



IMPORT/EXPORT/RE-EXPORT OF BIOLOGICAL SPECIMENS (CITES/ESA) FOR SCIENTIFIC RESEARCH



☐ New ☐ Reissue/Renew ☐ Amendment

Complete Sections **A** or **B**, and C, D, and E of this application. U.S. address may be required in Section C.**

A. Complete if applying as an individual							
1.a. Last name		1.b. First name		1.c. Middle name or initial		1.d. Suffix	
2. Date of birth (mm/dd/yyyy)		5.a. Telephone number		5.b. Alternate telephone number		6. E-mail address	
[REDACTED]		[REDACTED]		[REDACTED]		[REDACTED]	

B. Complete if applying on behalf of a business, corporation, public agency, Tribe, or institution							
1.a. Name of business, agency, Tribe, or institution		1.b. Doing business as (dba)					
2. Tax identification no.		3.a. Description of business, agency, Tribe, or institution		3.b. Website URL (if applicable)			
4.a. Principal officer (P.O.) last name		4.b. P.O. first name		4.c. P.O. middle initial		4.b. P.O. Title	
5. Primary contact name		6. Primary e-mail address					
7.a. Business telephone number		7.b. Alternate phone no.		8.a. Primary contact telephone no.			

C. All applicants complete address information									
1.a. Physical address (Street address; Apartment #, Suite #, or Room #; no P.O. Boxes)									
1.b. City		1.c. State		1.d. Zip code/Postal code		1.e. County/Province		1.f. Country	
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable)									
2.b. City		2.c. State		2.d. Zip code/Postal code		2.e. County/Province		2.f. Country	

D. All applicants MUST complete	
1. Include a check or money order, payable to the U.S. FISH AND WILDLIFE SERVICE, a nonrefundable processing fee [50 CFR 13.11(d)(4)]. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – attach documentation of fee exempt status as outlined in instructions. (50 CFR 13.11(d))	
2. If you are requesting a reissue/renew/amendment, what is your permit/file number?	
3. Certification: I hereby certify that I have read and am familiar with the regulations contained in Title 50, Part 13 of the Code of Federal Regulations and the other applicable parts in subchapter B of Chapter I of Title 50, and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and belief. I understand that any false statement herein may result in civil or criminal penalties under the provisions of 18 U.S.C. 1001.	
[REDACTED] (Andrew Burrell) 11/22/2021	
The individual/principal officer of the business must print and sign the application. (No photocopied or stamped signatures) Date (mm/dd/yyyy)	

** Further instructions for the above application may be found on our ePermits website. See the last page for information on the Privacy Act, Paperwork Reduction Act, Estimated Burden, and Freedom of Information Act aspects of this application form.

Mail your application(s) to Division of Management Authority, Branch of Permits, MS:IA 5275 Leesburg Pike, Falls Church, VA 22041-3803.

E. IMPORT/EXPORT/RE-EXPORT OF BIOLOGICAL SPECIMENS (CITES/ESA) FOR SCIENTIFIC RESEARCH

General Information

This application covers activities involving CITES and ESA-listed animal specimens used for scientific research, including any readily recognizable parts, products, or derivatives unless otherwise noted in the Appendices.

Review this application carefully and **provide complete answers to all of the questions**. If you are applying for multiple species, be sure to indicate which species you are addressing in each response. **If more space is needed, attach a separate sheet with your responses numbered according to the questions.**

Please allow at least 90 days for the application to be processed.

How do I determine whether the species is protected under CITES and/or the ESA?

CITES	ESA
To determine whether an animal species is protected under CITES, when the species was listed, or whether exemptions apply to your requested activity, see the list of CITES species	<p>To determine whether an animal species is protected under the ESA, please review the list of ESA-listed species in the Code of Federal Regulations.</p> <p>Please be aware that any permit request involving an ESA endangered species must be published in the Federal Register for a required 30-day public comment period.</p>

- If applying as an **individual or institution** please note that you will have to pay the appropriate permit fee.
- If applying as an **institution** that is (or is acting) on behalf of a Federal, Tribal, State, and/or local government agency, no permit fee is required. Provide fee exempt documentation with your application materials.
 - The individual signing the permit must have legal authority to do so if applying on behalf of the institution.

Questions

If you have any questions regarding an action you are requesting authorization for please contact the Division of Management Authority at managementauthority@fws.gov.

Please note: for renewal or amendment of a multi-use permit being requested **within the 5 year** Federal Register public notice period, use application [3-200-52](#)

This form should NOT be used for:

- Captive Bred Wildlife Registration (use application [3-200-41](#))
- ESA Plants (use application [3-200-36](#))

Electronic Information Submission

Electronic submission of inventories, photographs, and receipts: For hard copy applications, if you wish to provide information electronically, please include a flash drive containing this information with your physical application.

All Applicants Must Complete

1. Name and address where you wish the permit to be mailed, **if different from physical address**. If you would like expedited shipping, please enclose a self-addressed, pre-paid, computer-generated, courier service airway bill. If unspecified, all documents will be mailed via regular mail through the U.S. Postal Service.

