SMBE 2024
PUERTO VALLARTA

Annual Meeting of the Society for Molecular Biology and Evolution

July 7–11, 2024
Puerto Vallarta, Mexico

Smbe
Society for Molecular Biology & Evolution

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SMBE2024 Gallery

¡Bienvenidos a nuestro video memoria de SMBE 2024!

RESULTS ANNOUNCEMENT:

More than 1000 abstracts have been selected and the scientific program is under construction. Stay tuned!

SUBMISSION OF ABSTRACT IS CLOSED

Deadline for **Early bird registration fees**:

May 20, 2024

Arrange your travel

REGISTRATION SMBE 2024

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SMBE 2024

Keynote Speakers

Alicia Mastretta-Yanes

CONAHCYT - UNAM.

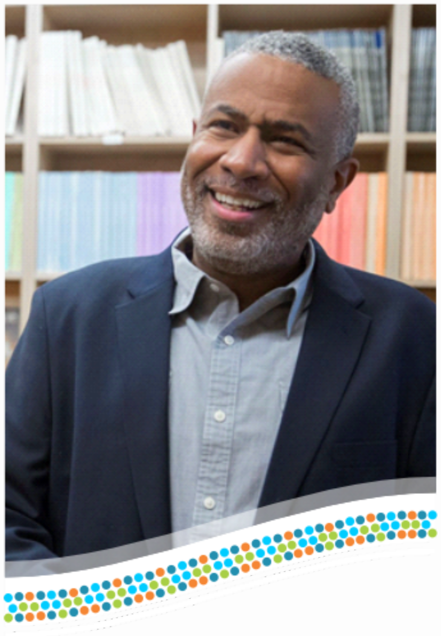
Alicia is a biologist from the National Autonomous University of Mexico (UNAM), and holds a PhD from the University of East Anglia, England. She currently Works as a CONAHCYT Research Fellow at Instituto de Ecología - UNAM. Her research focuses on incorporating genetic diversity into conservation using evolutionary approaches, spanning diverse ecosystems such as the Lacandona jungle, sky-islands, polluted forests, and Mexican

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 agroecosystems. She contributed to the development of genetic diversity indicators, now adopted by the Global Biodviersity Framework, and she is actively involved in co-formulating approaches for nations to monitor and safeguard genetic diversity on a global scale.

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

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 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.

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.

Graduate Student Excellence Awards Winners

Sung-Ya Lin

I grew up in Taiwan, where I completed a bachelor's degree in Life Science at National Taiwan University (NTU). During that time, I worked in Dr. Hsueh-Chi Sherry Yen's lab at Academia Sinica studying protein degradation and learned the fundamental concepts of scientific research and molecular biology techniques. After graduation, I continued to pursue a master's degree and joined Dr. Chau-Ti Ting's lab at NTU, where I studied the sex-ratio meiotic drive in Drosophila and became fascinated with selfish genetic elements and genetic conflict. My fascination for these rapidly changing parts of the genome led me to join Dr. Mia Levine's lab at the University of Pennsylvania as a PhD student. Currently, my research combines genetic, evolutionary, and cell biological approaches to understand the causes and consequences of the rapid evolution of telomere binding proteins that shape essential cellular functions.

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Christopher Blake

I am an evolutionary microbiologist conducting my PhD at Monash University in Melbourne, Australia with Mike McDonald. Before joining Mike's lab, I received my training in Biology (B.Sc.) at Kiel University in Germany and in Microbiology (M.Sc.) at Copenhagen University in Denmark, where I was working with Ákos T. Kovács. I am mainly interested in how complex microbial communities evolve together and adapt to rapidly changing environments. My research focuses on how evolution can alter the stability landscape of microbial communities, both as free-living communities and within host systems.

