster* and its environmental and genetic dependence

16:45-17:00

Thea Rogers

Novel topological units characterise a distinct regulatory architecture underlying the evolution of complex traits in coleoid cephalopods

17:00-17:15

Christabel-Floi Bucão

Gene expression variability implies stable cis-regulation of brain genes across non-nervous organs

17:15-17:30

Justin Wilcox

Population genomics of wild avian embryos uncovers hidden genetic diversity

17:30-17:45

Gabriela Santos Rodriguez

The evolution of transcriptome complexity using Oxford Nanopore long-read sequencing technology.

17:45-18:10

Aurora Ruiz-Herrera

Plasticity of 3D chromatin folding across timescales

15:50 -18:10

S1- Structural phylogenetics: investigating deep evolutionary history using protein structure

Las Pilitas

15:50-16:15

Martin Steinegger

Supercharged Protein Analysis in the era of AI

16:15-16:30

Hector Romero

Exploring protein evolution through natural and simulated sequences using experimental and modeled 3D structures

16:30-16:45

Stefano Pascarelli

AlphaHOG, a protein structure-based reference classification to improve orthology inference

16:45-17:00

David Moi

Foldtree. Empirical benchmarking of structural phylogenetics methods

17:00-17:25

Betul Kaçar

Early protein evolution using deep time sequence and structure reconstructions

17:25-17:40

Desiree Langer

Structural phylogenetics of the jelly roll fold sheds light on viral evolution

17:40-17:55

Claudia Alvarez Carreno

Polyphyletic insertions in the bacterial DNA-directed RNA polymerase

17:55-18:10

Charles Carter, Jr

Structural Enzymology, Phylogenetics, Differentiation and Symbolic Reflexivity at the Dawn of Biology

15:50 -18:10

S3- Progress and challenges for understanding the molecular evolution of sex chromosomes across Eukarya

Costa Alegre

15:50-16:15

Gabriel Marais

The *Silene latifolia* genome and its giant Y chromosome

16:15-16:30

Erik Fogh Sorensen

The struggle of being a sex chromosome: Why X has a lower diversity than expected in primates

16:30-16:45

Claudia C Weber

Do Z chromosomes in Butterflies and Moths Show Evidence of Increased Rates of Adaptation?

16:45-17:00

Josué Barrera-Redondo

The UV sex chromosomes of brown algae act as genomic cradles for new genes that evolve de novo

Scientific Program

Day 2 (8 July)

15:50 -18:10	S3- Progress and challenges for understanding the molecular evolution of sex chromosomes across Eukarya	Costa Alegre
17:00-17:15	Sophia Catherine MacRae Orzechowski Shining a light on early stages of neo-sex chromosome evolution in Australian honeyeaters (Aves: Meliphagidae)	
17:15-17:30	Gabrielle Coffing Cephalopod sex determination and its ancient evolutionary origin revealed by chromosome-level assembly of the California two-spot octopus	
17:30-17:45	Sarah Carey Using phased genome assemblies to examine the evolution of heteromorphic sex chromosomes in Cannabaceae	
17:45-18:10	Melissa Wilson Alignment and Variant Calling in Reference Genomes to Improve Sex Chromosome Comparative Genomics	
20:00 - 22:00	Event: MBE Editors Dinner	Mayapán Restaurant at Paradise Village Resort

Day 3 (9 July)

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

Scientific Program

Day 3 (9 July)

10:30 - 12:20

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

Olas Altas

11:50-12:05

Gillian Meeks

Accounting for common genetic variation improves chronological age prediction in African populations

12:05-12:20

Eugenio Mancera

Exploring the chronological lifespan spectrum of Candida species

10:30 - 12:20

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

Las Pilitas

10:30-10:55

Pier Palamara

Inference of recent effective population size from high and low coverage DNA data

10:55-11:10

Katia Bougiouri

How to paint a dog: limits of local ancestry inference in ancient genomes

11:10-11:25

Eduardo González Orozco

Archaic ancestry fragment calling using wavelet decomposition

11:25-11:40

Amy Williams

Reconstructing parent genotypes at genotyping array accuracy using siblings and other relatives

11:40-11:55

Jazeps Medina Tretmanis

Improving Local Ancestry Inference through Neural Networks

11:55-12:20

Amy Goldberg

Ancestry-based approaches for inference of evolutionary history on short timescales

10:30 - 12:20

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

Costa Alegre

10:30-10:55

Elinor Karlsson

Title to be confirmed

10:55-11:10

Alexandra Keene

Viral and host metagenomics of 100-year-old insect museum specimens

11:10-11:25

Eucharist Kun

The trait specific timing of accelerated genomic change in the human lineage.