2. Point of contact if we have questions about the application (name, phone number, and email).

3. Have you or any of the owners of the business (if applying as a business, corporation, or institution), been assessed a civil penalty or convicted of any criminal provision of any statute or regulation relating to the activity for which the application is filed; been convicted, or entered a plea of guilty or nolo contendere, for a felony violation of the Lacey Act, the Migratory Bird Treaty Act, or the Bald and Golden Eagle Protection Act; forfeited collateral; OR are currently under charges for any violation of the laws mentioned above?

___ No ___ Yes

If you answered "Yes" to Question 3, provide: a) the individual's name; b) date of charge; c) charge(s); d) location of incident; e) court, and f) action taken for each violation. Please be aware that a "Yes" response does not automatically disqualify you from getting a permit.

Proposed Activity

- ☐ Import
- ☐ Export
- ☐ Re-export (e.g. export of a specimen that was previously imported into the United States)

4. The **current** location of the samples (if different from the physical address provided):

Name:

Address:

City:

State/Province:

Postal Code:

Country:

5. **Recipient/Sender:**

- If **export or re-export**, provide name and **physical address** of the recipient in the foreign country.
- If **import**, provide name and **physical address** of the exporter/re-exporter in the foreign country.

Name:

Address:

City:

State/Province:

Postal Code:

Country:

6. Information on the type of **biological samples** involved in the import/export/re-export, provide for **each species** (you may use the table located below):

- Scientific name (genus, species, and, if applicable, subspecies);
- Common name;
- Number and type of sample(s) (e.g. 10 blood samples, ear clips, etc.)
- Source (wild or captive-born)
- Approximate date of collection (MM/YYYY)
- Description of packaging (vials, slides, envelopes, etc.)
- Total # of all samples in shipment.

Please see attached table - we have 26 listed species

a. Scientific name (genus, species, and, if applicable, subspecies)	b. Common Name	c. Number & type of sample/part	d. Wild or Captive born	e. Approximate date of collection (mm/yyyy)	f. Description of packaging (vials, slides, envelopes, etc)
EXAMPLE: <i>Pan troglodytes</i>	Chimpanzee	10 blood samples; 4 hair samples	W	08/2015	Vial Envelope
				g. TOTAL # of all samples in the shipment:	

Source of Specimen

7. For **each biological sample taken from a captive-born/captive hatched animal(s)**, provide a signed and dated statement from the breeder or appropriate documentation (e.g. Species 360 report) that includes the following:
- Scientific name (genus, species, and *if applicable*, subspecies),
 - Common name,
 - Name and address of the facility where the animal was bred and born;
 - Birth/hatch date (mm/dd/yyyy),
 - Identification information (studbook #, microchip, leg band, etc.),
 - Name and address of facility where the parental stock is located; and
 - A statement from the breeder that the animal was bred and born at the breeder's facility (including the facility's name and address), and
 - If not the breeder, documentation demonstrating the history of transactions (e.g., chain of custody or ownership of the sample(s), *if applicable*).
8. For **each biological sample taken from an animal in the wild**, provide:
- Scientific name (genus, species, and *if applicable*, subspecies),
 - Common name,
 - Specific location (e.g., county, state, province, country) where the samples were taken from the wild,
 - The name of the individual(s) who collected the animal/samples and their authorization to do so including (but not limited to) copies of foreign and domestic (Federal, State, and/or Tribal) government collecting permits, licenses, contracts, and/or agreements.
 - Method of collection: sampling protocol, approximate length of time held in captivity, any injury and/or mortality experienced during collection, transport, or holding;
 - Information related to any remuneration, either financial or in-kind, provided for acquiring the sample(s);
 - Efforts to use captive specimens (e.g., captive-born, captive-held) in lieu of taking samples from wild animals.
9. For **each biological sample being re-exported** (e.g., exporting a specimen that was previously imported into the United States), provide:
- A copy of the **canceled** CITES export or re-export document issued by the appropriate CITES office in the country from which the wildlife was imported;
 - A copy of your Declaration for Importation or Exportation of Fish or Wildlife (Form 3-177), **cleared** by USFWS Office of Law Enforcement.
 - A copy of the ESA permit that authorized the original import.
 - If you did not make the original import, please provide documentation outlining chain-of-ownership since import, including:
 - A copy of the importer's CITES, ESA, and declaration documents (a, b, & c above) and,
 - Subsequent invoices (or other documentation) showing the history of transactions leading to your ownership of the sample(s) after import (provenance).

Description and Justification For Requested Activity

10. Describe the purpose of the scientific research and include:
- A copy of the research proposal (outlining the purpose, objectives, methods),
 - How long the research has been (or will be) conducted,

- c. Detailed information on sampling methods including:
 - i. who will be taking the samples
 - ii. equipment and methods used
 - iii. measures taken to prevent injuries and mortalities during collection
- d. A copy of the study's Institutional Animal Care and Use Committee (IACUC) form (*if applicable*),
- e. Peer-reviewed scientific papers published from this research (*if applicable*),
- f. An explanation of whether similar research has already been conducted or is currently being conducted.

