FINAL PROGRAM

4th MEXICO POPULATION GENOMICS MEETING
January 11th, 2019-01-07
Mexico City
PROGRAM OF THE
4TH MEXICO POPULATION GENOMICS MEETING
JANUARY 11, 2019

School of Sciences, UNAM
Ciudad Universitaria
Mexico City

Organizing committee

Alicia Mastretta (CONACYT-CONABIO)
Andrés Moreno (LANGEBIO-IPN)
Azalea Guerra (UNAM)
Idalia Rojas (UNAM)
Karla Sandoval (LANGEBIO-IPN)
María C. Ávila (LIIGH-UNAM)
Víctor Acuña (ENAH-INAH)
Miriam Bravo (LIIGH-UNAM)
Acknowledgments

#mexpogen4 was possible thanks to the kind support of our sponsors:
Useful Information

Venue

Conjunto Amoxcalli,
Facultad de Ciencias (UNAM),
Ciudad Universitaria,
Circuito Exterior s/n,
Coyoacán, C.P 04510, Mexico City.

Oral presentations

The oral presentations will be held at the Auditorium “Carlos Graef Fernández”, in the Conjuto Amoxcalli.

Poster session

All posters will be installed in the coffee break area (lobby of Conjunto Amoxcalli) on designated panels between 9.00-9.30 hrs. Presentations will take place after lunch break (14:45 - 16:00hrs). During poster presentation we will have a "postres&posters" exchange. Each poster presenter will offer a dessert (provided by the organizers) to those who stop by their poster.

Registration Desk

The MEXPOPGEN Registration area will be open in the lobby of Conjunto Amoxcalli from 9.00 to 9.30 hrs.

Coffee Breaks and Lunch

Coffee and lunch will be provided only for registered attendees in the lobby of Conjunto Amoxcalli during the designated times. It is highly encouraged that participants bring their own cup, this is to avoid waste and have an ecofriendly #mexpopgen.
Ciudad Universitaria’s Map

* School of Sciences
School of Sciences, UNAM

*Amoxcalli
The closest **metro** station to the venue is Universidad, pumabus (UNAM free buses) line 4 takes you to the School of Science, or a 13 min walk.

The closest **metrobus** station is Ciudad Universitaria, pumabus line 2 takes you to the School of Sciences, or a 17 min walk.
Pre-congress Workshop

Hierarchical co-demographic inference with Multi-DICE R package

This workshop requires pre-registration. Due to space constraints only #mexpopgen4 participants or members of Posgrado en Ciencias Biológicas who pre-registered will be allowed in this workshop.

Instructor: Alexander T. Xue. Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, USA.

This workshop will focus on implementation of the R package Multi-DICE for model-based comparative phylogeographic inference given next generation sequencing data. Multi-DICE is deployed for construction of co-demographic models with many taxa, which may be unrelated, and generation of data under such models using the coalescent simulator fastsimcoal2. Data are in the form of the aggregate site frequency spectrum (aSFS), an efficient and informative summary of genome-scale data aggregated across independent taxa. The aSFS allows statistical inference of hyperparameters that describe degree of congruence in evolutionary histories among multiple taxa, such as synchronicity in co-expansion times. After simulation with Multi-DICE, probabilistic inference on empirical data can be conducted with a variety of other software packages and approaches, such as the abc or randomForest packages in R. Both foundational concepts underlying this methodology as well as practical hands-on application to perform these tasks from start to finish will be covered during this workshop.

Session on day 1 would cover the theory and basic analyses, on day 2 we will extend the discussion and allow time for students to discuss their own datasets.

When: 9- 10 January 2019, 9:30-18 hrs (with lunch and coffee breaks)
Where: Sotero Prieto 2, Amoxcalli, School of Science, UNAM

Language: English

Cost: FREE. Lunch and coffee not included. Thanks to PAEP and Posgrado en Ciencias Biológicas for their support to make this course possible.
Short Program

9:00-9:30 Registration

9:30 – 11:30 Session I

9:30 – 9:35 – Opening remarks

9:35 – 10:20 - Keynote talk 1 by Diego Cortez Quezada, Center for Genomics Sciences, UNAM.

10:20 – 11:00 - Short talks

11:00 – 11:30 - Lightning talks

11:30 – 12:00. Coffee break

12:00 – 13:45 Session II

12:00 – 12:45 -Keynote talk 2 by Araxi Urrutia Odabachian, University of Bath, UK.

12:45 – 13:25 - Short talks

13:25 – 13:45 - Lightning talks

13:45 – 14:45 Lunch

14:45 – 16:00 Posters & Postres

16:00 – 17:55 Session III

16:00 – 16:45 - Keynote 3 by Alexander T. Xue. Cold Spring Harbor Laboratory, USA.

16:45 – 17:55 - Lightning talks
Detailed Program

9:00-9:30 Registration

9:30 – 11:30 Session I

Auditorium “Carlos Graef Fernández”, Amoxcalli

9:30 – 9:35 – Opening remarks Alicia Mastretta, CONACYT-CONABIO, Mexico.

Keynote Talk 1
9:35 – 10:20 “Genomics of sexuality in vertebrates” Diego Cortez Quezada, Center for Genomics Sciences, UNAM.

Short Talks 1

10:20 – 10:40 “New Digs: Revisiting Paleoanthropology in the Genome Editing Era” Keolu Fox, University of California, San Diego, USA.

10:40 – 11:00 “Genetic structure of Mexican population”. Juan Carlos Guevara López, ENAH, INMEGEN, Mexico.

Lightning talks 1

11:00 – 11:10 “Dissimilar evolutionary processes drive morphological and genetic differentiation across a subtropical fir species complex”. Jorge Cruz Nicolas, Institute of Ecology, UNAM, Mexico.

11:10 – 11:20 “Can Mexico City’s peripheral forest adapt to tropospheric ozone pollution?: Transcriptome analysis of the sacred fir (Abies religiosa) in a natural setting”. Verónica Reyes Galindo Institute of Ecology, UNAM, Mexico.
11:20 – 11:30 “From microendemic to invasive species: evolutionary genomics, range changes, and fundamental niche of *Trachemys* turtles”. **Ella Vázquez-Domínguez.** Institute of Ecology, UNAM, Mexico.

11:30 – 12:00. Coffee break

12:00 – 13:45 Session II

Auditorium “Carlos Graef Fernández”, Amoxcalli

**Keynote Talk 2**
12:00 – 12:45 “Comparative genomics of longevity in mammals”
**Araxi Urrutia Odabachian,** University of Bath.

**Short Talks 2**

12:45 – 13:05 “Domestication of maize: the importance of wild relatives in assessing the center of origin”. **Alejandra Moreno-Letelier,** The Botanical Garden, Institute of Biology, UNAM, Mexico.


**Lightning talks 2**

13:25 – 13:35 “Reticulate evolution and relaxed selection shaped the temperate to subtropical transition in Mexican firs”. **Juan Pablo Jaramillo-Correa.** Institute of Ecology, UNAM, Mexico
13:35 – 13:45 “Surveying pathogens in the oral cavity of Pre-Hispanic and Colonial individuals from Central Mexico through paleogenomics”. Miriam Bravo López, LIIGH-UNAM, Mexico.

13:45 – 14:45 Lunch

14:45 – 16:00 Posters & Postres

Lobby of Conjunto Amoxcalli, School of Sciences

16:00 – 13:45 Session III

Auditorium “Carlos Graef Fernández”, Amoxcalli

Keynote Talk 3
16:00 – 16:45 “Comparative population genomic inference of demography and selection” Alexander T. Xue. Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, USA.

Lightning talks 3

16:45 – 16:55 “Genomic perspectives on the Afro-Caribbean diaspora in the Lesser Antilles”. Maria A. Nieves Colón, Arizona State University, USA, LANGEBIO-CINVESTAV, Mexico.

16:55 – 17:05 “Anolis lizards, an interesting model for tropical forest fragmentation studies”. Sandra Itzel Vera Paz, Institute of Biology, UNAM, Mexico.

17:05 – 17:15 “Natural variation and regulation of ribosomal RNA genes”. Fernando A. Rabanal, Max Planck Institute for Developmental Biology, Germany.
17:15 – 17:25 “Combining pairs of archaic and present-day samples to infer past demographic events”. Diego Ortega Del Vecchyo, LIIGH-UNAM, Mexico.


17:35 – 17:45 “Ancient Brazilian Genomics”. Diana Ivette Cruz Dávalos, University of Lausanne, Switzerland.

17:45 – 17:55 “Relatedness and differentiation in arbitrary population structures”. Alejandro Ochoa. Duke University, USA.
Keynote Speakers

**Diego Cortez Quezada**

Associate Professor, Systems Biology and Synthetic Biology Laboratory. Center of Genomics Sciences, UNAM.

Diego Cortez was born in Mexico D.F. and obtained his biology and master's degrees at the Faculty of Sciences of the UNAM. He received his PhD at the Pasteur Institute and the University of Paris XI in France working with Dr. Patrick Forterre and Dr. Simonetta Gribaldo on the origin of new genes and their connection with the virosphere. Diego also worked on the functional characterization of the Xer proteins in archaea (thermococcales), which happened to be involved in the resolution of the chromosomes. These findings had major implications in the evolution of the cell cycle. Diego pursued his post-doctoral research at the University of Lausanne, Switzerland, studying the functional evolution of the Y chromosomes in mammals. Diego currently works at the Center for Genomic Sciences of the UNAM studying the evolution, origin and sexual turnovers in different groups of amniotes.

**Araxi Urrutia Odabachian**

Dr Senior Lecturer, Department of Biology & Biochemistry. Centre for Networks and Collective Behaviour. Milner Centre for Evolution, University of Bath.