11:25-11:40

Lucas Rocha Moreira

Evolutionary paths to thermal resilience in placental mammals: functional genomics insights from the Frozen Zoo Biobank

11:40-11:55

Michelle Stitze

From swampy ancestors to modern maize: tracing the allopolyploid origins of Zea

11:55-12:20

Nico Franz

Title to be confirmed

12:20- 13:20

LUNCH BREAK

12:20 - 13:20

Event: SMBE Business Meeting

Boca de Tomates

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

Boca de Tomates

Scientific Program

Day 3 (9 July)

14:50 -17:10	S16- Evolutionary Medical Genomics	Los Tules
14:50-15:15	Pleuni Pennings Why aren't all E. coli resistant to antibiotics?	
15:15-15:30	Imroze Khan Rapid evolution of mutation rate and germline maintenance under strong pathogen selection: new insights from experimental evolution experiments	
15:30-15:45	Cara Love Radiation-induced stress and signatures of selection on anti-tumor immunity in Chornobyl wolves	
15:45-16:00	Daniel Jordan Deep learning phenotype imputation to measure dominance of rare variant effects on rare disease in UK Biobank	
16:00-16:15	Alief Moulana Epistasis and pleiotropy constrain and expand the evolution of SARS-CoV-2 Omicron lineage	
16:15-16:30	Helena Hopson Interactions between sickle cell and Plasmodium falciparum genotypes in asymptomatic malaria	
16:30-16:45	Evan Irving-Pease The evolutionary origins of autoimmune and infectious disease risks	
16:45-17:10	Shamil Sunyaev Evolutionary perspective on human polygenic traits	
14:50 -17:10	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	
15:15-15:30	Marco Rosario Capodiferro Archaic ancestry inference in imputed ancient human genomes	
15:30-15:45	Yulin Zhang Reconstructing mutation patterns over the course of human evolution	
15:45-16:00	Stéphane Peyrégne A high-quality genome from a 200,000-year-old Denisovan	
16:00-16:25	Maanasa Raghavan Human genetic histories at the Himalayan frontiers	
16:25-16:40	Dilek Koptekin Overcoming bias and postmortem damage to improve the accuracy of ancient genome analysis	
16:40-16:55	Sandra Oliveira Tracing admixture in European early farmers using local ancestry inference	
16:55-17:10	Hugh McColl Steppe Ancestry in western Eurasia and the spread of the Germanic Languages	
14:50 -17:10	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 -17:10	S6- Molecular evolution through metagenomics	Las Pilitas
14:50-15:15	Gabriela Olmedo Álvarez Clues to the Evolution of Antibiotic resistance from bacteria and ancient communities from pristine sites in Cuatrociénegas, 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-Diaz 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 <i>Treponema</i> 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 -17:10	S27- Transposable elements in the population genomics era: towards a better understanding of their contribution to evolution.	Costa Alegre
14:50-15:15	Grace Yuh Chwen Lee How transposable element shapes genome evolution through epigenetic mechanisms?	
15:15-15:40	Leandro Quadra 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 <i>Drosophila</i> species within the last 50 years	
16:10-16:25	Jilong Ma Independent transitions to sociality in <i>Stegodyphus</i> 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	S18- One Health and microbial evolution: New ideas and perspectives	Los Tules
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 <i>Pseudomonas aeruginosa</i> 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	

Scientific Program

Day 3 (9 July)

17:40-19:30

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

Los Tules

18:40-19:05

Santiago Elena

An evolving world for evolving pathogens: ecological drivers of virus diversification and adaptation

19:05-19:30

Fernando González Candelas

Evolutionary genomics and the one health approach to AMR

17:40 - 19:30

S34- Going local: Using engaged research practices to understand regional-scale interactions.

Boca de Tomates

17:40-18:05

María Ávila-Arcos

Community engagement experiences of the Afromexico Genomics Project

18:05-18:20

Eleni Seferidou

An ancient genetic insight into pre-colonial Trinidad.