11. Please provide a detailed description on how the proposed activities will **enhance or benefit the wild population within its native range** (e.g., direct or indirect **conservation efforts**) and provide documentation (e.g., signed memorandums of understanding) demonstrating your commitment to supporting the program and how the program contributes directly to the species identified in your application.

Technical Expertise & Authorizations

12. CV or resume outlining the technical experience of the researchers and field technicians collecting the samples, as it relates to the proposed activities, including experience with other similar species.

Shipment Information

- 13. Please indicate if this is a one-time shipment or if you anticipate needing to import/export/re-export samples multiple times within one year or over multiple years.
- 14. How will the samples be imported or exported (e.g., personally carried or shipped)?
- 15. If personally carried, please specify the individual(s) who will be transporting the samples.

All international shipment(s) must be through a designated port. A [list of designated ports](#) (where an inspector is posted) is available. If you wish to use a port not listed, please contact the Office of Law Enforcement for a Designated Port Exemption Permit (form 3-200-2).

CITES Appendix I & Marine Mammal Species

- For **export** of a **CITES Appendix I-listed species**, provide a copy of the CITES import permit, or evidence one will be issued by the Management Authority of the country to which you plan to export the specimen(s). In accordance with Article III of the CITES treaty, it is required that import permits are issued before the corresponding export permit.
- For **import** of **CITES Appendix-I listed species**, provide information to show the import is not for primarily commercial purposes as outlined in [Resolution Conf. 5.10 \(Rev CoP15\)](#).
- For **import** of **CITES Appendix-I marine mammal samples**, please provide a copy of your FWS or NMFS Marine Mammal Protection Act (MMPA) permit or authorization.



New York University
A private university in the public service

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November 22, 2021

U.S. Fish and Wildlife Service
Division of Management Authority
Branch of Permits, MS: IA
5275 Leesburg Pike
Falls Church, VA 22041-3803
1-800-358-2104 or 703-358-2104

To whom it may concern:

I am writing to apply for a permit to import 217 samples of 26 species of African primates, all in the tribe Cercopithecini. These samples are from dried, preserved skins in the collections of the Royal Museum for Central Africa in Tervuren, Belgium. The biomaterial from each specimen consists of about 5 grams of skin, roughly 1-2 square centimeters in size. The samples have already been collected and I am applying for permission to import them into the United States.

These samples are for scientific research as part of a fully funded National Science Foundation grant ("The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini", BCS-1718339). The skin snips are used as sources of DNA for genetic analyses.

The application form 3-200-37e is included, along with 1) a spreadsheet detailing the samples I am asking to import (for section E6); 2) a letter from Dr. Emmanuel Gilissen, Curator of Mammals at the Royal Museum of Central Africa, stating that I have permission to take the samples from the museum; 3) the description of the project I require the samples for (E10a); 4) my CV (E12); 5) a statement that I am not using the samples for commercial purposes.

I hope all of my documentation is in order.

Thank you for your attention.

Sincerely yours,

[REDACTED]

Andrew Burrell

6. For **EACH** animal/specimen involved in the proposed activity provide:

A. Scientific name	B. Common name	C. Number and type of sample	D. Wild or captive born	E. Date of collection	F. Description of packaging	G. Total # of samples
Allenopithecus nigroviridis	Swamp monkey	4 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	217
Cercopithecus albogularis	Sykes's monkey	3 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus ascanius	Red-tailed monkey	23 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus cephus	Mustached guenon	8 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus diana	Diana monkey	9 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus doggetti	Silver monkey	4 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus dryas	Salongo monkey	1 dry-preserved skin samples, ~5 g	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus erythrotis	Red-eared guenon	2 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus hamlyni	Owl-faced monkey	5 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus kandti	Golden monkey	6 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus lhoesti	L'Hoest's monkey	6 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus mitis	Blue monkey	25 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus mona	Mona monkey	22 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus neglectus	De Brazza's monkey	6 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus nictitans	Greater spot-nosed monkey	9 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus petaurista	Lesser spot-nosed monkey	7 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus pogonias	Crested mona monkey	11 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus solatus	Sun-tailed monkey	1 dry-preserved skin samples, ~5 g	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Cercopithecus wolffi	Wolf's mona monkey	29 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Chlorocebus cynosuros	Malbrouck's monkey	8 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Chlorocebus pygerythrus	Vervet monkey	6 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Chlorocebus sabeus	Green monkey	2 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Chlorocebus tantalus	Tantalus monkey	7 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Erythrocebus patas	Patas monkey	6 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Miopithecus ogouensis	Gabon talapoin	3 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	
Miopithecus talapoin	Angolan talapoin	4 dry-preserved skin samples, ~5 g each	wild born but housed in museum collections	not precisely known but before 1980	8 ml polypropylene vials with o-ring caps	

02.06.2022

Statement

To whom it may concern,

In 2017, it was with great pleasure that I provided permission for Anthony Tosi and Andrew Burrell to study and sample skin material of museum specimens for their research projects. Among these specimens, the Royal Museum for Central Africa houses *Cercopithecus diana*, *Cercopithecus erythrotis*, and *Cercopithecus lhoesti* that fall under the U.S. Endangered Species Act. The attached list contains all the available information on the history of these specimens, which were collected during biological expeditions over the 20th century. If necessary, please contact me at the address indicated herewith below.