Araxi’s interested in the evolution of genes and genomes and how it impacts on the evolution of phenotypes. Her research projects relate to the study of gene transcription changes during evolution and disease states and the evolution of gene and genome’s sequence, structure and organization. How and what drives gene expression evolution and what are the consequences of particular gene activity levels? Gene activity regulation is a major factor for understanding normal processes of development and senescence, disease states, and how individuals learn and cope with environmental events. Changes in gene activity are also thought to account for a large proportion of the differences in phenotype observed between species.
Alexander T. Xue

Computational Postdoctoral Fellow; Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory.

Alexander’s research interests consist of developing and applying novel comparative population genomic methods. He is currently a postdoc in Adam C. Siepel’s lab, where he’s working on a project that involves building a likelihood model to detect the selective dynamics underlying a complex polygenic trait by using GWAS summary statistics. In his former postdoc with Andrew D. Kern, he developed a machine learning approach that deployed deep convolutional neural networks for detecting selective sweeps, notably partial/incomplete hard and soft sweeps. This method was applied to whole-genome data for eight Anopheles mosquito populations to infer genomic responses to insecticide use, which will be used to inform malaria management. For his PhD, he primarily developed hierarchical co-demographic modeling approaches given genomic-scale data across multiple independent taxa.
Poster presentations


2. “Characterization of the genetic diversity and structure of Cucurbita pepo ssp. pepo in Mexico”. Carmina Martínez González et al.


4. “The Oceanian Genome Variation Project”. Consuelo Dayzú Quinto Cortés et al.

5. “The ChileGenomico Project creates a public resource to test association between socioeconomic and epidemiologic variation among communes of Chile and ancestry”. Ricardo Verdugo et al.


7. “Effect of the polygenic mating system on the structure and genetic diversity of the iguana Ctenosaura similis on Cozumel Island, Quintana Roo, Mexico”. Óscar Romero-Báez et al.

8. “Mycobacterium tuberculosis complex genomes from the Postclassic Basin of Mexico (1300-1521 CE)”. Kelly Blevins et al.
9. “Partial human parvovirus genome obtained from an archeological site associated to an epidemic at the Colonial period of Mexico City”. **Axel Arturo Guzmán Solís** et al.

10. “Genetic and phenotypic characterization of three taxa of *Agave salmiana* (Asparagaceae) in the Puebla-Veracruz region, México”. **Rogelio Lara González** et al.

11. “The virome of ancient DNA samples from Brazil”. **Yami Ommar Arizmendi Cárdenas** et al.

12. “Alellic variants associated to metabolic syndrome and it’s components in Amerindian population”. **Miguel Angel Cid Soto** et al.

13. “Species delimitation and demographic history of *Juniperus deppana*”. **Rodrigo Martínez de León** et al.


15. “Population genomics of herbicide resistance in *Alopecurus myosuroides*”. **Sonja Kersten** et al.

16. “Genetics of *Agave lechuguilla* populations and their possible response to climate change”. **Giovanna Karina Baltazar Valdez** et al.

17. “Phylogeography of *Agave striata Zucc*”. **Jorge Luis Cabral Avila** et al.


20. “Identificación local de Pinus pinceana”. Laura Figueroa Corona et al.

21. “Establishment of evolutionary populations in the Olotillo maize race as an option to recover diversity and local adaptation”. Duhyadi Oliva García et al.

22. “Genomic differentiation of an ectomycorrhizal fungus (Laccaria trichodermophora) is limited by its host distribution in Mexican sky-islands”. Christian Armando Quintero Corrales et al.

ABSTRACTS

Oral presentations
Short Talks

Presenter’s name: Keolu Fox
Email: pkfox@ucsd.edu
Institution: UCSD
Title: New Digs: Revisiting Paleoanthropology in the Genome Editing Era
Authors and affiliations: Keolu Fox (UCSD), Maya Parish (UCSD), Alexis Komor (UCSD), Alysson Muotri (UCSD).

Abstract: Mining paleogenomic datasets allows us to understand hominin population history at a higher resolution, including the confirmation of previously theorized ancient hominin introgression (Slon et al. 2018). While these analyses/methods have been used to impute ancient hominin disease susceptibility, one particular challenge working with paleogenomic data is that there is scant phenotype information to accompany degraded genome sequences. Intermediary methods have proposed to utilize both in vitro and in vivo systems to evaluate ancient hominin variations’ contribution to the human genepool via “human-Neanderthal hybrid induced pluripotent stem cells (iPSC’s) resources” and “Neanderthal transgenic mice.” I will discuss methods to functionally evaluate the role of ancient hominin-specific variation (i.e. coding and regulatory variants not found in any modern human population) discovered in publicly available paleogenomic datasets. I will highlight emerging methods to systematically isolate and explore ancient hominin allele function via endogenous introduction of ancient hominid-specific alleles using a precision form of genome editing (i.e. base-editing). Once these ancient hominin-specific mutations are endogenously introduced in diverse cell types (e.g. mesenchymal and iPSC), and differentiated in controlled 3D culture environments, the paleoanthropology community can begin the previously unexplored study of ancient hominin genotype to phenotype relationships, including neurological development, metabolism, immune system variation, and the potential role of each of these in ancient hominin disease susceptibility and “extinction.”
Abstract: Contemporary Mexican genomic diversity could be understood as a result of its plural ecosystems and a complex cultural history that underlies indigenous groups settlement and subsequent admixture mainly with European and African populations. Understanding this diversity is useful for anthropologic and medical studies as different genetic structures implies important relations among contemporary Mexican indigenous and mestizo populations. In this study, we analyze the genetic structure of 1,264 Mexican mestizo from the CANDELA project dataset, in contrast with 3,594 individuals from 56 reference populations from the HAPMAP3 and Mexican population datasets. CANDELA individuals exhibit a genetic structure that has two main components: a Southern European and an indigenous component that characterize the central groups of Mexico. We also correlate this structure with phenotypic and anthropometric traits collected by the CANDELA project. We found a positive correlation between some ancestral indigenous population with the body-waist index. Our results depict the complex genomic diversity of both nowadays Mexican indigenous and mestizo populations and its association with metabolic and anthropometric traits.
Title: Domestication of maize: the importance of wild relatives in assessing the center of origin.

Abstract: The study of maize domestication has overlooked the genetic structure within maize’s wild relative teosinte. Prior to investigating the domestication history of maize (Zea mays spp. mays), one should first understand the population history of teosintes and how they relate to maize. To achieve this, we used 32,739 SNPs obtained from a broad sampling of teosinte populations and 43 maize landraces and a) inferred current and past gene flow among teosinte populations and maize, b) analysed the degree of introgression among Zea mays subspecies, and c) rethink the putative domestication location of maize based on the teosinte analysis. We found geographic structure and introgression between Zea mays taxa. Teosinte subspecies have diverged significantly from maize, which indicates that current teosinte populations have evolved independently from maize since the domestication. Our results further suggest that the likely ancestor of maize may have been domesticated, not in the Balsas as previously thought but in Jalisco or the Pacific coast.
Abstract: Legumes are of great economic importance in agriculture as they are a major source of protein for humans, and their ability to fixate nitrogen through endosymbiosis is unique. Nevertheless, they have not been studied as extensively as other crops. The barrel medic (Medicago truncatula) is an invaluable model for studying local adaptation in legumes. Previous research on M. truncatula has identified loci potentially responsible for adaptation to climatic variables. However, other environmental variables can pose selective pressures on adaptive genomic variation. In the present study, we used a landscape genomics approach to identify candidate loci for adaptation to 10 environmental variables (including climatic, soil and atmospheric) among > 40,000 SNPs from 202 accessions of the model legume Medicago truncatula. Most candidate loci were associated with soil variables, highlighting the importance of soil environment as driver of local adaptation. Candidate SNPs associated with drought and soil salinity tagged genes with known functions in response to abiotic and biotic stress, while candidates associated with atmospheric and soil nitrogen tagged genes involved in stages of the legume-rhizobia symbiosis. Candidate SNPs identified explained up to 56% of variance in growth and flowering time, supporting the adaptive relevance of these traits in M. truncatula. Our findings highlight the importance of variables other than climate in promoting local adaptation in the system, and suggest that global climate change and anthropogenic alteration of the nitrogen cycle could disrupt local adaptation.
Lightning talks

Presenter’s name: Jorge Cruz Nicolas
Email: jorgecruzn@gmail.com
Institution: Universidad Nacional Autonoma de Mexico

Title: Dissimilar evolutionary processes drive morphological and genetic differentiation across a subtropical fir species complex

Authors and affiliations: Jorge Cruz-Nicolás 1, Gustavo Giles-Pérez1, Eréndira González-Linares1, Julia Múgica-Gallart1, Andrés Lira-Noriega2, David Gernandt3, Luis Eguiarte1, Juan P. Jaramillo-Correa1

1 Department of Evolutionary Ecology, Institute of Ecology, Universidad Nacional Autónoma de México, AP 70-275, Mexico City, CDMX 04510, Mexico. 2 CONACYT Research Fellow, Instituto de Ecología A.C., Red de Estudios Moléculares Avanzados, Xalapa, Mexico. 3 Department of Botany, Institute of Biology, Universidad Nacional Autónoma de México, AP 70-275, Mexico City, CDMX 04510, Mexico