18:20-18:35

Daniela Orozco-Perez

Paleogenomic analyses of archaeological remains reveal sex roles and mobility of ancient families in central Mexico

18:35-18:50

Esha Bandyopadhyay

Distinct positions of genetic and oral histories: Perspectives from India

18:50-19:05

Constanza de la Fuente Castro

Conversations in community-based genomic research: Showcasing a platform from Chile to integrate Indigenous engagement and representation

19:05-19:30

Laura Weyrich

Uncovering the global origins of an Industrialized microbiome using regionally focused studies

17:40 - 19:30

S22- Impact of environmental changes on agrobiodiversity and strategies for resilience.

Olas Altas

17:40-18:05

Brandon Gaut

Crop wild relatives, climate change and genomic diversity

18:05-18:20

Luis Eguiarte

Population genomics of tequila and mezcal (Agave spp.): Unexpected findings and lessons for these Mexican industries in the face of climate change.

18:20-18:35

Mirte Bosse

A boaring story of hybridization and adaptation in wild boars, domestic pigs and feral swine

18:35-18:50

Alejandra Hernandez-Teran

Disentangling microbiome effects on plant adaptation

18:50-19:05

Ayelet Salman-Minkov

Strategies for mining useful alleles for climate change adaptation

19:05-19:30

Azalea Guerra-García

Building agroecosystems resilience by fostering native crops and their wild relatives

17:40 - 19:30

S13- Animal paleogenomics beyond higher latitudes.

Las Pilitas

17:40-18:05

Selina Brace

Museomics and the Tropics: occasionally vexing, but a rewarding partnership

18:05-18:20

Alida de Flamingh

Compacted hair in broken carnivore teeth reveal dietary prey of historic lions

18:20-18:35

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.

18:35-18:50

David Ledesma

Small but mighty: ancient DNA analyses of late Pleistocene and Holocene microvertebrates from Central Texas

18:50-19:05

Federico Sánchez Quinto

The evolutionary origin of the Columbian mammoths from the Basin of Mexico and its implications for the *Mammuthus* genus

19:05-19:30

Viviane Slon

Sedimentary ancient DNA studies in challenging preservation contexts: Insights from the southern Levant

Scientific Program

Day 3 (9 July)

17:40 - 19:30

S35-Genetics, Molecular Biology, and the Future of Forensic Science

Costa Alegre

17:40-18:05

Rori Rohlf

Quantifying the accuracy of forensic genetic technologies

18:05-18:20

Anne Stone

The recovery of DNA from burned forensic contexts.

18:20-18:35

Feriel Ouerghi

How should we report genetic matches following an Investigative Genetic Genealogy search?

18:35-18:50

Meghna Swayambhu

Highly accurate predictions indicating sexual activity using microbiome-based analyses in forensic settings

18:50-19:05

Maria Flores

Construction of Epigenetic Clock using Cell-Free DNA

19:05-19:30

Jaehee Kim

Population genetics approaches for forensic genetic record-matching

20:00 - 22:00

Event: GBE Editors Dinner

Mayapán Restaurant at Paradise Village Resort

Day 4 (10 July)

9:00-10:00

Keynote Speaker

Los Tules

Aida Andrés

Local genetic adaptation in humans and other primates

10:00- 10:30

COFFEE BREAK

10:30 - 12:20

S2-Novel approaches to study plant domestication: disentangling the complex evolutionary history of crops

Los Tules

10:30-10:55

June Simpson

Exploring the fructan syndrome in Agave tequilana-a non-typical crop plant

10:55-11:10

Xianran Li

Deciphering Sorghum Domestication: The Pivotal Role of Condensed Tannins in Co-evolution Among Plants, Humans, and Birds

11:10-11:25

Arthur Wojcik

Meta-analysis of wild and domesticated crop phenotypic spaces

11:25-11:40

Laura Botigué

Wheat domestication and adaptation to new environments: the role of wild emmer.

11:40-11:55

Miriam Ferrer

Multipurpose species domestication in Mayan homegardens

11:55-12:20

Alejandro Quintero

Exploring the patterns of microbiota recruitment and inheritance on the chocolate tree, *Theobroma cacao* L

10:30 - 12:20

S10- Genomes and Generations: Mapping Health and Heritage Through African Genomics.