With best wishes,



Dr. Emmanuel Gilissen
Curator of Mammals
Royal Museum for Central Africa
Department of African Zoology
Leuvensesteenweg 13
3080 Tervuren, Belgium
Phone: 32 (2) 769 56 22
Fax: 32 (2) 769 56 42
Email: Emmanuel.Gilissen@africamuseum.be

Genus	Species	Subspecies	RMCA #	Sex	Locality	Country	Collector	Year collected
Cercopithecus	diana	roloway	23726	F	Prestea	Ghana	A.H. Booth	1952
Cercopithecus	diana		34964	?	Matonguine	Ivory Coast	?	prior 1973*
Cercopithecus	diana	roloway	34971	F	Bakanou	Ivory Coast	?	prior 1973*
Cercopithecus	diana	roloway	34972	M	Bakanou	Ivory Coast	?	prior 1973*
Cercopithecus	diana	roloway	34973	F	Bakanou	Ivory Coast	?	prior 1973*
Cercopithecus	diana		35699	?	Putto	Liberia	?	prior 1973*
Cercopithecus	diana		35778	?	Fassawalazu	Liberia	?	prior 1973*
Cercopithecus	diana		36278	?	Makai Bomi	Liberia	?	prior 1973*
Cercopithecus	diana		1977-048-M-0066	F	Berebi	Ivory Coast	Mr. Belline	1977
Cercopithecus	erythrotis		28426	?	Fernando Po	Equatorial Guinea	Mr. Schouteden	prior 1973*
Cercopithecus	erythrotis		1974-032-M-0016	F	Antwerp Zoo	?	Antwerp Zoo	1974
Cercopithecus	lhoesti		1271	M	Kivu meer	DRC	Lt. Moulron	1918
Cercopithecus	lhoesti		2891	F	Mawombi	DRC	Mr. Christy	prior 1973*
Cercopithecus	lhoesti		9652	?	Ruhengeri	Rwanda	Mr. Philippart	prior 1973*
Cercopithecus	lhoesti		9761	?	Lungu	DRC	?	prior 1973*
Cercopithecus	lhoesti		17673	?	Bujumbura	Burundi	Mr. Tujdaqb	prior 1973*
Cercopithecus	lhoesti		1988-047-M-001	F	Kisangani	DRC	?	1988

* RMCA modernized sample identification numbers after agreement on CITES treaty in 1973

E. 10 Description and Justification for Requested Activity

E. 10. a – copy of research proposal; please see attached pdf of our funded NSF proposal

E. 10. b. How long the research has been (or will be) conducted:

The samples were collected in June 2018 and stored at the RMCA in Tervuren, Belgium. Once imported into the USA, we will extract DNA and conducted genetic analyses. We anticipate completion of the project by end of 2022.

E. 10. c. Detailed information on sampling methods

i. Who will be taking the samples

Dr. Burrell collected the samples at the RMCA Tervuren in June 2018.

ii. Equipment and methods used

No special equipment was used. Skin samples, roughly 2 x 2 cm in size, were cut from edges of primate pelts using sterilized surgical scissors and placed in 8 ml polypropylene vials with o-ringed caps.

iii. Measures taken to prevent injuries

Burrell wore PPE (gloves, goggles, coat) while sampling the primate skins.

E. 10. f. Is similar researched being conducted or already been conducted?

Some genetic work has been done on this group of primates in the past, focusing on mitochondrial DNA (Guschanski, Katerina, et al. "Next-generation museomics disentangles one of the largest primate radiations." *Systematic biology* 62.4 [2013]: 539-554.). As far as my colleagues and I are aware, no one else is currently gathering whole genome and exome data from these primates using museum specimens.

E. 11. How will this proposed research benefit conservation of imported species?

This project will generate an enormous amount of genomic data for a highly speciose group of African primates, tribe Cercopithecini (aka the guenons). The data include whole genomes of individual representatives of each guenon species as well as population level "exome plus" data for >200 more individuals. While our primary goal is to explore the evolutionary impact of hybridization and admixture on primates, the data we will generate will have definite conservation implications such as measuring genetic diversity within populations and identifying genetically distinct populations in need of conservation. And because we use specimens from museums, we are not disturbing any current primate populations.

E. 12. Technical expertise.

Dr. Burrell has >20 years of experience working on the genetics of nonhuman primates. Please see attached CV.

Shipment information

E. 13 This is a one-time shipment

E. 14 The samples will be hand-carried (unless travel is restricted due to COVID-19; then we would have the samples shipped).