Abstract: Interacting stochastic and selective forces drive both the genetic and phenotypic divergence of populations and species. Depending on the predominant evolutionary factor, which according to theory is related to population size and the amount of genetic diversity, contrasting clines related to either geographical or environmental variation may arise. Herein, we asked whether the morphological and genetic differentiation across a fir species complex in central Mexico fits isolation by distance (IBD) or isolation by environment (IBE) frameworks. This complex includes two species with partial morphological differences, and contrasting range sizes and environmental requirements. After comparing the variation at neutral SSRs and diagnostic morphological traits with climate variables contributing to ecological differentiation, we found that the geographically restricted A. flinckii had less genetic diversity and was more morphologically homogeneous than the widely distributed A. religiosa. The morphological differentiation at three physiologically important traits (needle thickness, number of stomata rows and location of the resin ducts) was significantly correlated with geography in this taxon (indicative of IBD), while it was associated with climate variation in A. religiosa (suggesting IBE). Consistent with quantitative genetics theory, PST - G’ST comparisons
indicated contrasting contributions of putatively adaptive and stochastic factors to the morphological differentiation of species related to their population size and genetic diversity. The integration of such quantitative genetics/evolutionary aspects to reinforce species descriptions may help disentangling resilient taxonomic discordances in plants.
Title: Can Mexico City’s peripheral forest adapt to tropospheric ozone pollution?: Transcriptome analysis of the sacred fir (Abies religiosa) in a natural setting

Abstract: Air pollution produced in Mexico City has caused harmful effects in its population and even in the near forests. Tropospheric ozone is one of the most abundant pollutants. This gas increases its presence through photochemical reactions between the products resulting from the burning of fuels and weather conditions, (insolation, humidity, temperature and wind) that are intensified in Mexico City’s basin due to its topographic characteristics. As a consequence, since few decades ago high levels of tropospheric ozone are present in the city. Among others, this is known to have caused the decline of A. religiosa in peripheral forests. Years of reforestation efforts have had limited success. However, in recent years individuals with less leaf damage can be spotted at the same exposure site were damaged trees are, suggesting that there is genetic variability within sacred fir populations, which allows some individuals to tolerate ozone pollution. Such diversity could be targeted by reforestation programs to improve forest recovery. Here, we compared healthy and ozone-damaged individuals from a natural population exposed to ozone, at the histologic, metabolic, genomic and transcriptomic level. For this, leaf tissue was collected from the same...
individuals in days of high (170 ppb) and low (87 ppb) tropospheric ozone concentration. The histological sections evidenced damage at the structural level and showed organelles associated with metabolic compounds such as tannins. Gas chromatography–mass spectrometry (GC-MS) allowed the identification of compounds associated with ozone metabolism in other studies, such as α-pineno, α-caryophyllene and limonene. GBS data was used to identify the individual ancestry (local, introduced by reforestation). The transcriptome analysis was used to identify genetic and gene expression differences among damaged and healthy individuals, particularly in pathways like hormones, terpenoids, flavonoids and polyamines. In all cases, differences were found at the histological, metabolic and transcriptomic levels between the groups.
**Title:** From microendemic to invasive species: evolutionary genomics, range changes, and fundamental niche of Trachemys turtles

**Authors and affiliations:** Ella Vázquez-Domínguez y Sayra Espindola Barrientos. Departamento de Ecología de la Biodiversidad, Instituto de Ecología, UNAM

**Abstract:** Natural habitat perturbation and fragmentation, exotic species introduction, and hybridization have severe negative effects on wild animals and their genetics. We examined four turtles encompassing remarkable distributional and ecological ranges, from freshwater microendemic (Trachemys taylori), to temperate (T. scripta) and tropical (T. cataspila, T. venusta) coastal inhabitants, to one of the 100’s worst invasive species (T. scripta). We evaluated their evolutionary and contemporary genetic/genomic patterns along their native Gulf of Mexico distribution. We assessed T. scripta’s invasion potential using genetic data and species distribution approaches (SDA). We show that the four species are clearly divergent; only T. taylori shows some geographic structuring. Although individual ancestry coefficients indicate some degree of admixture for all species, effective migration is low, and gene flow and introgression is ancient, all in agreement with their separation as distinct lineages and genetic clusters. Interestingly, while T. scripta has established invasive populations worldwide, not so along the Gulf of Mexico, where genetic and geographic borders between species are clearly defined, as a result of the presence of its congeners: SDA results show a low niche overlap between T. scripta and the other Trachemys, whereas significantly overlapping with other turtle species worldwide. Moreover, our results based on physiological tolerance limits for T. scripta evidence that it occupies just a portion of its fundamental niche. Because of the ongoing movement into new environments via human introductions and the wide range of environmental conditions suitable and not yet occupied by this turtle species, the risk of invasion is significant.
Title: Reticulate evolution and relaxed selection shaped the temperate to subtropical transition in Mexican firs


Abstract: Tropical trees face the dichotomy of being long-lived taxa with predominant positions on the ecosystem (which prompts evolutionary stasis), but which inhabit heterogeneous environments (which favours disruptive selection and species divergence). Such a dichotomy is amplified in conifers that have migrated south from boreal regions. These taxa not only accumulate mutations more slowly than angiosperm trees, but have highly conserved genomes with low levels of recombination. We surveyed several aspects of this evolutionary puzzle on the genus Abies (firs), which expanded into Mexico from northern North America some 5Ma ago, and then underwent a relatively rapid diversification. According to a phylogeny constructed from variation on 15 candidate nuclear genes, firs colonized Mexico in at least two independent waves, which resulted in as many as four modern lineages. These lineages encompass northern Abies durangensis var durangensis, and A. durangensis var. coahuilensis-A. vejari, central A. religiosa-A. flinckii-A. jaliscana and southern A. hickelii- A. guatemalensis. However, phylogenetic relationships of these lineages do not fit a classic bifurcating model in which sister taxa diverge at similar rates from an outgroup; they are better depicted as a reticulated network in which incomplete lineage sorting and introgressive hybridization are commonplace. All lineages have accumulated relatively low amounts of nucleotide diversity since their separation, fitting the expectations of the nearly neutral theory of evolution. However, the central and southern clades accumulated more non-synonymous mutations than the other two clades, suggesting relaxed purifying selection. A more detailed study of
the central lineage revealed that this is not only related to population size, but to the relative distance to the optimal ecological conditions that these populations have had during the last ~20Ka. The existence of a long-lasting, continuum process of adaptation, genetic drift and introgression should be thus considered for managing and protecting this economically important group of trees.
Title: Surveying pathogens in the oral cavity of Pre-Hispanic and Colonial individuals from Central Mexico through paleogenomics

Authors and affiliations: Miriam J. Bravo López 1, Viridiana Villa Islas 1, Axel Solís Guzmán 1, Elizabeth Mejía Campos 2, Alberto Herrera Muñoz 2, Jorge Gómez Valdés 3 and María c. Ávila Arcos 1. 1 Population & Evolutionary Genomics Lab, International Laboratory for Human Genome Research, 2 Centre INAH Querétaro, Centre INAH Querétaro (National Institute of Anthropology and History), 3 Postgraduate Studies Division, National School of Anthropology and History, UNAM.

Abstract: Genome-wide studies of ancient pathogens have proven instrumental in both identifying and characterizing past human infectious diseases. To gain insights into past human infectious diseases in indigenous populations in Mexico, we analyzed seven Pre-Hispanic and twenty-nine Colonial teeth from ancient individuals from Central Mexico. We generated low-depth shot-gun sequencing data from these two sample sets and used KRAKEN to compare the reads to a database with complete bacterial, archaeal, and viral genomes in RefSeq. Based on the taxonomic assignments specific to known pathogenic species, we identified one individual from the pre-contact period with a high fraction of reads assigned to Tannerella forsythia. This Gram-negative anaerobic bacteria belongs to the so-called “red-complex” bacteria involved in periodontal disease, and has also been associated with the progression of cardiovascular disease. Furthermore, four individuals from Colonial period also yielded reads matching to T. forsythia in important amounts. Mapping these data to the T. forsythia KS16 genome revealed the characteristic DNA damage patterns expected in ancient DNA, thus supporting its ancient nature. Undoubtedly, the drastic changes that took place as a result of colonization influenced the type of diet and lifestyle of the native population, and, consequently of their oral health. Further phylogenetic and comparative genomics analyses of T. forsythia spanning this transition will help to understand the evolution of their pathogenicity, and open up
questions regarding past lifestyle, diet and genetic makeup of pathogens and hosts for both time periods.
**Title:** Genomic perspectives on the Afro-Caribbean diaspora in the Lesser Antilles

**Authors and affiliations:** Maria A. Nieves Colón 1,2, Jada Benn Torres 3, Andrés Moreno Estrada 2 and Anne C. Stone 1. 1 School of Human Evolution and Social Change, Arizona State University, Tempe, AZ. 2.Laboratorio de Genómica para la Biodiversidad (LANGEBIO), Unidad de Genómica Avanzada CINVESTAV, Irapuato, Guanajuato, MX. 3.Department of Anthropology, Vanderbilt University, Nashville, TN

**Abstract:** Over 7 million African peoples were forcibly transported to the Caribbean during the Atlantic Slave Trade. However, research into the biohistories of contemporary Afro-Caribbean communities is still lacking. Here we use genomics as part of an integrative toolkit, which also draws upon historical and anthropological sources, to investigate the African diasporic experience in the Lesser Antilles. We examine high-density nuclear SNP genotypes from 73 individuals sampled in self-identified Afro-Caribbean communities from St. Kitts, St. Lucia, St. Vincent, Grenada, and Trinidad. Our findings indicate that all communities have large components of African ancestry and low proportions of Native American ancestry; a significantly different ancestry pattern from that of Caribbean Latinos and other islanders. We also found variation in global admixture patterns between communities. Trinidadian Afro-Caribbeans for instance, carry large components of East and South Asian ancestry. To examine subcontinental ancestry patterns further, we used ancestry-specific PCA (ASPCA), to compare masked genomes from the admixed Afro-Caribbeans with continental reference panels from Africa and South Asia. We found that the African ancestry component is most similar to that of present-day peoples living in Lower Guinea, a region that includes Ivory Coast, Togo, Benin and Ghana. This is consistent with historical records that indicate that Lower Guinea was a major exporter of enslaved peoples to the British Caribbean colonies in the 17th century. Using the same technique, we found that the South Asian ancestry component is most similar to populations living in present-day South India. This finding likely reflects admixture with Indian migrants who arrived in the Antilles during the 19th
century Asian Indentureship period. Overall, these findings underscore the large impact of colonial and post-colonial migrations, on Afro-Caribbean ancestry, and increases understanding of how the African diaspora has shaped the genomic and cultural variation of Caribbean peoples.
Title: Anolis lizards, an interesting model for tropical forest fragmentation studies.