Boca de Tomates

10:30-10:55

Brenna Henn

A Rich Resource of African-Descent Genomes (CAAPA2)

10:55-11:20

Dhriti Sengupta

Impact of Khoe-San gene flow in phenotypic variation of anthropometric and cardiometabolic traits

11:20-11:35

Jeremy Choin

Genomic Insights into the population history of southern-central Africa

11:35-11:50

Rohini Janivara

Heterogeneous genetic architectures and evolutionary genomics of prostate cancer in Sub-Saharan Africa

11:50-12:05

Esther Brielle

Sudanic, Central, and Western African ancestry contributions to ancient Ugandan Populations

12:05-12:20

Jasmin Rees

Evolutionary History of Transient Receptor Proteins in Sub-Saharan Africa

Scientific Program

Day 4 (10 July)

10:30 - 12:20	S29- Advances in Machine Learning for Evolutionary Genomics.	Olas Altas
10:30-10:55	Sara Mathieson Interpreting deep learning methods for population genetic inference	
10:55-11:20	Siavash Mirarab Metric learning for phylogenetic placement	
11:20-11:35	Carina Cornejo Paramo A Bag-Of-Motif Model Captures Context-Specific Distal Regulatory Elements	
11:35-11:50	Steven Reilly Interrogating the relationship between conservation and regulatory function across all human promoters using machine-learning variant effect predictions	
11:50-12:05	Murillo Rodrigues A deep learning framework for evolutionary inference using ancestral recombination graphs	
12:05-12:20	Zhengting Zou Sequence embeddings by pretrained language model indicate adaptive convergence of high-order protein features.	

10:30 - 12:20	S14- Unveiling the evolutionary history of pathogens through paleogenomics	Las Pilitas
10:30-10:55	Tanvi Honap Exploring oral microbial evolution in the context of European colonization of the Americas	
10:55-11:10	Laura Carrillo-Olivas Exploring Pathogens and Demographic Dynamics in Colonial Mexico City through Paleogenomics	
11:10-11:25	Paola Campos Deciphering the emergence and evolutionary history of a bacterial crop pathogen: insights from historical herbarium specimens	
11:25-11:40	Sojung Han RNA virus genomes from historical specimens of great apes	
11:40-11:55	Nasreen Broomandkhoshbacht Characteristics of a 5,500-year-old Treponema pathogen from Colombia	
11:55-12:20	Elizabeth Nelson Tuberculosis and Sociocultural Dynamics: Critical Insights from Paleogenomics in South America and Beyond	

10:30 - 12:20	S33- Science in the Spotlight: Empowering Education and Public Engagement with Cutting-Edge Science in Molecular Evolution.	Costa Alegre
10:30-10:55	Roberto Torres Melanogaster Catch The Fly! Rural high schools committed to frontier research on genomics and evolution through citizen science	
10:55-11:10	Sarah Schaack TE Hub: A Community for Developing Tools, Trainings, and Resources to Analyze DNA Repeats	
11:10-11:25	Kate Duggan Disease Detectives: Using Minecraft to explore virus evolution and epidemiology	
11:25-11:40	Sònia Casillas Adopting ESG principles in PopLife, the population genomics browser across the tree of life	
11:40-11:55	Rebecca Siford Evaluating community perceptions and ethical considerations in genetics research in small scale northern Kenyan populations	
11:55-12:20	Nicolette Caperello Engaging the Public on Biology's Moonshot: The Earth BioGenome Project	

12:20- 13:20 **LUNCH BREAK**

12:20 - 13:20 **Event: MBE & GBE Editors 'Q&A session'** Boca de Tomates

Scientific Program

Day 4 (10 July)

13:20 - 14:50

Poster session 3

Advances in Machine Learning for Evolutionary Genomics.
Deciphering the functional and adaptive effects of genomic structural variation.
Decoding the past to safeguard the future.
Epigenetic inheritance: from molecular mechanisms to evolutionary consequences.
Evolution of microbial communities: is the sum of parts greater than the whole?
Genomes and Generations: Mapping Health and Heritage Through African Genomics.
Human population demography and adaptation signals in the Americas.
Mitochondria: from powerhouse to processor and from marker to meaning.
New computational approaches to estimate past demographic events and natural selection.
Novel approaches to study plant domestication: disentangling the complex evolutionary history of crops
Open Symposium 2
Spatial population genetics: where are we now?
Unveiling the evolutionary history of pathogens through paleogenomics.