E. 15 The samples will be personally carried by Andrew Burrell (the applicant).

ANDREW STEPHEN BURRELL

Department of Anthropology
New York University
25 Waverly Place
New York, NY 10003
Tel: [REDACTED] Fax: 212-995-4014
E-mail: andrew.burrell@nyu.edu

EDUCATION

January 2009	Ph.D. Anthropology, New York University, NY
May 2000	M.A. Anthropology, New York University, NY
May 1995	B.A. Biology, Amherst College, MA <i>Magna cum laude</i>

PROFESSIONAL EXPERIENCE

2020-present	<i>Visiting Assistant Professor</i> , Anthropology Department, New York University
2009-2019	<i>Research Scientist</i> , Anthropology Department, New York University
2002-3; 2008	<i>Research Assistant</i> , Anthropology Department, New York University
2001-2002	<i>Editorial Assistant</i> , Journal of Human Evolution
1996-1998	<i>Laboratory Technician</i> , Department of Anatomy, Physiology, and Genetics, Uniformed Services University of the Health Sciences

PEER-REVIEWED PUBLICATIONS

2019	Janiak M, Burrell AS , Orkin JD, Disotell TR. Duplication and convergent evolution of the pancreatic ribonuclease gene (<i>RNASE1</i>) in folivorous non-colobine primates, the howler monkeys (<i>Alouatta</i> spp.). <i>Scientific Reports</i> (in review)
2019	Rogers J, and the Baboon Genome Consortium. The comparative genomics and complex population history of <i>Papio</i> . <i>Science Advances</i> 5 eaau6947. [Note: Burrell was responsible for gene tree-species tree analysis and write-up]
2015	Burrell AS , Disotell TR, Bergey CM. The use of museum specimens with high-throughput sequencing. <i>Journal of Human Evolution</i> 79:35-44.
2015	Clarke T, Gould L, Gray O, Burrell AS . Genetic diversity of the ring-tailed lemur (<i>Lemur catta</i>) in south-central Madagascar. <i>Folia Primatologica</i> 86:76-84.
2014	Pozzi L, Hodgson JA, Burrell AS , Sterner KN, Raaum RL, Disotell TR. Primate phylogenetic relationships and divergence dates inferred from complete mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> 75:15-183.
2014	Pozzi L, Bergey CM, Burrell AS . The use (and misuse) of phylogenetic trees in comparative behavioral analyses. <i>International Journal of Primatology</i> . 35:32-54.

- 2013 Bergey CM, Pozzi L, Disotell TR, **Burrell AS**. A new method for genome-wide marker development and genotyping holds great promise for molecular primatology. *International Journal of Primatology* 34: 303-314.
- 2012 Hart JA, Detwiler KM, Gilbert CC, **Burrell AS**, Fuller JL, Emetshu M, Hart TB, Vosper A, Sargis E, Tosi AJ. Lesula: A remarkable new species of Cercopithecus monkey from Congo's Central Basin. *PLoS ONE* 7: e44271.
- 2012 Ting N, Astaras C, Hearn G, Honarvar S, Corush J, **Burrell AS**, Phillips N, Morgan B, Gadsby E, Raaum R, Roos C. Genetic signatures of a demographic collapse in a large-bodied forest dwelling primate (*Mandrillus leucophaeus*). *Ecology and Evolution* 2: 550-561.
- 2011 Pozzi L, Hodgson JA, **Burrell AS**, Disotell TR. Saadanius: stem fossils cannot date the origins of crown groups. *Journal of Human Evolution* 61: 209-210.
- 2011 Jolly CJ, **Burrell AS**, Phillips-Conroy JE, Bergey C, Rogers J. Kinda baboons (*Papio kindae*) and grayfoot chacma baboons (*P. ursinus griseipes*) hybridize in the Kafue River Valley, Zambia. *American Journal of Primatology* 73: 291-303.
- 2010 Disotell TR, **Burrell AS**. Molecular taxonomy. In N Rowe (ed), *All the World's Primates*. Pogonias Press, New York.
- 2009 **Burrell AS**, Disotell TR. Panmixia postponed: ancestry-related assortative mating in contemporary human populations. Minireview in *Genome Biology* 10:245.1-245.4.
- 2009 **Burrell AS**, Jolly CJ, Tosi AJ, Disotell TR. Mitochondrial evidence for the hybrid origin of the kipunji, *Rungwecebus kipunji* (Primates: Papionini). *Molecular Phylogenetics and Evolution* 51: 340-348.
- 2009 Hodgson JA, Sterner KN, Matthews LJ, **Burrell AS**, Raaum RL, Stewart CB, and Disotell TR. Successive radiations, not stasis, in the South American primate fauna. *Proceedings of the National Academy of Sciences, USA*. 106: 5534-5539.
- 2009 **Burrell AS**. "Phylogenetics and Population Genetics of Central African Baboons". Doctoral Dissertation, New York University.
- 2005 Detwiler KM, **Burrell AS**, Jolly CJ. Conservation implications of hybridization in African cercopithecine monkeys. *International Journal of Primatology* 26:661-684.
- 2005 Perez-Sweeney BM, Valladares-Padua C, **Burrell AS**, Di Fiore A, Satkoski J, van Coeverden de Groot PJ, Boag PT, Melnick DJ. Dinucleotide microsatellite primers designed for a critically endangered primate, the black lion tamarin (*Leontopithecus chrysopygus*). *Molecular Ecology Notes* 5: 198-201.