Maria Jose Palma Martinez

Jaison Jeevan Sequeira

I am a PhD candidate at the Sohail lab at the Center for Genomic Sciences, UNAM. Previously during my master's, I had the amazing opportunity of working on the MXBiobank. Currently, my research focuses on promoting intentional decisions about the way we group humans in genetics and biomedical research. In this project, along with a trans-disciplinary team of collaborators, we developed a computational pipeline and web browser based on relational thinking.

I am a bioinformatician at heart and I am also interested in the study of non-human species. I truly believe in the role of science in the search for knowledge that allows us to make better decisions as a society.

Twitter account: **@MaxolotlMad**

I always find it challenging to introduce myself because I am passionate about many things, and I tend to get excited about new experiences. That's why I decided to study genetic variation and the ancestral origin of indigenous populations along the southwest coast of India. I have trained myself to become an aspiring population geneticist, and in my free time, I enjoy pursuing my other interests, such as singing and song writing, freelance sound engineering, and motivational speaking.

Twitter: **@jaisonjseq**

Ben Michael Moran

Ben Moran is a 5th-year PhD student in the Department of Biology at Stanford University. As part of the laboratory of Prof. Molly Schumer, he has spent his dissertation studying hybrids between swordtail fishes (*Xiphophorus* spp.) in the Sierra y Huasteca Hidalguense, with frequent trips to the CICHAZ field station in

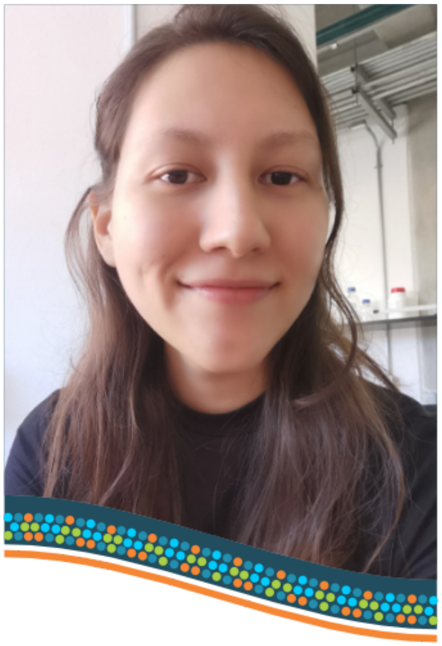
Meaghan Marohn

I am a PhD student in Priya Moorjani's lab at UC Berkeley as part of the department of Molecular and Cell Biology with a designated emphasis in Computational Biology. My current project aims to revisit the evolution of lactase persistence by leveraging data from South Asian populations. Prior to pursuing my PhD I received my B.A. from Barnard College in

Calnali, Hidalgo, México. Ben is interested in the eco-evolutionary processes that can be revealed in natural hybrid zones, as well as the relationship between human impacts on the environment and novel hybrid zones. Looking forward, he is excited to expand the role of population genomics in our understanding and conservation of biodiversity.

Twitter/X: **@Ben_M_Moran**

Biology and Anthropology. In addition to population genetics research, I have enjoyed learning more about the scientific writing community at Berkeley and partaking in education and outreach initiatives in the Bay Area to practice different science communication efforts. When I'm not trying to unravel the mysteries of human evolution and diversity, I enjoy exercising my creative side by drawing and painting.



Mariela Tenorio

I am a biologist who has had the privilege of working with and meeting special people who guided me on my scientific journey. I earned my Ph.D. at the Center for Genomic Sciences under the mentorship of Dr. Diego Cortez. Over the past five years, my research has focused on the expression of sex chromosomes in lizards, a project that has allowed me to develop extensive technical and bioinformatic expertise. I am committed to advancing our understanding of genomic sciences and contributing to the scientific community.

Siliang Song

I am a 5th-year PhD student at the University of Michigan, working in Prof. Jianzhi Zhang's lab. My research focuses on fitness landscape, molecular evolution, and human behavioral evolution. Currently, I utilize large-scale biobank data to investigate the evolution of human sex ratios. My broader research interests include adaptive tracking, the evolution of sex and its derivatives (sexual reproduction, sex chromosome, sex ratio, etc.). In my leisure time, I enjoy exploring the diversity of insects in the wild and learning physics.