Authors and affiliations: Biol. Sandra Itzel Vera Paz, Instituto de Biología, UNAM; Dra. Denise Arroyo Lambaer, Instituto de Biología; Dr. Víctor Hugo Reynoso, Instituto de Biología, Colección Nacional de Anfibios y Reptiles (CNAR)-UNAM.

Abstract: Habitat modification and disturbance severely affect the loss of genetic variation promoting among other aspects high levels of population genetic structure. The tropical forest of Los Tuxtlas, in Veracruz, México is a highly fragmented landscape with countless of native forest remnants of different size within a disturbed matrix. In this area the species Anolis uniformis is an excellent model to develop population genetics studies due to its high abundance, affinity to mature forest, short life cycles and low vagility. In this work, we use sequences data from two mitochondrial genes (ND4 and Cytochrome b) to evaluate composition and population genetic structure of populations inhabiting forest fragments of different size in Los Tuxtlas; then results were compared with a continuous population of the Lacandon rainforest. The results show that the habitat fragmentation in Los Tuxtlas does not have a negative influence in terms of genetic diversity loss, especially when comparing with the Lacandon population. Nonetheless, different forces are exerted on the populations. There is no direct relationship between the size of the forest fragments and genetic diversity in Los Tuxtlas (π mean = 0.000262; dh mean = 0.931). With regard to the population genetic structure, it is not observed a well-defined population structure (Fst mean = 0.04223333). The Analysis of Molecular Variance (AMOVA) shows that 91% of the variation is within the fragment populations and only 9% among them. This study suggests that the abundance of A. uniformis and its population dynamics, along with other features, have a great influence on genetic diversity maintenance.
Presenter’s name: Fernando A. Rabanal  
Email: fernando.rabanal@tuebingen.mpg.de  
Institution: Max Planck Institute for Developmental Biology  
Title: Natural variation and regulation of ribosomal RNA genes

Authors and affiliations: Fernando A. Rabanal (1), Magnus Nordborg (2), Detlef Weigel (1). (1) Max Planck Institute for Developmental Biology, Tübingen, Germany. (2) Gregor Mendel Institute, Vienna, Austria

Abstract: The central importance of ribosomal RNA (rRNA) genes for our understanding of biology cannot be overstated: they may well be evolutionarily the oldest genes; they are the most highly expressed genes in any organism; and their expression is central to cellular growth. rRNA genes in eukaryotic genomes are present in clusters of hundreds to thousands of nearly identical copies, only a subset of which are active at any given time while the rest is silenced by chromatin modifications. In the model plant Arabidopsis thaliana, 45S rRNA genes are found in two megabase-size ribosomal DNA (rDNA) clusters, and little is known about the contribution of each to the overall transcription pattern in the species. By taking advantage of genome sequencing data from the 1001 Genomes Consortium, we characterized rRNA gene sequence variation both within and among natural strains, including within the highly conserved ribosomal subunits. Through linkage mapping, we unambiguously assigned these variants to a particular rDNA cluster, and use them as reporters of rDNA cluster-specific expression. We demonstrated that rDNA cluster-usage varies greatly among strains, and that rDNA cluster-specific expression and silencing is controlled via genetic interactions between entire rDNA haplotypes. In light of these findings, we would like to investigate how variation in rDNA cluster-usage and its consequent reshaping of 3D genome architecture impact not only the expression of adjacent protein-coding genes, but also how genome-wide gene regulatory networks can adapt to such large-scale differences in gene expression.
Title: Combining pairs of archaic and present-day samples to infer past demographic events

Authors and affiliations: Diego Ortega Del Vecchyo Laboratorio Internacional de Investigación sobre el Genoma Humano - Universidad Nacional Autónoma de México

Montgomery Slatkin. Department of Integrative Biology - University of California, Berkeley

Abstract: The increasing abundance of DNA sequences obtained from fossils calls for new population genetics theory and methods that take account of both the temporal and spatial separation of samples. Here we will present results from two projects we are developing to study past demographic events combining pairs of archaic and present-day samples. First, we will show new analytic theory describing how FST depends on both the distance and time separating pairs of sampled genomes. We show that if there is a time series of samples, partial population replacement creates a discontinuity in pairwise FST values. The magnitude of the discontinuity depends on the extent of the replacement. In stepping-stone models, pairwise FST values between archaic and present-day samples reflect both the spatial and temporal separation. We illustrate our results with applications to archaic samples from European human populations. Secondly, we will show results from a composite-likelihood method we are developing to infer population sizes, divergence times and gene flow between pairs of populations in an isolation-with-migration (IM) model. Our method uses two samples, one from the present and one from an ancient individual. We take into account the possibility of low genomic coverage, the presence of contamination and sequencing errors on the ancient sample, along with the age difference between different fossils and present-day samples. We show that our method can be used to obtain accurate estimates of demographic parameters even when the genomic coverage is as low as 0.1X, and when the contamination rates are as high as 10%. We explore how the misspecification of the demographic model
affects the results, particularly when the real demographic model is a stepping-stone model or when there was a range expansion.
Title: Population structure, genomic diversity and phylogeographic patterns in the Virginia opossum (*Didelphis virginiana*)


Abstract: The Virginia opossum (*Didelphis virginiana*) is a marsupial species of tropical origin widely distributed in Central and North America. The fossil record shows the species was present in the southern part of the United States (US) 600 Ka, but only recently (~15 Ka) expanded its range to more temperate regions in North America. To determine the genetic structure of *D. virginiana* throughout its range and test if its northwards range expansion is reflected in the genome, we performed a population genomics study in this species. We used 127 samples collected along the geographic range of the species. Implementing a genotyping-by-sequencing (GBS) approach and using a draft genome as reference we identified ~20,500 SNPs. We did cluster and principal component analyses to identify the number of genetic groups in our sample. Also, we determined the phylogenetic relationships among groups and their genetic diversity to find patterns suggestive of the demographic scenarios that have shaped the genomic diversity in the opossum. We identified four main genetic groups, with three corresponding to previously described subspecies. Within each group we found further substructure. Northern populations are highly differentiated and have less genetic diversity (He=...
0.042) compared to southern populations (He= 0.11). Opossums from Cozumel show reduced genetic diversity (He= 0.05) and are distinct from other Yucatan Peninsula’s populations. Phylogeographic patterns do not coincide with a gradual northward expansion. The strong genetic structure observed might be explained by the low dispersion capability of the species and the presence of geographic barriers. The genetic diversity and phylogeographic patterns are not concordant with a northward expansion but with a glacial refugia in northern populations. Finally, the diversity and phylogeographic pattern of the Cozumel opossums suggests a prolonged isolation of this population. Our results have important evolutionary and conservation implications for opossum populations.
Despite decades of study into the peopling of the Americas, several key aspects remain contentious, such as the number of human waves that took place to people the continent. Most of the Native American genomic data available point towards a single ancestral population that entered the continent at most 15 kya. However, recent findings suggest that some Amazonian groups derive part of their ancestry from a second ancient population related to Australo-Melanesians. As ancient and modern genomic data have been scarce until recently in the Americas, it remains unclear whether other unsampled Native Americans are likewise related to Australo-Melanesians. Furthermore, the affinity to those old-world populations is absent in the ancient Native Americans sequenced to date, except for the oldest remains found in Brazil dated back to 11 kya.

To better understand the genomic background of the founding populations in the Americas, we tested for the contribution of distant worldwide populations into the indigenous populations of Brazil. We report preliminary genomic data from 22 ancient hunter-gatherers ("Botocudos") from Central-Eastern Brazil. To outline the origins and legacy of these populations, we assessed the relationships between the different populations included in our study and previously published Amerindian genomes. The results allow us to characterize some of the Anthropological collection from the National Museum of Rio de Janeiro,
recovered prior to the tragic fire that consumed the museum on September 2018.
**Presenter’s name:** Alejandro Ochoa  
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**Institution:** Duke University

**Title:** Relatedness and differentiation in arbitrary population structures

**Authors and affiliations:** Alejandro Ochoa[1,2] and John D Storey[3,4][1]
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**Abstract:** Several important biomedical applications, including genome-wide association studies and heritability estimation for complex traits, require accurate modeling of the covariance structure of genetic variants. This dependence structure between individuals is parametrized by kinship coefficients, which are defined as the probability that random alleles are "identical by descent" (IBD). The fixation index "F_ST" is also an IBD probability that measures the overall population structure. My work is focused on extending current models and estimation approaches for kinship and F_ST to arbitrary population structures, where individuals are not assumed to belong to subpopulations that are disjoint, homogeneous, and statistically independent. African-Americans and Hispanics are two examples of complex population structures without independent subpopulations that require my novel approaches. I will first show how my approach improves upon previous approaches in real human datasets containing world-wide samples and in simulations where the true parameters are known. I then present my theoretical findings that several widely-used previous approaches yield biased kinship matrices and F_ST estimates, which return abundant negative values and other systematic distortions. My work led to a novel kinship and F_ST estimation framework with greatly improved accuracy, implemented in the R package 'popkin' available on CRAN. These results have direct implications in the estimation of heritability, association studies, and other analyses where population structure is a confounder.
Poster presentations

1. **Presenter’s name:** Gabriela Díaz Juárez  
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   **Institution:** Instituto de Biología, UNAM

**Title:** Diversity and genetic structure of Ctenosaura oaxacana (Iguanidae) in hunted and fragmented populations in the Tehuantepec Isthmus, Oaxaca.

