

Iguanid Genetics Projects Summary

Below is a summary of ongoing and planned Iguanid projects utilizing genetic data. Names in brackets indicate only the primary contacts for a particular project; hence, several other collaborators may be participating in the project. A list of tissue needs can be found at the end.

IGUANIDAE

OPLURUS

(2017) Origin, taxonomy, and conservation of Madagascar's Oplurid Iguanas [Rachel Welt, et al.] rwelt@amnh.org

Ongoing: Comprehensive geographic sampling, combined with genomic sampling using SNPs across Opluridae should reveal phylogeographic structuring and may validate hypothesized cryptic species lineages. A subsequent revision of taxonomy will require conservation reassessment for adjusted species boundaries. A larger phylogeny incorporating representatives of genera across Iguania will be estimated using Ultraconserved Elements in order to date the divergence of Oplurids from their closest extant relatives to test biogeographic hypotheses explaining their origin on Madagascar.

IGUANINAE

(2017) Comparative transcriptomics of *Iguaninae* [Catherine Malone, Thijs van den Berg, Juan C. Santos, et al.] catherine.malone.isg@gmail.com

Ongoing: We have collected RNA transcriptomes from whole blood across four iguanid genera (*Ctenosaura*, *Sauromalus*, *Dipsosaurus*, *Cyclura*). These transcriptomes have been assembled and we will begin characterizing each one, beginning with *Dipsosaurus*. Results will be useful for a variety of comparative genomics projects (systematics and adaptive evolution) as well as marker development in Iguaninae taxa. Anyone with an interest in accessing the assembled data prior to publication, please email Catherine Malone.

(2017) Nex gen sequencing of *Amblyrhynchus* and *Conolophus* spp. [Gabriele Gentile] gabriele.gentile@uniroma2.it

Beginning: both methylated and non-methylated mtDNA and nucDNA genomes are currently being sequenced in collaboration with the Genome Center of Malaysia. Results will provide insights in the patterns and mechanisms of evolution within this monophyletic group of iguanas.

AMBLYRHYNCHUS

MacLeod, A. and S. Steinfartz. 2016. The conservation status of the Galápagos Marine Iguanas, *Amblyrhynchus cristatus*: a molecular perspective. *Amphibia-Reptilia* 37(2016): 91-109.

BRACHYLOPHUS

(2016) Phylogeography and population genetics of *Brachylophus* [Heidi Davis, Robert Fisher, Peter Harlow] rfisher@usgs.gov

Ongoing: Two mitochondrial loci, ND4 and cytochrome b, have been sequenced in 209 individuals collected in Fiji between 2010 and 2016. Eighty-six of those individuals were sequenced in 2016. At least 86 concatenated haplotypes have been found in captive and wild *Brachylophus*. These haplotypes are comprised of 60 ND4 and 66 cytochrome b haplotypes.

Bayesian phylogenetic analysis yields four reciprocally monophyletic groups corresponding to the three existing species plus individuals from Gau Island, which may represent a new species. Iguanas from six other islands that were identified as *B. bulabula* grouped more closely with either *B. vitiensis* or *B. fasciatus*. Microsatellite analysis was performed using 17 highly polymorphic loci, and while previous Structure results indicated 12 population clusters in the wild individuals, discriminant analysis of principal components (DAPC) suggests fewer clusters. Current work includes analysis of samples collected in Fiji between 2013-2016. Currently these tissues are in San Diego and are being utilized for analysis, most of the mitochondrial work is completed and the microsatellite work is ongoing. The morphological analysis of iguanas from across Fiji needs to be completed to determine how many populations merit new species status.

CACHRYX

Malone CL, Reynoso VH, Buckley L 2017. Never judge an iguana by its spines: systematics of the Yucatan spiny tailed iguana, *Ctenosaura defensor*. *Molecular Phylogenetics and Evolution*. 115: 27–39

CONOLOPHUS

(2016) Hybridization and introgression between *Conolophus marthae* and *C. subcristatus* in Volcan Wolf, Isabela Island [Gabriele Gentile] gabriele.gentile@uniroma2.it

Concluded: through the use of about 30 microsatellite loci, the direction and deepness of introgression following hybridization between the two syntopic populations has been evaluated. The project has been partly financed by the MBZ Foundation in 2012 and was also aimed at complete genetic characterization of *C. marthae* for the purposes of a starting pilot captive breeding program. Results indicated that no hybridization occurred at least in the last two generations and genetic introgression, if any, plays a negligible role.