Bárbara Sousa da Mota

Born and raised in Portugal, I studied physics in my home country before switching to biology. I have spent the last five years studying population history using ancient DNA at the University of Lausanne in Switzerland. In particular, I worked on implementing imputation techniques for ancient genomes and then leveraged these methods to study the genomic history of the Rapanui. I have very recently finished my PhD and am very much looking forward to my future projects. During my time in Switzerland, you could often find me hiking the magnificent mountains.

⊕ GENHIST kickoff at SMBE

⊕ Introduction to programmatic access to EnsE...

⊕ Introdution to STDPOPSIM workshop

Key dates

Call for Symposia
October 2023

Selection of Symposia
November 2023

Announcement of Selected Symposia
January 2024

Call for abstracts Submission
February 2024

Deadline for submitting abstracts
March 15, 2024

Deadline for Early Bird Registration
May 10, 2024

Fun begins

July 7, 2024

Preliminary Program

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 "Introdution 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				
ROOM	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				
ROOM	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				
ROOM	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				
ROOM	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				

PROGRAM OVERVIEW

Accepted Symposia

Topic 1:

Phylogenetics and Comparative Genomics.

- ⊕ 1. Structural phylogenetics: investigating deep evolut…
- ⊕ 2. Novel approaches to study plant domestication: di…
- ⊕ 3. Progress and challenges for understanding the mol…
- ⊕ 4. Everything that is old becomes new: comparative g…

Topic 2:

Evolutionary Genomics.

- 5. Human evolution in the genomic era.
- 6. Molecular evolution through metagenomics.
- 7. Epigenetic inheritance: from molecular mechanism…
- 8. Clustering of human cohorts beyond race and ance…

Topic 3:

Population Genetics and Demography.

- 9. Human population demography and adaptation sig…
- 10. Genomes and Generations: Mapping Health and H…
- 11. Spatial population genetics: where are we now?
- 12. Exploring the Evolutionary Effects of Admixture.

Topic 4:

Paleogenomics and Ancient DNA.

⊕ 13. Animal paleogenomics beyond higher latitudes.

⊕ 14. Unveiling the evolutionary history of pathogens thr...

⊕ 15. Paleogenomics and human evolutionary history: n...

Topic 5:

Evolutionary Medicine and Microbial Evolution.

⊕ 16. Evolutionary medical genomics.

⊕ 17. Aging from a multidisciplinary overview: evolution, ...

⊕ 18. One Health and microbial evolution: New ideas an...

⊕ 19. Evolution of microbial communities: is the sum of p...

Topic 6:

Conservation Genomics and Biodiversity.

⊕ 20. Pushing the frontiers of conservation genomics.

⊕ 21. Decoding the past to safeguard the future.

⊕ 22. Impact of environmental changes on agrobiodiver…

Topic 7:

Functional Genomics and Regulatory Evolution.

⊕ 23. Exploring the Frontiers of Single-Cell Biology in Di…

⊕ 24. Unlocking the hidden dimensions of genomic dive…

⊕ 25. Mitochondria: from powerhouse to processor and…

Topic 8:

Genomic Structural Variation.

⊕ 26. Deciphering the functional and adaptive effects o…

⊕ 27. Transposable elements in the population genomic…

⊖ 28. Human genetic variability in the Pangenomic era.

28. Human genetic variability in the Pangenomic era.

Organizers: Davide Bolognini, Giulio Formenti, Andrea Guarracino, Alessandro Raveane.
Invited speakers: Arang Rhie, Erik Garrison.