**Authors and affiliations:** M. en C. Gabriela Díaz-Juárez, Instituto de Biología. UNAM. Dr. Víctor H. Reynoso, Instituto de Biología. UNAM

**Abstract:** As many other microendemic species, during the last decades the Oaxacan Spiny-tailed iguana, Ctenosaura oaxacana, has suffered a drastic population drop, caused by habitat fragmentation and hunting. Our study was to determine whether fragmentation and hunting impact has affected the genetic diversity of the species. We evaluated nine populations of these iguanas under three scenarios: a) within a continuous preserved forest; b) within the fragmented forest; and, c) within sites with extreme hunting. Our results indicated that genetic diversity is low (Het=0.296) and different between scenarios (F =2.063, P=0.04), showing a high inbreeding coefficient (F=0.391). We believe that the loss of genetic diversity is an effect of gene flow reduction between populations (Nm=1.649). Genetic differentiation was within individuals (61%, Fis=0.269, P=0.001; Fst=0.157, P=0.001) that has generated some genetic structure. The individual homozygosity analysis of the three scenarios showed a moderate loss of heterozygous individuals (PHt=0.368). However, the fragmentation scenario in the population of StoDom obtained greater loss of genetic diversity (PHt = 0.304). Within the conserved forest, the Mata population obtained the highest value (PHt = 0.410). The number of homozygous loci per individual in the three scenarios was high (IR = 0.399), as was the individual homozygosity value per locus (HL=0.595). The highest homozygosity value was presented by the StoDom population (HL=0.664) and the lowest value by La Mata (HL=0.553). Our results show that hunting and habitat fragmentation exert an impact on the genetic structure and diversity of C. oaxacana. Now, it is possible to identify areas of high and low genetic diversity, which will lead to the development of accurate conservation and management programs for the species.
2. **Presenter’s name:** Carmina Martínez González  
   **Email:** carmimaglez@gmail.com  
   **Institution:** Instituto de Ecología

**Title:** Characterization of the genetic diversity and structure of Cucurbita pepo ssp. pepo in Mexico

**Authors and affiliations:** Carmina, Martínez-González; Castellanos-Morales, Gabriela; Moreno Letelier, Alejandra; Eguiarte Fruns, Luis E.; Lira Saade, Rafael.

**Abstract:** Genetic diversity is the source of variation that allows species to diversify and adapt to new selective pressures. In most cultivated species, man management has caused a decrease in genetic diversity, reflecting changes in the morphology and physiology of cultivated species, generating what is known as the domestication syndrome. Among the most important plant genetic resources in the world are pumpkins, squashes and gourds (Cucurbita spp.). In particular, C. pepo, which has a history of domestication and adaptation of at least 10,000 years, is considered the most economically important cultivated squash worldwide. In Mexico, C. pepo ssp. pepo has been cultivated extensively, both in the traditional cultivation system (milpa), and in more technified crops. As a result, farmers have developed high morphological diversity. Despite this, there are few studies that analyze the patterns of genetic diversity in C. pepo ssp. pepo in Mexico. The aim of this work is to determine the current status of genetic diversity and genetic structure between the different accessions of C. pepo ssp. pepo in Mexico. We analysed tGBS data from 14 localities (n = 92). Those individuals and sites with > 50% missing data were removed and the SNPs with two alleles were retained, resulting in a total of 3,817 informative SNPs. We found high genetic diversity when compared to that of other cultivated pumpkin species, such as C. argyrosperma spp. argyrosperma. Studied localities showed some degree of genetic structure. Criollo varieties, which are maintained in the milpa system, showed higher genetic diversity than improved varieties, so it is recommended to preserve the local varieties under traditional management.
3. **Presenter’s name:** Andres Jimenez Kaufmann  
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**Institution:** UGA-LANGEBIO, Cinvestav, Mexico

**Title:** Imputation performance in Latin American populations: Expanding the imputation reference panel with Native American Genomes.

**Authors and affiliations:** Andrés Jiménez Kaufmann(1), Adrián Cortés(2), Selene Fernandez-Valverde(1), Andrés Moreno-Estrada(1)  
1. UGA-LANGEBIO, Cinvestav, Mexico. 2. Wellcome Center for Human Genetics, University of Oxford, United Kingdom

**Abstract:** Current Genome-Wide Association studies (GWAS) rely on genotype imputation to increase power, improve fine-mapping of association signals and to facilitate meta-analyses. However, Native American (NAM) genomes are underrepresented in current imputation reference panels, hence, interpretation of studies performed in Latin American populations is limited. Here, we expand the 1000 Genomes reference (1KGP) with 34 Native American genomes (1KGP + NAM) to increase imputation performance in Latin American individuals. To evaluate our reference panel we performed imputation with IMPUTE2 utilizing the Latin American individuals from 1KGP as targets. First, we assigned an ancestry to each position by inferring local-ancestry. Then, we simulated a microarray experiment, performed imputation using both references and compared the imputation accuracy score (INFO) and genotype concordance for each diploid ancestry as a measure of performance. We show that by expanding the current reference with NAM genomes we improve imputation performance specifically in positions with low minor allele frequency and NAM ancestry. The fact that we obtain these results by adding a small number of NAM genomes shows the striking imbalance and underrepresentation in current references. We demonstrate the necessity of balancing the representation of diverse genomes to fully grasp the genetic variation of underrepresented populations.
4. **Presenter’s name:** Consuelo Dayzú Quinto Cortés  
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**Institution:** LANGEBIO

**Title:** The Oceanian Genome Variation Project

**Authors and affiliations:** Consuelo D. Quinto-Cortés, National Laboratory of Genomics for Biodiversity, Irapuato, Guanajuato, Mexico  
Alexander Ioannidis, Computational and Mathematical Engineering, Stanford University, Palo Alto, CA, USA; Julian R. Homburger, Department of Genetics, Stanford University, Stanford, CA, USA; Genevieve L. Wojcik, Department of Biomedical Data Science, Stanford University, Stanford, CA, USA; Javier Blanco Portillo, National Laboratory of Genomics for Biodiversity, Irapuato, Guanajuato, Mexico; Kathryn Auckland, University of Oxford, United Kingdom; Alissa Severson, Department of Genetics, Stanford University, Stanford, CA, USA; Carmina Barberena Jonas, Undergraduate Program on Genomic Sciences, UNAM, Cuernavaca, Morelos, Mexico; Jennifer Blanc, University of California, Davis, Davis, CA, USA; Gillian M. Belbin, Icahn School of Medicine at Mount Sinai, New York, NY, USA; Stephen Oppenheimer, University of Oxford, United Kingdom; Tom Parks, University of Oxford, United Kingdom; Maude Phipps, Monash University, Malaysia; Kathryn Robson, University of Oxford, United Kingdom; Eimear E. Kenny, Icahn School of Medicine at Mount Sinai, New York, NY, USA; Adrian V. S. Hill, University of Oxford, United Kingdom; Alexander J. Mentzer, University of Oxford, United Kingdom; Carlos Bustamante, Department of Biomedical Data Science, Stanford University, Stanford, CA, USA; Andrés Moreno-Estrada, National Laboratory of Genomics for Biodiversity, Irapuato, Guanajuato, Mexico; Christopher R. Gignoux, Colorado Center for Personalized Medicine and Department of Biostatistics and Informatics, University of Colorado, Aurora, Colorado, USA. On behalf of the Oceanian Genome Variation Consortium.

**Abstract:** Oceania comprises the region from Southeast Asia throughout the South Pacific and has a rich demographic history, with the first human settlements in Papua New Guinea dating to ~40,000 years ago. Multiple migration and admixture events have occurred throughout the region, like the Lapita expansion that reached Tonga and Samoa and the colonization of Remote Oceania. Despite the richness of different peoples and cultures, this area of the world remains almost entirely left out of the global genetic
mapping efforts. Here, we present the Oceanian Genome Variation Project (OGVP), the largest collection of historic genotyped DNA samples collected by the University of Oxford. The main aims of this project are to reconstruct the population genetic history of the major human migrations into the Pacific and to increase resolution on the characterization of understudied regions. We generated genome-wide SNP data for 980 individuals using the MEGA platform and identified genetic clusters of population differentiation with ADMIXTURE. They broadly correspond to Melanesia, Micronesia and Polynesia, recapitulating cultural and linguistic differences among the islands. In particular, there is decreasing continental East Asian ancestry throughout Malaysia and Indonesia, including some of the remote islands as we move east away from the mainland. The ADMIXTURE patterns seen in the westernmost islands (Tonga, Samoa, and Tuvalu) contrast with the remainder of the Polynesian islands as they have both of the components seen in Polynesia and Melanesia. In addition, Remote Polynesia shows patterns of pervasive European admixture, which contact can be dated to reconstruct the recent demographic dynamics of the region triggered by intercontinental travel. We used BEAGLE to find identity-by-descent (IBD) segments between individuals in Oceania and found that the amount of IBD shared between different populations increases in an eastward direction and that Polynesian populations share the highest amount of IBD. Lastly, we identified maternal and paternal lineages in this dataset. The most common mitochondrial haplogroups were B (namely B4a1), Q and M. Most of the Y chromosome lineages found in Oceania were O, C, K, M and R. The OGVP initiative represents an important effort to include a historically underrepresented area of the world in the publicly available genetic databases and to facilitate genetic research in the Pacific.
Title: The ChileGenomico Project creates a public resource to test association between socioeconomic and epidemiologic variation among communes of Chile and ancestry.