(2016) Mechanisms of haemoparasite dispersal throughout Galápagos Iguanas [Gabriele Gentile] gabriele.gentile@uniroma2.it

Ongoing: Traditional and PCR based methods will be used to understand how *Hepatozoon* parasite is transmitted to iguanas.

(2016) Phylogeny and phylogeography of *Hepatozoon* parasite of Galápagos Iguanas [Gabriele Gentile] gabriele.gentile@uniroma2.it

Ongoing: Traditional and PCR based methods are used to understand clarify taxonomy, phylogeny, and phylogeography of Galápagos *Hepatozoon*.

(2016) Genetic assignment of fecal samples of *Conolophus* spp. [Gabriele Gentile, Livia Di Giambattista] gabriele.gentile@uniroma2.it

Concluded: A PCR-based protocol has been designed and is currently applied to assign unknown fecal samples to the original species. Submitted to Conservation Genetic Resources.

(2016) Genetic determination of diet in *Conolophus marthae* and *C. subcristatus* from Volcan Wolf, by combining a PCR-based protocol and a traditional fecal inspection approach [Gabriele Gentile] gabriele.gentile@uniroma2.it

Funds requested: As the logistics of the site is very difficult, long permanence on the volcano is prohibitive. Thus, long lasting direct observations can not be carried out. For the purposes of diet assessment, the analysis of stomach-content remains obtained through stomach flushing is possible. However, this technique is invasive, logistically difficult, and ultimately not recommendable, as it may affect survival in lizards (Luiselli et al., 2011). Indirect methods, by

both traditional scat inspection and more recent PCR-based methods prove very useful in situations like ours, when animals are predominantly herbivores (Soininen et al., 2009). These latter methods are particularly well suited in our case as the two sympatric species of land iguanas occur at the same time, in the same places on Volcan Wolf. As the scats are morphologically identical in the two species, the correct species assignment of each scat is impossible, if not by using molecular tools. The use of such tools have also additional advantage as they provide indirect information about the geographic occurrence of the species, providing further data respect to direct capture or sighting.

(2016) Hybridization and introgression between *Conolophus subcristatus* and *Amblyrhynchus cristatus* in Plaza Sur Island [Gabriele Gentile, Livia Di Giambattista] gabriele.gentile@uniroma2.it

Concluding: through the use of about 30 microsatellite loci, the direction and deepness of introgression following hybridization between the two syntopic species is being evaluated. The origin of Marine Iguana males is currently being investigated in depth, via genetic characterization of individuals from other islands.

CTENOSAURA

(2016) Phylogeographic history of *Ctenosaura* [Larry Buckley, Victor Reynoso] ljbsbi@rit.edu

Ongoing: Nuclear DNA and mtDNA sequence data is currently being collected in order to establish the phylogenetic relationships between the species of *Ctenosaura* and to examine their current distributions in relation to the geographic history of Central America.

(2016) Contact zones between *Ctenosaura* species [Victor Reynoso, Eugenia Zarza, Alfredo Romero-Mariscal-Borbolla] vreynoso@ib.unam.mx

Ongoing: Using ND4, Alpha enolase, and microsatellites, Zarza and Reynoso will evaluate the genetic dynamics of the contact zone of *C. pectinata* and *C. hemilopha*.

(2017) Investing the current rate of hybridization between *C. bakeri* and *C. similis* on Utila, Honduras [Daisy Maryon] dfmaryon@gmail.com

Ongoing: Samples have been collected from both species in 2016 fieldwork, with more samples being taken in 2017. We will look at the current rate of hybridization between *C. bakeri* and *C. similis* on Utila, Honduras. Additionally, we plan to see if it is possible to determine sex ratio of *C. bakeri* in nests using egg shells. Twenty-seven egg shells have been collected so far. Work will take place at the University of South Wales, UK, in the lab of Dr Emma Hayhurst.