Description or the symposium:
Pangenome graphs serve as a powerful tool for modelling genomic variation across multiple samples without the bias associated with a single genome reference. While their extensive application was initially observed in the field of microbiology, recent advancements in sequencing and computational methods have facilitated their expansion to include plant and animal species. Large efforts have led to the release of human population-scale pangenomic data representing the genetic variability across every continent, and new algorithms and data structures have become available to deal with such complexity. These pangenomic resources empower the exploration of human genomic variability at unprecedented levels. They offer numerous possibilities, including I) a more comprehensive understanding of the evolution of highly repetitive regions linked to specific traits; II) the unveiling of molecular mechanisms that were only previously hypotheses in the field of cytogenetics; and III) a deeper understanding of recent and ancient human evolutionary history. In the upcoming symposium, we will assemble a collection of applications and methodologies that leverage population-scale pangenomic data to examine structure from local to global genomic perspectives for both human datasets and non-model species relevant to biodiversity genomics.

Topic 9:

Methods and Computational Approaches.

⊕ 29. Advances in Machine Learning for Evolutionary Ge…

⊕ 30. New computational approaches to estimate past …

⊕ 31. Haplotype-based methods and frameworks for inf…

⊕ 32. Not just Ne Ne-more: New applications for SMC fr…

Topic 10:

Research Ethics, Equity, Outreach and Open Symposium

⊕ 33. Science in the Spotlight: Empowering Education a…

⊕ 34. Going local: Using engaged research practices to …

⊕ 35. Genetics, Molecular Biology, and the Future of For…

⊕ 36. Greener and Sustainable Computing in Molecular …

⊕ 37. IDEA symposium

⊕ 38. Open Symposium

⊕ 39. Editors symposium

Dr. Maria Avila-Arcos

Associate Professor, International Laboratory for Human Genome Research (LIIGH), National Autonomous University of Mexico (UNAM)

Prof. Valeria Souza

Professor, Institute of Ecology, National Autonomous University of Mexico (UNAM)

Dr. Andres Moreno-Estrada

Professor, National Laboratory of Genomics for Biodiversity (LANGEBIO), CINVESTAV

Dr. Federico Sanchez-Quinto

Associate Professor, International Laboratory for Human Genome Research

Dr. Selene Fernandez-Valverde

Senior Lecturer, RNA Institute / School of Biotechnology &

Dr. Karla Sandoval

Equity and Gender Office of the Centre for Research and Advanced Studies

(LIIGH), National Autonomous University of Mexico (UNAM)

Biomolecular Sciences, UNSW Sydney

(CODIGO-C), CINVESTAV

Dr. Diego Cortez

Associate Professor, Center for Genomics Sciences (CCG), National Autonomous University of Mexico (UNAM)

Dr. Mashaal Sohail

Associate Professor,Center for Genomic Sciences (CCG), National Autonomous University of Mexico (UNAM)

Dr. Diego Ortega Del Vecchyo

Assistant Professor, International Laboratory for Human Genome Research (LIIGH), National Autonomous University of Mexico (UNAM)