14:50 -17:10

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

Los Tules

14:50-15:15

Paul Rainey

Communities, lineages, and the evolution of evolvability

15:15-15:30

José Flores-Uribe

Experimental evolution of synthetic phototrophic communities

15:30-15:45

Mike McDonald

A new genome from the pangenome - experimental evolution with horizontal gene transfer.

15:45-16:00

Pu Wang

Eco-evolutionary feedbacks promoted by hypermutation rate in a predator-prey microcosm

16:00-16:15

Edmund Moody

The nature of the Last Universal Common Ancestor and its impact on the early Earth system

16:15-16:30

Autumn Peterson

Disentangling the evolutionary impacts of relatedness and facultative/obligate life cycles during the transition to multicellularity

16:30-16:55

Sarit Avrani

Tradeoffs between phage resistance and nitrogen fixation drive the evolution of multicellular cyanobacteria

14:50 -17:10

S9- Human population demography and adaptation signals in the Americas

Boca de Tomates

14:50-15:15

Cosimo Posth

The genetic history of early Americans

15:15-15:30

Santiago Medina-Muñoz

Inferring fine-scale demography of indigenous lineages from 500 whole genomes across Mexico

15:30-15:45

Valeria Anorve-Garibay

The contribution of Neanderthal introgression to the heritability of human complex traits in Mexico

15:45-16:00

Esther Brielle

Adaptation in Ancient Maya

16:00-16:25

Tábita Hünemeier

Evolutionary Changes Throughout Human History in America

16:25-16:40

Epifanía Arango Isaza

Uncovering South American genomic diversity in the Southern Cone

16:40-16:55

Marisol Espitia Fajardo

Colombian Arawak genomes shed light on population demography of South America

16:55-17:10

Thomaz Pinotti

Picuris Pueblo oral history and genomics reveal genetic continuity in North American Southwest

14:50 -17:10

S11- Spatial population genetics: where are we now?

Olas Altas

14:50-15:15

Alison Feder

Spatial drivers of disease progression in bacteria and viruses

15:15-15:30

Alessandro Lopez-Hernandez

A space-time model for jointly inferring gene flow and natural selection

15:30-15:45

Clara Rehmann

In space no one can hear you sweep: a novel signal of selective sweeps in continuous geographic space

Scientific Program

Day 4 (10 July)

14:50 - 17:10	S11- Spatial population genetics: where are we now?	Olas Altas
15:45-16:00	Jack Harper Using biological invasions to understand rapid adaptation to new environments: a genomic reconstruction of the house sparrow global spread	
16:00-16:25	Andy Kern Deep Space– supervised machine learning methods for spatial population genetics	
16:25-16:40	Gilia Patterson A spatially explicit close kin mark recapture method for estimating census size from genetic data	
16:40-16:55	Vivaswat Shastry Inference of long-range gene-flow events in a background of spatially heterogeneous isolation-by-distance	
16:55-17:10	Michael Grundler Spatial ancestry reconstruction using parsimony on tree sequences	
14:50 - 15:50	S25- Mitochondria: from powerhouse to processor and from marker to meaning	Las Pilitas
14:50-15:15	Dennis Lavrov Evolution of mitochondrial mRNA editing and linear multipartite mt-genome architecture in calcaronean sponges	
15:15-15:30	Vaishali Katju No passive sidekick: a substantial role for mitochondrial compensatory evolution during adaptation of ETC-deficient strains of <i>Caenorhabditis elegans</i>	
15:30-15:45	Toni Gossmann Phylonomtomics uncovers diverse evolutionary trajectories of mitogenomic fossils buried in mammalian and avian genomes	
15:45-16:00	Dennis Lavrov Evolution of mitochondrial mRNA editing and linear multipartite mt-genome architecture in calcaronean sponges (invited talk)	
16:00-16:15	Konstantin Popadin Decoding the Puzzle of Human Somatic mtDNA Mutagenesis: Bridging Species Life-History Traits and Organ-Specific Cellular Properties	
16:15-16:30	Leah Darwin The contribution of within- and between-species mitochondrial variation to adaptation in experimental <i>Drosophila</i> populations	
16:30-16:45	Wei-Chin Ho Population-Genetic Environment of Genome Retention and Reduction in Mitochondria	
16:45-17:10	Michael Garvin The Importance of Mito-nuclear Epistasis in Evolutionary Genetics	
14:50 - 15:50	S26- Deciphering the functional and adaptive effects of genomic structural variation	Costa Alegre
14:50-15:15	Mia Levine DNA satellite evolution triggers a cross-species incompatibility	
15:15-15:30	Julie Chuong DNA replication errors are a major source of gene amplification in adaptive evolution	
15:30-15:45	Elli Cryan Molecular evolution of a maize hybrid barrier over 12 million years suggests epistatic silencing	
15:45-16:00	Samuel Bogan Convergent Structural Variation of Antifreeze Proteins in Polar and Deep Sea Fishes	
16:00-16:15	Tristram Dodge Intergenic structural variation and ancient gene duplication underpin pigmentation diversification in swordtail fish	
16:15-16:30	Diego Hartasánchez The role of structural variation in clownfish adaptive radiation	
16:30-16:45	Megan Dennis Gene expansions contributing to human brain evolution	
16:45-17:10	Christine Beck Repetitive sequences drive genomic variation and vary regulatory landscapes	
19:00-23:00	GALA DINNER	Host Hotel Paradise Village