(2016) Systematics of *Ctenosaura hemilopha/macrolopha* [Victor Reynoso, Eugenia Zarza, Nohelia Pacheco, Carmina Martinez] vreynoso@ib.unam.mx

Ongoing: We are trying to understand the genetic relationships and phylogeography between the different species of the *C. hemilopha* complex based on microsatellites, mitochondrial, and Rad-seq DNA sequences. The validity of suggested species and subspecies is being evaluated. We are particularly interested in evaluating evidence of hybridism in the *C. hemilopha* complex, particularly in Nolasco islands, and measuring genetic flow between islands and islands and the Baja Peninsula or the Continent.

Pasachnik, S.A. and S. Hudman. 2016. Conservation genetics of Roatán Spiny-tailed Iguanas, *Ctenosaura oedirhina*. Pp. 187-196 In Iguanas: Biology, Systematics, and

Conservation. Iverson, J.B., T.D. Grant, C.R. Knapp, and S.A. Pasachnik (Eds.). Herpetological Conservation and Biology 11(Monograph 6).

(2016) Dynamics between *C. pectinata*, *C. acanthura* and *C. similis* [Victor Reynoso, Eugenia Zarza, Alfredo Romero-Mariscal-Borbolla] vreynoso@ib.unam.mx

Ongoing: We want to compare gene flow dynamics in intraspecific and interspecific contact zones and the influence of environmental variables on the location of the contact zones using geographic distribution modeling.

(2016) Linkage map of *C. pectinata* [Eugenia Zarza. Víctor Reynoso] eugenia.zarza@gmail.com.

Planning: We are planning a project to build a linkage map of *C. pectinata* that will serve to localize genomic regions relevant for speciation in contact zones. For this, we will use methods to reduce genome complexity (RAD-sequencing). This project will help to identify and quantify adaptive genomic diversity across the species distribution and in the contact zones.

Zarza, et al. 2016. Genetic tools for assisting sustainable management and conservation of the spiny-tailed iguana, *Ctenosaura pectinata*. Pp. 255-264 In Iguanas: Biology, Systematics, and Conservation. Iverson, J.B., T.D. Grant, C.R. Knapp, and S.A. Pasachnik (Eds.). Herpetological Conservation and Biology 11(Monograph 6).

(2016) Phylogeography of *Ctenosaura oaxacana* [Victor Reynoso, Gabriela Diaz, Carmina Martinez] vreynoso@ib.unam.mx

Ongoing: Using mitochondrial and microsatellite markers, we are evaluating the distribution of genetic variation within *C. oaxacana*, and its relationship to *C. quinquecarinata* and sister species *C. flavidorsalis* and *C. praeocularis* throughout its distribution.

(2016) Phylogeography of *Ctenosaura clarkii* [Victor Reynoso] vreynoso@ib.unam.mx

Stalled: Reynoso and Quijada will evaluate the distribution of the genes ND4, Cyt B, Alpha enolase, and OD in *C. clarkii*, and its relationship to *C. quinquecarinata*, throughout its range.

(2017) *Ctenosaura similis* phylogeography [Stesha Pasachnik, Victor Reynoso, Larry Buckley] sapasachnik@gmail.com

Ongoing: This is an in-depth look at the variation within *C. similis* throughout its range. Thorough sampling has now been conducted from Mexico through Costa Rica, leaving only sampling needed in Panama and the islands of San Andres and Providencia, Columbia. Preliminary sequence data has been collected by for ND4, PACs, CytB, and Rhodopsin by Pasachnik and Buckley. Laboratory work will continue.

(2016) Genetic variability and structure of *Ctenosaura similis* and *Iguana iguana* from Cozumel Island [Ella Vázquez, Alfredo Cuarón] evazquez@ecologia.unam.mx

Ongoing: we have started fieldwork and have now collected behavioral data and tissue samples for populations of *Ctenosaura similis* on Cozumel Island. Laboratory work will initiate early 2016 to assess their population ecology and genetics.

(2017) Assessing the genetic origins of introduced populations of *Ctenosaura similis* in Florida [Leroy Nunez, Kenneth Krysko, Michael Avery, Larry Buckley, Stesha Pasachnik]. Manuscript draft undergoing revisions.