Authors and affiliations: Verdugo R.A.1,10, Araneda P.1, Di Genova A.2, Herrera L.1, Moraga M.1 Acuña M.1, Berrios S.1, Llop E.1, Valenzuela C.Y.1, Bustamante M.L.1,3, Digman D.1, Symon A.1, Asenjo S.1, Pezo-Valderrana P.1, López P.1, Blanco A.1, Suazo J.4, Caba F.5, Barozet E.6, Salgado K.7, Naranjo A.M.7, Portales P.8, Loira N.9, Maass A.2,9 and Cifuentes L.1
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Abstract: Introduction and objectives. The Chilean population is the result of a process of admixture between Europeans, Africans and Amerindians since the XXVI century. The genetic variation between them allows estimating the proportion of ancestors of each of these origins in current individuals. Estimates of ancestry show significant differences
between subpopulations of Chile, related to latitude and social stratum. However, a systematic study of the differences in the ancestry components of Chileans has not been carried out. Material and methods The ChileGenomico project carried out the largest sampling to date of mixed Chilean population (n = 3200), recruiting healthy individuals in nine urban centers from Arica to Puerto Montt. The genome of 48 individuals with Amerindian ancestry was typified by complete genomic sequencing (3.6x) or microarrays. Using a genetic algorithm to maximize genomic coverage and ancestry normativity, we selected 147 autosomal SNPs, then genotyped by KASP in 2,843 individuals. Results. The average ancestry was 51% European, 5% African and 44% Amerindian (20% Aymara and 25% Mapuche). The Amerindian ancestry is lower in the central zone, the Aymara decreases with latitude and the Mapuche increases. The Amerindian component rises 5-10% per level of decline in socioeconomic stratification. Average ancestry estimates for 39 communes of Chile were estimated and made available through an online that allows identifying association to socio-economic and epidemiological data (http://genoma.med.uchile.cl/ancestry). In addition, we have added average polygenic risk scores per commune for nine diseases that are prevalent in Chile. Conclusions. We have created a public resources that will be allow controlling for ancestry heterogeneity of the Chilean population in public health studies and scientific research.
6. **Presenter’s name:** Joseph Yracheta  
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**Institution:** Missouri Breaks Industries Research, Inc.

**Title:** Improving multi-omic approaches on Rheumatoid Arthritis with Indigenous Communities.

**Authors and affiliations:** J. Yracheta1, J. Li-Pook-Than2, M. Anderson3, M. Snyder2. 1) John Hopkins University, MD; 2) Stanford University, Genetics Department, CA; 3) Ohio State University, Dept of Microbiology, Dept of Microbial Immunity and Infection, OH.

**Abstract:** The frontiers of precision health science research reside in combining multi -omics high-throughput approaches (including exome, transcriptome, proteome and microbiome data) with clinical and epigenetic data. In relation to disease onset and progression, the integration of these -omes better captures the biological and cellular mechanisms underlying the phenotype, and subsequently allow for better diagnosis and targets for therapeutics. Studies of complex diseases as the auto-immune illness Rheumatoid Arthritis (RA) greatly benefit from this type of multi-omic analysis, capturing the interplay between genetic and environmental components. To date, multi-omic research has focused on individuals with European ancestry, while under serving groups with diverse ancestry such as the indigenous populations of America. Studies of Auto-immune Illnesses with the Lakota (SAIL) is a first-of-its-kind multi-omic approach focusing on RA. RA is highly prevalent in the Lakota community. Here, preliminary work on exome, transcriptome and auto-antibody-ome will be discussed and paired with select environmental data. Moreover, RA and variation in the human microbiome have been correlated. Our SAIL team will describe the optimization and effectiveness of capturing human microbial components, particular interesting in distinct environments as Indian Country. At the forefront of this work, will be the importance of fair bio-ethical co-education between indigenous and scientific partners; with improving practices to innovate in community engagement, upgrading policy on data stewardship/ownership, education programs on pros and cons of multi-omics precision health approaches and overall improving research disparity by inclusivity and tangible translation in tribal community setting.
Title: Effect of the polygenic mating system on the structure and genetic diversity of the iguana Ctenosaura similis on Cozumel Island, Quintana Roo, Mexico

Abstract: The study of mating systems in animals allows to describe aspects about features differentiation between sexes, the way in which individuals achieve copulation, and its effects at the genetic level, topics that together help to understand the evolution of species. In the present study we evaluated the effects of the polygynous mating system on the structure and genetic diversity of the iguana Ctenosaura similis on Cozumel Island. Based on 11 microsatellite loci, we show that the populations studied are structured as three different genetic groups, one in a more conserved area (Inter-Island) and two with anthropogenic influence (City and South), of which Inter-Island presented evidence of genetic bottleneck. The genetic structure showed low differentiation (FST=0.020-0.061) with a certain level of migration, where the urban area represents a barrier for individual movement. Results also exhibit moderate genetic diversity (HO=0.545-0.612; HE=0.552-0.587), with moderate effective population sizes (Ne=15.8-30.4) and low kinship relationship among individuals (79.92-83.55%). Our results suggest that C. similis behavior influences the genetic structure of its populations throughout the island, where adults maintain a certain fidelity to the microhabitat that meets its requirements of survival and reproduction. Also, that genetic diversity is maintained by the ability of individuals to recognize family conspecifics through chemical signaling; the mating system dynamism plays a key role by a change of dominant individuals at each reproductive season due to agonistic encounters. We also recognize that anthropogenic factors most likely have an effect on the genetic structure, in particular by reducing genetic diversity as a result of habitat fragmentation.
8. Presenter’s name: Kelly Blevins
   Email: blevinske1@gmail.com
   Institution: Arizona State University

Title: Mycobacterium tuberculosis complex genomes from the Postclassic Basin of Mexico (1300-1521 CE).

Authors and affiliations: Kelly E. Blevins1, Elizabeth A. Nelson2, Alexander Herbig2, Johannes Krause2, Jane E. Buikstra1, Josefina Mansilla Lory3, Kirsten I. Bos2, and Anne C. Stone1
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Abstract: There is substantial bioarchaeological evidence of tuberculosis infection in the New World prior to European contact. Evidence in the form of Pott’s disease, or a collapsing spine, is found dating from 700 CE in Peru and 900 CE in the American southwest. In 2014, three whole Mycobacterium tuberculosis complex (MTBC) genomes were recovered from pre-contact coastal Peru. These strains were most closely related to M. pinnipedii, the contemporary MTBC strain that infects seals and sea lions. This evidence was key in the formulation of a new hypothesis about pre-contact MTBC ecology, wherein sea mammals were suggested as having played a central role in its introduction to humans in the Americas. Discovery of this zoonotic event raised questions about the other cases of skeletal tuberculosis throughout the Americas and whether they resulted from a human-to-human adapted variety of the M. pinnipedii form, or a different source. Here, we present the molecular screening results of seventeen samples of bone and calculus from pre-contact Mexican sites: Monte Alban (n=1), Tlatelolco (n=8), and two salvage excavations along the Sistema de Transporte Colectivo (STC) metro routes near Tenochtitlan in Mexico City (n=8). DNA was extracted using silica-based methods and screened using quantitative PCR assays targeting a MTBC-specific region of the rpoB gene and two insertion sequences, IS6110 and IS1081. Samples that amplified for more than one assay (n=6) were prepared into double-indexed libraries and target enriched for the whole MTBC genome using in-solution capture. Our
preliminary capture data results are discussed, as well as the significance of ancient MTBC strains in the urban marketplace of Tlatelolco and urban center of Tenochtitlan. All samples were exported and processed with permission from the Instituto Nacional de Antropología e Historia (Oficio 401.B(4)19.2016/36/2099). This work was supported by funding from the National Science Foundation (BCS-1063939 and BCS-1515163) and the Max Planck Society.
Title: Partial human parvovirus genome obtained from an archeological site associated to an epidemic at the Colonial period of Mexico City.

Authors and affiliations: Axel A. Guzmán-Solís (1), Viridiana Villa-Islas (1), Miriam Bravo-Lopez (1), Marcela Sandoval-Velasco (2), Julie Wesp (3), Daniel Blanco-Melo (4), María C. Ávila-Arcos (1) .
1. International Laboratory for Human Genome Research, Universidad Nacional Autónoma de Mexico. 2. Center for GeoGenetics, Natural History Museum of Denmark. 3. Department of Anthropology, American University. 3. Icahn School of Medicine, Mount Sinai.

Abstract: The study of ancient organisms provides important clues about their evolutionary history and relationships with their host. With the development of next generation sequencing, it is now possible to obtain whole genomes from ancient pathogens as molecular fossils. In the case of viruses, whole genomes have been recovered for variola virus, hepatitis B, and parvovirus from archeological remains or museums specimens. The introduction of viral pathogens during European colonization of the Americas had a dramatic impact on the immunologically naïve Native population, causing epidemics that devastated the population. To understand better the role of pathogens introduced upon colonization, we studied archaeological remains from a Colonial hospital in Mexico City designated for the Native population, with historical and archaeological evidence of having experienced a mass epidemic. We extracted and sequenced DNA from teeth using ancient DNA facilities to screen for viruses through metagenomics. Furthermore, we designed an in-solution capture assay to retrieve DNA from viral pathogens of clinical importance, with this enrichment we obtained a partial genome (70%) from B19 Parvovirus, a pathogen with current exposures rates generally over 50% in adulthood, associated with erythema infectiosum in children, arthritis and arthralgias in adults, as well as fetal death in pregnant women. Despite having a single-stranded DNA genome, ancient DNA from B19 Parvovirus has been previously recovered from bones as old as 6.9 thousand years old. The DNA fragments recovered using our capture design were mapped to the B19 reference genome and the ancient origin of the viral DNA was corroborated by the presence of damage at the terminal bases. When assessing the similarity of the recovered genome to modern strains, we found it is more
related to an African genotype (genotype 3), in agreement with the inferred genetic ancestry of the human host from which the sample was retrieved.
Title: Genetic and phenotypic characterization of three taxa of Agave salmiana (Asparagaceae) in the Puebla-Veracruz region, México.