- 2001 McCabe JT, **Burrell AS**. Alterations of AP-1 and CREB protein DNA binding in rat supraoptic and paraventricular nuclei by acute and repeated hyperosmotic stress. *Brain Research Bulletin* 55: 347-358.
- 1995 Green GR, Collas P, **Burrell A**, Poccia DL. Histone phosphorylation during sea urchin development. *Seminars in Cell Biology* 6: 219-227.

GRANTS

- 2017 Tosi AJ (PI), **Burrell AS** (co-PI), Shriver M (co-PI). “Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation.” National Science Foundation BCS-1718339. \$135,093 to Burrell at NYU.
- 2017 **Burrell AS** (PI), Disotell TR (co-PI), Bergey CM (co-PI) “The evolution of the anthropoid genome”. National Science Foundation BCS-1640515. \$217,771.
- 2015 Disotell TR, **Burrell AS** (co-PI) Optimizing DNA enrichment methods from low-quality biosamples for genomic studies. New York University Research Challenge Fund, \$10,000.
- 2011 Disotell TR, **Burrell AS** (co-PI) A high throughput sequencing approach to *Alu* element discovery. New York University Research Challenge Fund, \$14,720.
- 2010 Disotell TR, **Burrell AS** (co-PI) Next generation sequencing of a baboon hybrid zone. Leakey Foundation, \$20,550.
- 2009 Disotell TR, **Burrell AS** (co-PI) Development of transposable-element genetic markers (SINES) for primate phylogenetics. New York University Research Challenge Fund, \$13,000.
- 2005 **Burrell AS** (doctoral candidate), Disotell TR, Jolly CJ. “Phylogenetic relationships and gene flow among southern African baboons.” National Science Foundation Doctoral Dissertation Improvement Grant BCS-0452835. \$5600.

TEACHING EXPERIENCE

- 2020-2021 *Visiting Assistant Professor*, New York University
Taught five graduate and undergraduate courses:
Human Genetics
Forensic Genetics
Human Origins
Molecular Anthropology
Emerging Diseases
- 2017-19 *Instructor*, New York University
• Research in Anthropology: Molecular Genetics Methods: Taught MA and PhD students molecular genetics techniques from DNA extraction to PCR to library prep for high-throughput sequencers.

- 2008 *Lecturer*, Lehman College, City University of New York
• Introduction to Human Variation: Lectured and taught laboratory sections for 30 students; wrote and graded exams; assigned and graded research papers; administered class Blackboard site
- 2005 *Lecturer*, New York University
• Introduction to Human Evolution: Lectured and taught laboratory sections for 20 students; designed and graded exams
- 2002-04 *Laboratory Teaching Assistant*, New York University
• Introduction to Human Evolution; Evolution of Language: Taught laboratory sections, graded papers and exams; prepared teaching supplements for students; administered class Blackboard site
- 1992-94 *Laboratory Teaching Assistant*, Amherst College
• Developmental Biology; Cell Biology; Genes, Cells, and Molecules; Adaptation and Organisms: Assisted professor during laboratory sections

INVITED TALKS

- 2014 “Museum specimens and population genomics.” New York University Ecology and Evolution Group.
- 2012 “Genetic insights into the behavior and evolution of the Kinda baboon.” Graduate Seminar in Animal Behavior, University of Pennsylvania.
- 2011 “Genetic traces of hybridization among southern African baboon species.” Biological Anthropology Colloquium Series, Yale University.
- 2010 “Molecular genetic perspectives on Afro-papionin evolutionary history.” New York Regional Primatology Group, City University of New York Graduate Center, New York.
- 2009 “Genetic studies of three baboon hybrid zones in Zambia”. Invited speaker for the symposium “Hybridization in Primates: Evidence, Extent, Evolutionary Impact and Problems.” Deutsches Primatenzentrum, Göttingen, Germany.