CYCLURA

(2017) A phylogenomic approach to estimating species diversity and evolutionary relationships in West Indian *Cyclura* [R. Graham Reynolds, Stesha Pasachnik, John Iverson] greynold@unca.edu

Ongoing: We are constructing a phylogeny for the genus *Cyclura* using genomic sequence data for both the entire mtDNA genome and for thousands of loci distributed across the nuclear genome. We will explicitly test hypotheses related to historical biogeography, morphological evolution, evolutionary ecology, and conservation biology in a phylogenomic framework. We are generating a wealth of new genomic data for the genus, including thousands of sequenced loci, entire mtDNA genomes, and dozens of microsatellite loci (Raposo do Amaral, et al. 2015; Streicher, et al. 2016) for all taxonomic units in the genus. These data, including alignments, phylogenetic trees, sequences, and microsatellite primers, will be made available via permanent accession in Dryad, and hence will be available to all other researchers wishing to pursue intraspecific molecular studies.

Welch M et al. 2017. Molecular variation and population structure in critically endangered Turks and Caicos Rock Iguanas: identifying intraspecific conservation units and revising subspecific taxonomy. Conservation Genetics 18: 479–493

(2017) Inbreeding and heterozygosity fitness correlations in isolated populations of the Turks and Caicos Rock Iguana, *Cyclura carinata* [Giuliano Colosimo, et al.] gln.colosimo@gmail.com

Completed: We analyzed the role of soft selection in generating patterns of inbreeding depression in the small isolated population of *C. carinata* iguanas on Little Water Cay. We found circumstantial evidence indicating that density-dependent selective pressure can play a role in regulating long time persistence of this population. However, reliable quantification of the relative role of competition was not feasible in this study. These results are now being organized for peer review publication.

(2017) Assessing the genetic impact of headstarting and current diversity of the recovering population of *Cyclura collei* [Mark Welch, Tandora Grant, Byron Wilson] welch@biology.msstate.edu

Ongoing: Since the 1990 rediscovery of *Cyclura collei* in Jamaica's Hellshire Hills, hatchlings have been collected for headstarting at the Hope Zoo in Kingston. Animals were first released from the headstart program in 1996. While the recovery program has dramatically increased the population size, headstarting may have favored offspring from a limited sample of the original remnant population. Results using twelve polymorphic microsatellites (designed for congeners) suggest that only 3-5% of the genetic variation that was present prior to headstarted releases is absent from recent cohorts of hatchlings. Individual genetic diversity has been informative to fully optimize the breeding strategy for the captive assurance colony in the United States. This project has been published as Armed Raspberry's MSc. Thesis.

(2017) Understanding the genetic diversity and structure of *Cyclura cornuta* throughout the Dominican Republic and Mona, and assessing the origins of captive individuals in the DR [Stesha Pasachnik] sapasachnik@gmail.com

Ongoing: Sampling and analyses have been completed. A draft should be submitted by the end of 2017.

(2016) Host-parasite-superparasite interactions in *Cyclura cyclura* [Giuliano Colosimo, et al.] gln.colosimo@gmail.com

Completed: We investigated the host-parasite-superparasite distribution in the system *Cyclura-Amblyomma-Rickettsia* in The Bahamas. We found strong evidence of vertical dispersal and restricted gene flow in this system indicating that different populations of iguanas may be exposed to unique selective pressures. These results are currently being organized for peer review publication.

Aplasca, et al. 2016. Genetic diversity and structure in the Endangered Allen Cays Rock Iguana, *Cyclura cyclura inornata*. PeerJ 4:e1793. <https://doi.org/10.7717/peerj.1793>

(2017) Population genetic analysis and implications for species management for *Cyclura lewisi* [Fred Burton, Tandora Grant, Mallory McKinney, Mark Welch, et al.]