Authors and affiliations: Rogelio Lara-González1, Alejandra C. Moreno-Letelier2, Ángel I. Ortiz-Ceballos3, Lev O. Jardón-Barbolla4, Alejandra Vazquez-Lobo1.
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4.Centro de Investigaciones Interdisciplinarias en Ciencias y Humanidades, Universidad Nacional Autónoma de México.

Abstract: Agave salmiana Otto ex Salm-Dyck is one of the most plastic species of the Agave genus, and thus has a greater number of varieties, able to survive in anthropogenic environments as rangeland and plantations. Today is one of the most economically important species; because all components of the plant and the associated fauna (including its pests) are utilized and have immeasurable ecological value. However, reproduction and morphological diversity has been modified by the type of management, making field identification difficult. Therefore, the present study aims to characterize and compare the levels of phenotypic variation within and between three taxa of Agave salmiana (maguey pulquero) in the Puebla-Veracruz region, Mexico. Plant morphometric characters were recorded in an experimental plantation, along with the number of leaves and tillers produced per plant. Phenotypic variation through these morphometric variables was assessed using principal component analysis and discriminant analysis. Molecular markers type SNP's will be used by genotyping by sequencing (GBS) to know the genotype of the individuals. The results showed that over 75% of the total cumulative variance is explained by the first four major components. The height, diameter, coverage of the plant, the length of the apical meristem and leaf length comprising the first component and explain
51.17% of the variability for the three varieties of Agave salmiana, (P < 0.05). The discriminant functions show that except the length, width and number of leaves, most characters are grouped better in the first discriminant function and allow to distinguish the three separate groups, similarly to the reported by Alfaro-Rojas et al in 2007. It is concluded that in the region, the study allowed to recognize the presence of the three taxa as different. This suggests the usefulness of morphological characters in the selection of promising material for use as parents in breeding and conservation programs.
Abstract: The human body is home to a whole ecosystem including bacterial, viral and fungal species. Metagenomic studies have contributed to our understanding of the composition of such a complex habitat. By exploring ancient samples, changes in the microbiota composition across tissues and across time can be assessed. Furthermore, ancient DNA allows to track ancient pathogens and study their evolutionary history using direct snapshots into the past. Most of the metagenomic studies have focused on the most abundant organisms in the microbiome, namely the bacteria. In the present study, we zoom in the viral fraction by analysing the viruses found across ancient samples from Brazil. These come from distinct tissues, populations and are both pre and post-Columbian. We use the software DIAMOND (Buchfink et al. 2015) to study the viral composition at the species level. Among the viruses, we found the bacteriophages to be the most abundant ones, while the coliphages are the most prevalent phages. We observe that the virome profile differs across tissues, but we found no obvious correlation with the age of the samples, perhaps due to our sample size. Finally, we investigate in more details viruses of potential health relevance.
Title: Allelic variants associated to metabolic syndrome and its components in Amerindian population.

Authors and affiliations: Miguel Angel Cid Soto INMEGEN. Angelica Martínez Hernández INMEGEN. Lorena Orozco Orozco INMEGEN

Abstract: Metabolic syndrome is a multifactorial disorder defined by a cluster of metabolic factors, such as high levels of fasting glucose and triglycerides, elevated blood pressure, low levels of high-density lipoprotein cholesterol, and central obesity. MetS increase the risk for develop type 2 diabetes coronary heart disease, and cardiovascular diseases (1). The estimated prevalence of MetS in Mexican adults was 36.8% in 2006, making a public health problem. There are several evidences that Amerindian derived populations have a high susceptibility for develop metabolic diseases such as hypertriglyceridemia, type 2 diabetes and obesity (2). A total of 2051 Mexican Amerindian individuals were included in the present study to made a GWAS for metabolic syndrome and its components in 690,893 SNPs. The average of Amerindian ancestry was 95.5% ± 5. The aim of the present study was to made a GWAS to evaluate the association single-nucleotide polymorphisms (SNPn) and metabolic syndrome and its components in amerindian populations from Mexico. Analysis of the data showed an association of the KIF1B SNP rs17034615 with high glucose levels P=0.06; OR=4.74 (IC 0.9-25.01), P=3.307E-12; Beta=101 (IC 73.9-128.2) in amerindian population. In adition there was also associated with type 2 diabetes in amerindians populations Mixe, Otomí, Chinanteco, Mazateco, Popoluca y Totonaca in subjects older tan 40 years old P=4.60E-03; OR=9.13 (IC 1.97-42.25). This association was not found in mestizo population. Our findings suggest that the KIF1B gene play a role in the metabolic syndrome pathophysiology.

REFERENCES
Abstract: Speciation can be defined as the process in which one lineage diverges into at least two evolutionary independent lineages. Despite this definition consensus, species delimitation often lays purely on morphological differentiation, ignoring the historic view of the speciation process. Differentiation between taxa and late species recognition requires a set of criteria from different fields that also gives information about the history of the populations of such taxa and that leads us to a less partial view of the process of speciation. Juniperus deppeana, also known as the “alligator juniper”, is a well-distributed species across the Mexican Highlands, Guatemala and the south of the USA. There are 4 varieties described so far, each one with a specific distribution in a different Mexican mountain system. The aim of this work is to evaluate the hypothesis in which each one of these varieties actually represents a fully independent lineage. This hypothesis was tested using 3 different information criteria that had been helpful in taxonomy before and that can be measured at a population level, genetic variation, ecology, and morphology. Genetic variation was evaluated using two molecular markers from genomic DNA and one from chloroplast as well, the genetic structure was determined as well as demographic history. Climate niche was described using 19 bioclimatic variables plus soil type and soil’s pH. Niche divergence was tested using a background test in ENMTools and projections at Las Glacial Maximum (LGM) were also made. Finally, a morphometric analysis of leaf margin was carried out, to determine the differentiation at a morphologic level among populations and its utility in species delimitation.
14. Presenter’s name: Jazeps Medina Tretmanis  
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Title: Measuring the phasing accuracy of modern tools on ancient DNA

Authors and affiliations: Jazeps Medina Tretmanis – UNAM. María del Carmen Ávila Arcos – UNAM. Emilia Huerta-Sanchez - Brown University

Abstract: In the fields of paleogenomics and population genetics, ancient samples have been used to study the relationships between ancient and modern populations. It is useful to have phased ancient data as this gives researchers more information when testing for demographic events. However, it is not clear how accurate this phasing can be after we factor in the modern contamination, low coverage, and genetic distance from modern human reference panels found in ancient samples. This research will test different phasing methods that have been used for real ancient data, both with and without a reference panel. We will test several combinations of low coverage, contamination, sample age, and demographic events. Finally, the effects of all these sample parameters and phasing methods on phasing accuracy will be shown along with guidelines for the minimum sample quality required for acceptable phasing.
Abstract: Unintendedly, humans have been carrying out a series of – often alarming– evolutionary “experiments” that have led to the selection for resistance to herbicides in agricultural weeds over the past several decades. The repeated exposure of Alopecurus myosuroides (Alomy), a major weed in cereal crops of the temperate climate zone, to high selective pressures through herbicide applications gives us the opportunity to look into the underlying evolutionary processes of rapid adaptation. In particular, we aim at understanding whether adaptation to herbicides evolves from new mutations, standing genetic variation, or geographic spread of adaptive alleles through gene flow. Due to the large size of Alomy's genome (~4.2 Gb), we have exploited two complementary sequencing methods, Amplicon sequencing (Amplicon-Seq) and Restriction site Associated DNA Sequencing (RAD-Seq), to characterize genetic variation at different genomic scales in field populations across Europe. At a scale of specific loci, variation in and around three known Target Site Resistant genes (ACCase, ALS, psbA) obtained by Amplicon-Seq will tell us how and how often resistance alleles –or entire haplotypes– have appeared. At the genome-wide scale, RAD-Seq markers will reflect whether spread of resistance alleles is due to an overtake of entire genotypes or the introgression of specific haplotypes.
Title: Genetics of Agave lechuguilla populations and their possible response to climate change.

Authors and affiliations: Giovanna Karina Baltazar Valdez, Alejandra Citlalli Moreno Letelier.