Scientific Program

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, <i>Xiphophorus variatus</i>	
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	Hélène 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 <i>C. elegans</i> and beyond	
9:25-9:40	Elisa Israel MBD2/3 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)

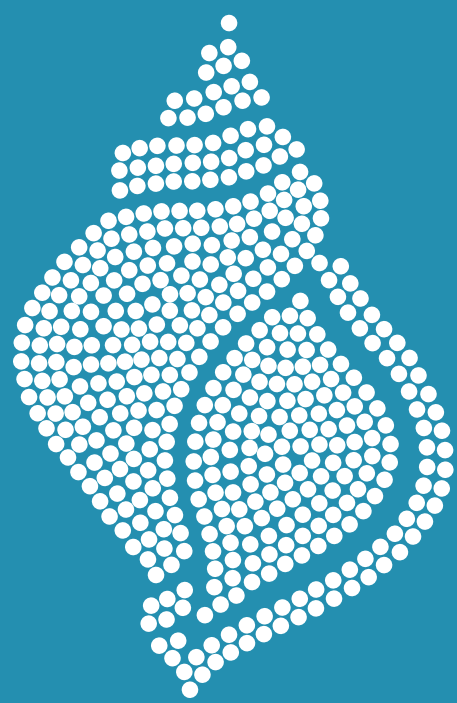
09:00- 10:50	S21- Decoding the past to safeguard the future.	Las Pilitas
9:50-10:05	Germán Hernández-Alonso Exploring the Rock Dove's (<i>Columba livia</i>) Genetic Diversity: Insights into the Species' Evolutionary History and Conservation Challenges	
10:05-10:20	Chenyu Jin Metagenomic reconstruction of the plant community in the stomach content of a steppe bison living over 48,000 C14 years ago	
10:20-10:35	Maria Zicos Reconstructing the population history of the endangered Hispaniolan solenodon, one of the most evolutionary distinct mammals on earth	
10:35-10:50	Xuejing Wang Reviving from four birds: post-bottleneck overview of temporal genomics of Mauritius kestrel	

09:00- 10:50	S28- Human genetic variability in the Pangenomic era..	Costa Alegre
9:00-9:25	Erik Garrison Implicit pangenomics	
9:25-9:40	Gabriel Renaud Maximum-likelihood inferences from ancient environmental DNA using panmitogenomes	
9:40-9:55	Runyang Nicolas Lou Global diversity, recurrent evolution, and recent selection on amylase structural haplotypes in humans	
9:55-10:10	Joana Rocha A Pan-pangenome captures the full spectrum of genetic variation in humans, chimpanzees and bonobos	
10:10-10:25	Rick McLaughlin Pangenome assemblies reveal the evolution and recent in vivo activity of human LINE-1 retrotransposons	
10:25-10:50	Arang Rhie Living with your dynamic genome: lessons learned from T2T genomes	

10:50 -11:20 **COFFEE BREAK**

11:20-12:20	Closing Keynote Speaker	Los Tules
	Scott Edwards PhyloG2P: the new science of connecting genomes to phenotypes via phylogenies	

12:20-14:20 **Awards Ceremony and Introduction to SMBE 2025**



SMBE 2024

PUERTO VALLARTA