CONFERENCE ABSTRACTS

- 2018 **Burrell AS**, Janiak MC, Disotell TR, Bergey CM. Development of a taxonomically dense dataset of primate genomes. American Association of Physical Anthropologists, Austin, TX.
- 2016 **Burrell AS**, Disotell TR, Bergey CM. Patterns of past admixture in *Papio* inferred from RAD-Seq data. XXVI Congress of the International Primatological Society, Chicago, IL.
- 2015 **Burrell AS**, Disotell TR, Haueisen S, Bergey CM. High-throughput restriction site associated DNA sequencing (RAD-Seq) for genomic studies of primates

- using museum specimens. American Association of Physical Anthropologists, St. Louis, MO.
- 2014 **Burrell AS**, Disotell TR, Hauelsen S, Bergey CM. Using museum specimens for genomic analyses of primates. Northeastern Primate Ecology, Evolution, and Biology Group, Rutgers University.
- 2014 **Burrell AS**, Disotell TR, Jolly CJ, Bergey CM. A phylogenomic approach to understanding the diversification of common baboons. XXV Congress of the International Primatological Society, Hanoi, Vietnam.
- 2013 **Burrell A**, Jolly C, Bergey C, Phillips-Conroy J, Rogers J, Disotell T. Kinda baboons in phylogenetic and paleogeographic perspective. American Association of Physical Anthropologists, Knoxville, TN.
- 2012 **Burrell AS**. Dating the origin of the chacma baboon. XXIV Congress of the International Primatological Society. August, 2012, Cancun, Mexico.
- 2011 **Burrell AS**, Jolly CJ, Rogers J, Phillips-Conroy JE, Disotell TR. Inferring the dispersal behavior of the Kinda baboon (*Papio kindae*) from multilocus genetic data. American Association of Physical Anthropologists, Minneapolis, MN.
- 2010 **Burrell AS**, Jolly CJ, Phillips-Conroy JE, Disotell TR. Conflicting mitochondrial and Y-chromosomal phylogenies indicate complex evolutionary history of *Papio* baboons. American Association of Physical Anthropologists, Albuquerque, NM.
- 2009 **Burrell AS**, Jolly CJ, Tosi AJ, Disotell TR. Genetic data suggest the kipunji mangabey (*Rungwecebus kipunji*) is hybrid in origin. American Association of Physical Anthropologists, Chicago, IL.
- 2009 **Burrell AS**, Jolly CJ, Tosi, AJ, Disotell TR. Mitochondrial DNA evidence suggests the kipunji, *Rungwecebus kipunji*, is hybrid in origin. Poster at the conference "Darwin's Legacy: Early Human Evolution in Africa", New York Consortium in Evolutionary Primatology & American Museum of Natural History, New York.
- 2005 **Burrell AS**. Reliable mitochondrial DNA from non-invasively collected samples. American Association of Physical Anthropologists, Milwaukee, WI.
- 2005 **Burrell AS**. Nuclear/mitochondrial discordance in gray-footed chacma baboons. Poster at the conference "Monkeys old and new", New York Consortium in Evolutionary Primatology & City University of New York, New York.
- 2004 **Burrell AS**, Jolly CJ, Rogers J, Disotell TR. Mitochondrial phylogeny of southern African baboons. American Association of Physical Anthropologists, Tampa, FL.

AWARDS

- 1998-2004 MacCracken Fellowship, New York University
1994 Howard Hughes Summer Fellowship

FIELDWORK

- | | |
|------|---|
| 2008 | Northern and central Tanzania <ul style="list-style-type: none">• Conducted population surveys of primates, including baboons and vervet monkeys |
| 2002 | Kafue National Park, Zambia <ul style="list-style-type: none">• Collected non-invasive samples of Kinda, yellow, and chacma baboons• Currently an active field site for research on baboon hybrids |
| 2000 | Awash National Park, Ethiopia <ul style="list-style-type: none">• Trapped and sampled baboons in hybrid zone |

PROFESSIONAL ACTIVITY

Dissertation committees:

- | | |
|------|--|
| 2011 | Alba Lucia Morlaes Jimenez, “Evolutionary history, phylogeography and conservation priorities for the spider monkey (genus <i>Ateles</i>)”. Anthropology Department, New York University. |
| 2012 | Jason August Hodgson, “Population history and natural selection in the Yemeni”. Anthropology Department, New York University. |
| 2013 | Luca Pozzi, “Evolutionary history, systematics, and species boundaries in galagos (<i>Galagidae</i>)”. Anthropology Department, New York University. |
| 2015 | Christina Bergey, “Population genomics of a baboon hybrid zone”. Anthropology Department, New York University. |

Journal referee:

American Journal of Primatology, The Anatomical Record, Collection Forum, Conservation Genetics, Folia Primatologica, International Journal of Primatology, Journal of Biogeography, Molecular Ecology, Molecular Phylogenetics and Evolution, PLOS One

Grant referee:

National Science Foundation, Leakey Foundation, Wenner-Gren Foundation, Israel Science Foundation

Professional associations:

American Association of Physical Anthropologists, International Society of Primatology.

Workshop:

Andrew S. Burrell

2016 Analysis of Next Generation Sequence Data (ANGUS) at Michigan State University's Kellogg Biological Station. Selective two week intensive summer course on how to use bioinformatic tools to analyze large comparative genomic datasets.

EL-HI EDUCATIONAL OUTREACH AND TRAINING

2016-2018 summer ARISE Program; led eight NYC area high school students through development, execution, and presentation of projects including: identification of cryptic vertebrates in NYC via eDNA; relatedness inference in wild baboons via microsatellite genotypes; evaluation of NYC Dept of Health restaurant "grades" via eDNA

2012 Invited Speaker, "College for a Day" program, New York University. Interactive presentation to 4th and 5th graders from the Success Academy Network about science and science careers. Sponsored by NYU's Office of Civic Engagement.