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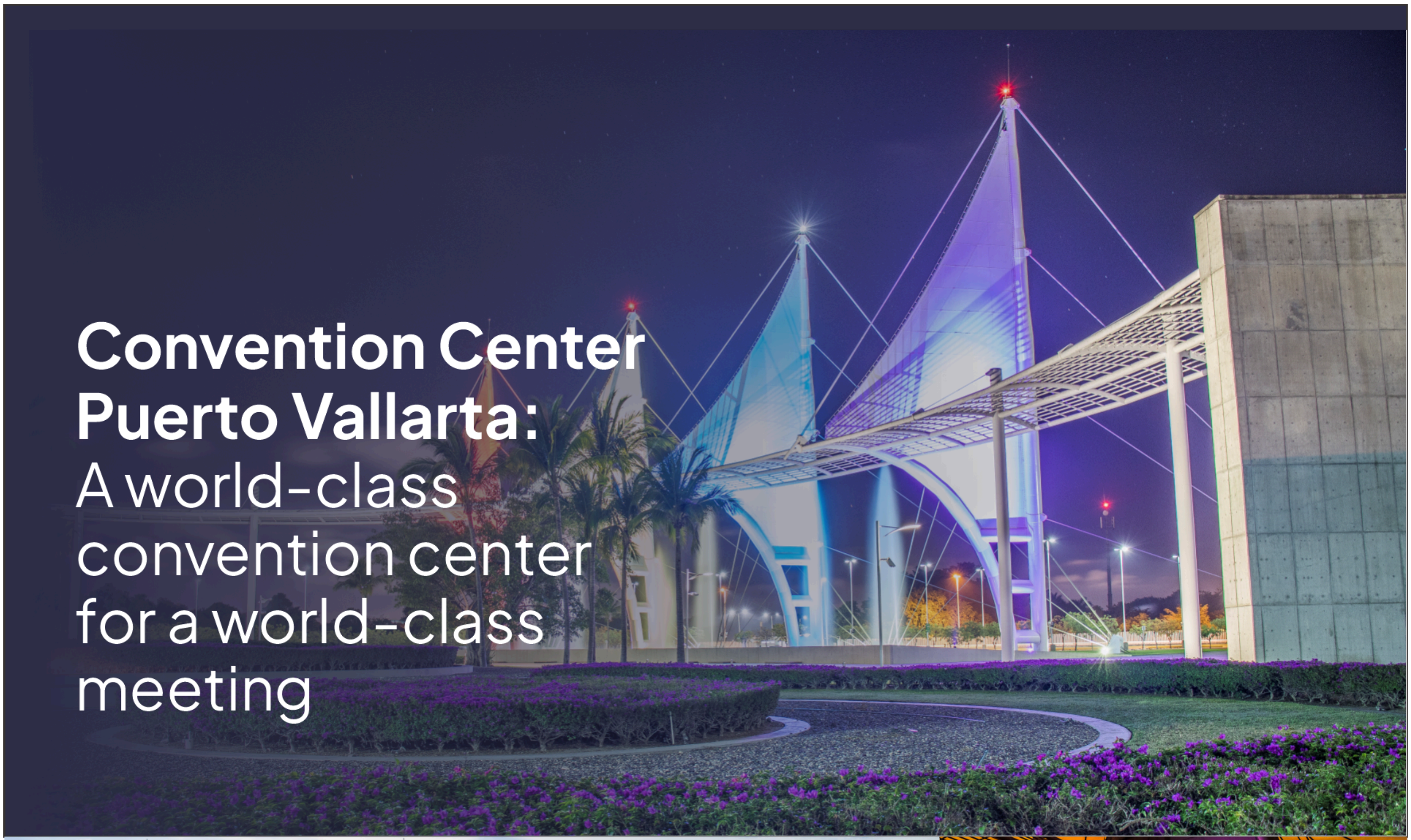

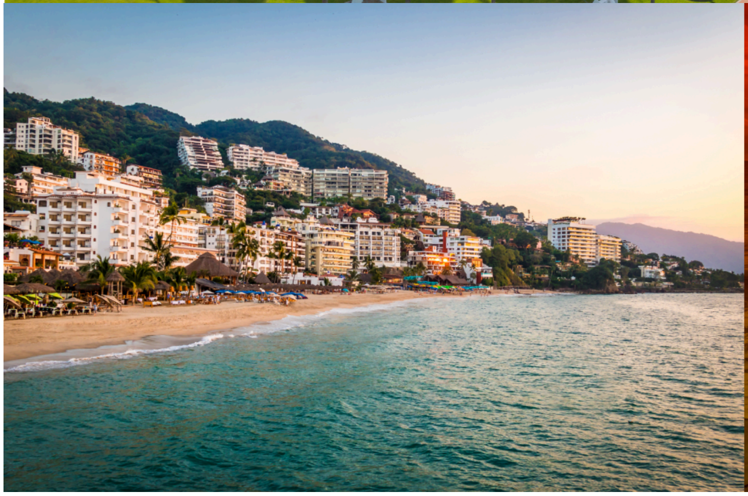

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