Abstract: Mexico is mostly occupied by deserts, arid and semi-arid zones, these zones are refugia of endemic plants with cultural and economic importance. One of the most representative genus in these ecosystems is Agave, which has a high diversity and endemism in the country. Within this genus is the species Agave lechuguilla, a native and widely distributed plant throughout the Chihuahuan Desert. Future scenarios on climate change suggest that arid ecosystems will be the most affected, the effect on this species will depend on the adaptive response it may have to changes in its habitat, so it’s important to know the genetic diversity of these populations for have knowledge of their vulnerability. We extracted nuclear DNA data of 30 A. lechuguilla populations along its distribution at the Chihuahuan Desert. The total genomic DNA is going to be amplified and sequenced through massive parallel sequencing using the GBS (Genotype by Sequencing) technique and the Illumina HiSeq2500 platform. Subsequently we will assemble de novo the sequences using as reference the published transcriptomes of Agave genus. To know which genes may be under selection of local adaptation, we will separate the polymorphisms under selection (Single Nucleotide Polymorphism) from the neutral ones to know which loci are being affected by environmental factors. Also, we will perform niche modeling with MAXENT, using databases of the geographical and ecological space in which Agave lechuguilla has been distributed over time, in order to be able to generate models that infer its distribution in the face of future climate changes and land use. Because it has been reported that Agave lechuguilla nuclear DNA have high levels of genetic variation among its populations and a complex population structure, we expect A. lechuguilla will have a greater distribution in the future despite the possible scenarios of climate change.
Abstract: Phylogeography determines the geographical distribution of genetic lineages, between and within species. The support in the coalescent theory shows the history of the current gene with its closest common ancestor. Suggest possible sites of diversification of species before environmental and geographic changes. Mexico has the largest number of Agave species. So study your phylogeography can show points of diversity and spatial differentiation. In particular, Agave striata is composed of two subspecies: A. striata subsp striata and A. striata subsp falcata; they are restricted to the Chihuahuense desert. This desert has a recent origin, 4-6 thousand years ago. Therefore, we can intuit a rapid differentiation between the subspecies to occupy different latitudes. The objective of this work is determine the relationships of the lineages, inferring the process of differentiation. With help of chloroplast fragments describe for the genus: psbJ-petA, rps16-trnK, rpl32-trnL and trnL-trnF. The structure among populations and the contact zone between the subspecies will be evaluated. Likewise, ecological niche models will be used at the Ultimate Glacial Maximum to evaluate if the distribution changes coincide with the genetic data.
**Title:** The Mexican Biobank Project: The genetic landscape of uniparental lineages

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**Abstract:** The Mexican Biobank Project (MXB) is a collaborative initiative committed to reduce the currently existing bias in medical genomics by increasing the representation of diverse populations. This project is undertaking the genetic profiling of ~6,000 individuals to generate the most comprehensive DNA Biobank of the Mexican population to date, with associated demographic and biomedical phenotypes. Since the genetic architecture of common diseases and traits is impacted by demographic history, the first phase of the project involves reconstructing the fine-scale population structure of the Mexican population using both autosomal markers and uniparental lineages. We estimate, mitochondrial DNA (mtDNA) and Y chromosome haplogroups for the Mexican Biobank, and make inferences about the diverse sources of ancestry contributing to present-day Mexicans, the sex-biased nature of admixture, and the regional variability of ancestries within Mexico.
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**Title:** Morphological and climatic patterns, genomic structure and phylogenetic analysis of teosinte (Zea spp.)

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**Abstract:** The wild species of the genus Zea comprise nine different taxa, including annual and perennial, diploid and tetraploid species, distributed from northern Mexico to Costa Rica. In order to understand the great variability that exists among the different species, the objective of the present work was to evaluate the diversity and genomic structure of teosinte. Two hundred and seventy-six teosinte populations were planted during the 2014 and 2015 summer cycles under greenhouse conditions. We evaluated 19 morphological characters and 23 climatic variables, foliar tissue was collected from each plant for DNA extraction, and sequencing was carried out in the genomic diversity laboratory of Cornell University, USA. Based on morphological and climatic variables, Discriminant Analysis of Principal Components (DAPC) were performed. Molecular analyzes were carried out with a sample of 3,604 plants with data of 33,929 SNP markers. Using the results of DAPC, the presence of 26 groups was determined; species, subspecies and races were found to be clearly delimited by geographic regions, climatic characteristics, altitudes and characters morphological. Admixture analysis revealed high genomic structure among different populations of teosinte, the best model was explained with K = 24 with high allocation percentages for individuals within groups and high values of differentiation. Based on several structure analyses, a recurrent grouping pattern was found for subspecies parviglumis including Villa Purificación, Guachinango, Manantlán, El Saucito and Ejutla from the Jalisco state and San Cristóbal Honduras from the state of Oaxaca. The results of the phylogenetic reconstruction include five main groups, which show in detail the
evolutionary relationships of teosinte at population level both within and among of taxa. In addition, this work provides useful insights into designing appropriate programs for the effective conservation of the different populations of teosinte.
Title: Identificación local de *Pinus pinceana*.

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Abstract *Pinus pinceana* es un pino piñonero endémico de México, que se distribuye en suelos calcáreos, rocosos y en condiciones de extrema aridez (Farjon y Styles, 1997). Se conocen pocas poblaciones pequeñas, dispersas y discontinuas, en la Sierra Madre Oriental (1480-3000 msnm). Forma parte de las especies de pinos que han sido descritas con mayor tolerancia a condiciones de sequía. Estudios genéticos previos en *P. pinceana* han mostrado a partir de diferentes marcadores, que existe una alta diferenciación genética entre sus poblaciones en comparación con otras especies de pinos. A nivel morfológico Martiñón-Martínez (et al., 2010) encontró que las poblaciones de *P. pinceana* presentan cambios en la longitud de su raíz correlacionados a localidad geográfica Ramírez-Herrera (et al., 2011) y la abundancia de cera en las hojas con la ubicación geográfica de los organismos poblaciones, sugiriendo una adaptación diferencial al estrés hídrico y las altas temperaturas; siendo que en las poblaciones del Norte hay un mejor desempeño de los individuos en condiciones de estrés hídrico y de temperatura elevada. En el presente trabajo se compara la respuesta transcripcional de individuos adultos a lo largo de la distribución natural, describiendo 46,805 genes completos y reconociendo la expresión diferencial de 848 genes que incluyen en la respuesta a cambios de regulación hídrica. En un enfoque poblacional se incluye en este trabajo la caracterización de 858 genes completos para caracterizar la diversidad genética, la estructuración poblacional y se efectúa un llamado de variantes que pretende detectar genes candidatos de respuesta presiones de selección para la adaptación local a condiciones climáticas diferenciales. La distribución, la heterogeneidad de hábitats, la alta diversidad genética y el aislamiento genético y geográfico entre sus poblaciones, además de cambios morfológicos hacen de *P. pinceana* un buen modelo para plantear una
hipótesis que explore el potencial adaptativo, las diferencias genéticas que modulen poblacionalmente distintas estrategias de resistencia a los cambios ambientales y de esa manera entender el papel de la adaptación al ambiente.
Abstract. About 60 maize races are registered for Mexico. This genetic diversity could be lost, as in the case of the race Olotillo, which is currently planted in small proportion, due to low yield. The proposal of this project focuses on taking advantage of the genetic diversity of the landraces of this race with the aim of recovering genetic diversity and yield through a method known as evolutionary breeding (EB). Evolutionary breeding involves the creation of evolutionary populations (EP) from mixing seeds with different evolutionary origin. For the construction of the EPs, the starting point will be local germplasm (Ocozocuatla, Chis.), local + regional (La Frailesca, Chis.) and local + national (Guerrero, Oaxaca and Nayarit). Establishing three types of parcels, local, regional, and national. The EPs will be evaluated during four productive cycles at the agronomic and genetic level. For the genetic level, genotyping-by-sequencing will be produced at different generations and analyses would focus on estimating the balance between deleterious and synonymous mutations (Ka / ks) in each of the
established EPs. The resulting results will allow the proposal of a strategy to improve varieties that could be of direct application to farmers.
**Abstract:** Mycorrhizal fungi play fundamental roles in terrestrial ecosystems by increasing the fitness of their hosts under abiotic stress. Sub-alpine forest at timberline harbor particularly stressful abiotic conditions, characterized by low temperatures, hypoxia, high insolation and frequent soil freezing-unfreezing cycles. Therefore, we expect natural selection to promote specialized strategies for increasing fitness at contrasting elevations in these ecosystems. To better understand the patterns of genomic diversity associated with altitude-driven adaptation, we conducted a population genomics study with the non-model ectomycorrhizal fungal species *Laccaria trichodermophora* in three sky-islands, sub-alpine pine forests of the Trans Mexican Volcanic Belt in Central Mexico, sampling at low (3,000 masl) and high (4,000 masl) elevations. We generated internal transcribed spacer sequences (ITS) and 2,638 SNPs for 75 individuals using a Genotyping by Sequencing method and the *Laccaria bicolor* genome as reference. Using this data, we
inferred population structure and tested for patterns of isolation by distance; and we searched for loci under potential divergent selection using $F_{ST}$ approaches. We identified three highly differentiated genetic clusters that coincided with each mountain peak and fitted them to a model of isolation by distance. Outlier loci reflecting unusual $F_{ST}$ values across mountains but not between low and high-altitude conditions. Our result suggests that *L. trichodermophora* populations went through recent geographic isolation and other environmental forces, other than elevation, are driving the genetic structure of this ectomycorrhizal fungal species.
Title: Genetic Origins of Easter Island and Remote Oceania


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Abstract: The settlement of Oceania represents a uniquely structured, final chapter in the historical founding events of the human species. Resolving the detailed sequences of islands settled and dates of settlement requires careful attention to both haplotype and genetic drift based methodologies. These must be developed within a framework that accounts for the confounding effects of subsequent waves of complex admixture (Melanesian and European). We present methodologies for analyzing these island populations that we have developed across two different large studies (the Oceanian Genome Variation Project: 980 individuals from 88 populations genotyped at 1.7M sites and an eastern Pacific dataset comprising 500 individuals from 20 populations genotyped at 700K sites). We introduce an algorithm for graph reconstruction based on combining directionality measures with dissimilarity measures, a method for dating settlement based on haplotypes, and a PCA-like matrix completion
method for visualizing ancestry specific patterns of population
differentiation. Based on these new methods we will present new findings
about the origin and timing of specific migrations, including strong
evidence for a complex pre-European admixture event between
Polynesians and Native Americans.