tandora@sandiegozoo.org Ongoing, and recently re-engaged: Over 350 samples have been collected since 2002 and represent the entire remaining genome of the wild population. No other iguana population has been so thoroughly sampled from the point of functional extinction. Goals for the project are: 1) to determine overall genetic diversity, relatedness, and confirm historic records of individual identities among the original founder population; 2) quantify genetic differentiation compared to *Cyclura nubila nubila* and *C. n. caymanensis* and determine if admixture has occurred; and 3) determine parentage for the hatchlings from nests of free-ranging iguanas in the QE II Botanic Park. Results from DNA analysis will be compared with the pedigree-based assumptions and models that have been implemented for the reintroduction program to date. The potential that breeding bias among founder lines may have occurred in the sub-populations after release may alter future management strategies. As the population grows, random sampling of the three release areas will provide information on the population structure. Occasionally, iguanas of unknown or suspect origin (both on and off island) need to be screened for species confirmation and genetic contribution. Progress on this project was stalled for several years but is currently being revisited with M. Welch's lab in conjunction with studies on the Sister Isles Iguana (*Cyclura nubila caymanensis*).

(2017) Inbreeding depression and mate choice in *Cyclura nubila caymanensis* on Little Cayman [Jen Moss, Mark Welch, et al.] jbm650@msstate.edu

Ongoing: Multilocus microsatellite genotyping is being conducted for large numbers of hatchling and adult genetic samples collected from Little Cayman's West End in Summer 2015. So far, 20 markers characterized for *C. nubila* (An, et al., 2004) and 67 additional markers for *Cyclura* spp. have been screened for use in this population. A subset of 25 polymorphic loci has been selected for further population genetic analysis. Age-dependent multilocus heterozygosity will be used as an indicator of inbreeding and half-sibling progeny arrays will be employed in the reconstruction of parental genotypes for mate choice analyses. Thus far, 16 full or partial clutches have been analyzed using the software, COLONY, to infer the most likely number of sires. More complete sampling in 2016 is expected to provide greater resolution into the population-level rates of polyandry, a possible inbreeding avoidance strategy. Taken together, we will use these genetic data to quantify the relative contributions of communal nesting sites to recruitment and maintenance of genetic diversity in the Little Cayman population.

(2015) Population genetics and divergence history of *Cyclura nubila nubila* from Cuba [Ella Vázquez, Grisell Díaz, Vicente Berovides] evazquez@ecologia.unam.mx

Ongoing: We have samples from throughout Cuba. We finished analyzing microsatellite and mitochondrial data to assess genetic diversity and structure within and between populations and

to infer the divergence of the Cuban populations in relation to other rock iguanas. We are working on the publication of this study.

**(2017) Genetic variation in a serially translocated population of highly endangered Caribbean iguanas (*Cyclura pinguis*) [Glenn Gerber, Heidi Davis, et al.]
ggerber@sandiegozoo.org**

Ongoing: Translocated populations of *Cyclura pinguis* may serve as a tool in managing the species. Seventy-three unrelated iguanas from Anegada, 65 from a first-order translocated population on Guana, and 38 from a second-order population on Necker have been genotyped at 23 microsatellite loci developed for *Cyclura pinguis* to compare the genetic diversity of the translocated populations to that of the source population. Reduced heterozygosity and allelic richness were observed in the translocated populations. We are preparing results for publication with recommendations for metapopulation management and genetic restoration of all introduced populations

(2017) Carreras De León, R. 2015. Spatial genetic structure of hatchlings of *Cyclura ricordii* (Reptilia: Iguanidae) in Pedernales Province, Dominican Republic is inconsistent with natal philopatry. Thesis is completed and manuscript is in preparation.

(2013) Population genetics of *Cyclura rileyi* [William Hayes] whayes@llu.edu

Beginning: We have procured fresh DNA samples to evaluate the population genetics of all three *Cyclura rileyi* subspecies using both mitochondrial and nuclear markers. We expect to present our results at the Natural History of the Bahamas Symposium in March 2013.

DIPSOSAURUS

(2017) Phylogeographic history of *Dipsosaurus* [Michael Packer, Catherine Malone, Robert Fisher] catherine.malone.isg@gmail.com

Ending: Morphological and DNA sequence data has been collected from individuals across the range of the genus. We used several nuclear loci (NT3, MLH3, Cmos) and the mtDNA ND4 locus. Drafting manuscript.

IGUANA

Judson JLM, Knapp CR, Welch ME (2018) Age-dependent, negative heterozygosity–fitness correlations and local effects in an endangered Caribbean reptile, *Iguana delicatissima*.

Ecology and Evolution DOI: 10.1002/ece3.3826

Vuillaume, et al. 2015. Genetic evidence of hybridization between the endangered native species *Iguana delicatissima* and the invasive *Iguana iguana* (Reptilia, Iguanidae) in the Lesser Antilles: management implications. PLOS One

<http://dx.doi.org/10.1371/journal.pone.0127575>

(2017) Investigating the population genetics from *Iguana delicatissima* on St.

Eustatius [Thijs van den Burg, Mark Welch, et al.] welch@biology.msstate.edu

Ending: All samples have been screened for 16 msats: D105, D110, D135, D136, 60HDZ13, 60HDZ148, Ccste02, IgdL11, IgdL12, IgdL14, IgdL17, IgdL19, IgdL20, IgdL21, IgdL22, and IgdL24). Genotypic data was used to estimate population structure, degree of inbreeding,

frequency of hybridization with *Iguana iguana* and effective population size to assess the population status. Drafting manuscript.

(2016) Assemblages and acquired antibiotic resistance traits in commensal Gram-negative aerobic microbiota from *Iguana delicatissima* (Squamata, Iguanidae) from Lesser Antilles [Gabriele Gentile] gabriele.gentile@uniroma2.it

Ongoing: Almost completed the investigation in St. Barthélemy and Chancel Island (Martinique). Funds needed for the molecular characterization of antibiotic resistance cassettes. The influence of human presence and activity on gut-associated coliforms in animal populations, has been demonstrated and can be tracked by assessing antimicrobial resistance patterns in gut-associated enterobacteria. Indeed, resistance associated traits, even in remote and uncontaminated settings, can be found in both human-associated strains and wildlife, including iguanas. In contaminated settings, of course, besides being exposed to colonization, wildlife can actually play a role as a reservoir of antibiotic resistance genes and resistant strains. By using a combination of microbiology and molecular biology techniques, we have been screening for antibiotic resistance in gut-associated aerobic microbiota for *Iguana delicatissima* throughout its range and investigating the molecular characterization of the genetic determinants of antibiotic resistance traits.

(2016) Genetic characterization, parasitemia, and prevalence of *Hepatozoon* haemoparasite in *Iguana delicatissima* of Lesser Antilles [Gabriele Gentile] gabriele.gentile@uniroma2.it

Ongoing: Several blood samples have been collected in two pops of *I. delicatissima* (Chancel Island, Martinique, and St. Barthélemy). Traditional and PCR-based methods were used to assess presence, prevalence, and parasitemia of such an *Apicomplexa*. Resulting data will be related to the larger database under construction. The work will be extended to other populations from other islands. Data will be also related to fitness estimators.

(2017) Conservation genetics and systematics of the Curacao population of *Iguana iguana* [Thijs van den Burg, Catherine Malone, Brian Bock] thijs_burg@hotmail.com

Beginning: Genetic data collected to date indicates the population of green iguanas on Curacao are highly distinct from other populations sampled across the species' range. Additionally, this population is highly specialized to dry forest habitat. Given the growing number of non native iguana releases across the Caribbean, research on the Curacao population is needed in order to inform future management decisions.

(2017) Invasive Green Iguana genetics: origin of invasive populations [Christina de Jesus, Wilfredo Falcon, Catherine Malone] chri360@gmail.com

Ending: Building on the work by Malone et al., 2012, our objective is to determine the origin of invasive populations and that of populations in the Caribbean of unknown origin. Using the same loci (ND4, NT3, and PAC), we began this project in spring 2013 in Dr. Riccardo Papa's Lab (University of Puerto Rico). We have sequenced and analyzed all of our data, spanning invasive populations from throughout the Caribbean and the continental U.S.A. Christina is finished her Master's thesis on this work. Additional samples from captive pet or pet-store iguana if acquired will be integrated into analysis. A draft manuscript is underway.

Valette, et al. 2015. Genetic evidence of hybridization between the endangered native species *Iguana delicatissima* and the invasive *Iguana iguana* (Reptilia, Iguanidae) in the Lesser Antilles: management implications. PLOS One

<http://dx.doi.org/10.1371/journal.pone.0127575>

(2016) Origin and differentiation of *Iguana iguana* in Lesser Antilles [Michel Breuil, Frédéric Grandjean, Barbara Vuillaume] breuil.michel@gmail.com

Ongoing: St. Lucia and Saba + Montserrat Common Green Iguanas are different; they have their own ND4 haplotypes but also some specific microsatellites which identify them among all other populations. Moreover, they are identifiable by morphology (Breuil 2016). The problem is that we have no data for Sainte-Croix, that has also black iguanas, to see if there are genetic exchanges between these populations. St. Lucia striped iguanas seem different from all others and are also endemic. To identify the origins of the different alien invasives found in the Lesser Antilles, it will be necessary to compare them with the sequences found in Central and South America. We sequenced the aliens in St. Lucia, Martinique, Guadeloupe (Les Saintes, Grande-Terre, Basse-Terre), St. Maarten, and St. Barts. The results of all these analyses will be soon ready for publication.

(2016) Differentiation and hybridization of *Iguana iguana* and *Iguana delicatissima* [Michel Breuil, Frédéric Grandjean, Victorien Valette, Barbara Vuillaume] breuil.michel@gmail.com

Ongoing: we are continuing our work with more samples and with the same team.

SAUROMALUS

(2017) Broader systematics of *Sauromalus* [Catherine Malone, Victor Reynoso et al.] catherine.malone.isg@gmail.com

Stalled: Tissue samples of *Sauromalus* have been gathered from museums, zoological collections, and wild specimens from throughout most of the range of this genus. DNA sequence data have been collected at several nuclear loci (NT3, PAC, RP40) and the mtDNA ND4 locus. The South Baja peninsula remains sparsely sampled and the putative *S. slevini* population has not been sampled. This project has stalled. Anyone interested in collaborating on this project for the final stages should email Catherine Malone.

(2016) Variation, genetic structure, and hybridization among *Sauromalus* species populations [Victor Hugo Reynoso, Nancy Gabriela Santos] vreynoso@ib.unam.mx

Beginning: Over 30 tissue samples per site have been collected in the Gulf of California including: Bahia Kino islands, Isla Tiburon, Bahia de Los Angeles islands, Bahia de Loreto islands, Bahia de La Paz islands, and several localities on the mainland. Morphological data and a large photographic collection has been gathered for every single specimen sampled. Samples are being sequenced for mtDNA and microsatellites.

McCaliley, RL et al. 2016. Captive breeding of the endangered San Esteban chuckwalla, *Sauromalus varius*: effects of a decade of captive breeding on maintaining genetic diversity. The Southwestern Naturalist 61: 279–285

TISSUE NEEDS

Amblyrhynchus

Brachylophus

Conolophus

Ctenosaura – *C. similis* from Panama and the Columbian Islands of San Andres and Providencia (requested by Stesha Pasachnik).

Cyclura – *C. cornuta* and *C. ricordii*, any samples available from Hispaniola, but particularly from Haiti (requested by Stesha Pasachnik).

Dipsosaurus – Samples of fresh scat are needed for parasitology work (requested by Robert Fisher).

Iguana iguana samples are needed from Venezuela (requested by M. Florencia Breitman and Thijs van den Burg).

Sauromalus – Samples of fresh scat are needed for parasitology work (requested by Robert Fisher).

Outgroups for *Oplurus* systematics (ideally ~2 samples per genus): *Corytophanes* sp., *Laemanctus* sp., *Crotaphytus* sp., *Enyalioides* sp., *Hoplocercus spinosus*, *Morunasaurus* sp., *Amblyrhynchus cristatus*, *Brachylophus* sp., *Conolophus* sp., *Leiocephalus* sp., *Anisolepis* sp., *Enyalius* sp., *Leiosaurus* sp., *Urostrophus* sp., *Eurolophosaurus* sp., *Microlophus* sp., *Stenocercus* sp., *Uracentron* sp. (requested by Rachel Welt).