2009, 2012 Invited Speaker, Career Day, PS 124 Yung Wing School, New York City.



New York University

A private university in the public service

Andrew S. Burrell
Visiting Assistant Professor
Department of Anthropology
Center for the Study of Human Origins
25 Waverly Place
New York, NY 10003-6790
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E-mail: andrew.burrell@nyu.edu



November 22, 2021

U.S. Fish and Wildlife Service
Division of Management Authority
Branch of Permits, MS: IA
5275 Leesburg Pike
Falls Church, VA 22041-3803
1-800-358-2104 or 703-358-2104

To whom it may concern:

These samples will not be used for commercial purposes. The samples themselves will likely be fully consumed during DNA extraction; any remaining sample cannot be used for other purposes without the permission of the Royal Museum of Central Africa. All genetic data generated from these samples will be made publicly available on standard repositories of genetic information (e.g., NCBI's GenBank), as per National Science Foundation regulations.

Sincerely yours,

[REDACTED]

Andrew Burrell

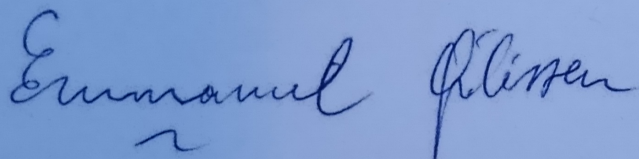
15.06.2018

attestation

To whom it may concern,

This is to certify that Drs. Anthony Tosi, Kent State University, USA, and Andrew Burrell, New York University, USA, worked in the collections of the Royal Museum for Central Africa on 8-15 June 2018. The package of samples contains dead museum specimens (preserved dried non endangered mammal skins) for scientific research. These specimens are non-infectious, non-contagious, non-venomous, unfit for human consumption. Preservation agrees with requirements for SAFE TREATMENT laid down in Point (8) (a) (d) in the ANNEX to the Commission Regulation (EU) No 294/2013. The specimens in the package are on loan for scientific research from the Royal Museum for Central Africa. Please see attached specimen list for further information.

Sincerely Yours,



Dr. Emmanuel Gilissen

Curator of Mammals

Royal Museum for Central Africa

Department of African Zoology

Leuvensesteenweg 13

3080 Tervuren, Belgium

Phone: 32 (2) 769 56 22

Fax: 32 (2) 769 56 42

Email: Emmanuel.Gilissen@africamuseum.be

List of Suggested Reviewers or Reviewers Not To Include (optional)

SUGGESTED REVIEWERS:

Brenda Bradley, George Washington University, [REDACTED]
Alan Templeton, Washington University, temple_a@wustl.edu
Mike Bruford, Cardiff University, brufordmw@cardiff.ac.uk
Cristian Apetrei, University of Pittsburgh, apetreic@cvr.pitt.edu

REVIEWERS NOT TO INCLUDE:

Not Listed

List of Suggested Reviewers or Reviewers Not To Include (optional)

SUGGESTED REVIEWERS:

Not Listed

REVIEWERS NOT TO INCLUDE:

Not Listed

List of Suggested Reviewers or Reviewers Not To Include (optional)

SUGGESTED REVIEWERS:

Not Listed

REVIEWERS NOT TO INCLUDE:

Not Listed

COLLABORATORS AND OTHER AFFILIATIONS

PI: ANTHONY J. TOSI

Collaborators and co-authors during previous 48 months (21 total):

Muhammad Abdul-Latiff	National University of Malaysia
Christina Bergey	University of Notre Dame
Kai Böker	German Primate Center
Markus Brameier	German Primate Center
Andrew Burrell	New York University
Kate Detwiler	Florida Atlantic University
Maurice Emetsu	Lukuru Wildlife Foundation, DR Congo
Ben Evans	McMaster University
James Fuller	Columbia University
Christopher Gilbert	Hunter College, CUNY
John Hart	Lukuru Wildlife Foundation, DR Congo
Terese Hart	Lukuru Wildlife Foundation, DR Congo
Jakob Kolleck	German Primate Center
Rasmus Liedigk	German Primate Center
Badrul Md-Zain	National University of Malaysia
Erik Meijaard	Australian National University
Don Melnick	Columbia University
Christian Roos	German Primate Center
Eric Sargis	Yale University
Ashley Vosper	Wildlife Conservation Society, DR Congo
Dietmar Zinner	German Primate Center

Graduate advisors and postdoctoral sponsors (3 total):

Don Melnick	Graduate Advisor, Columbia University
Osamu Takenaka	Postdoctoral Sponsor, Kyoto University
Todd Disotell	Postdoctoral Sponsor, New York University

Graduate advisees/committee memberships (6 total):

Paul Telfer	PhD Advisee, New York University 2003
Wesley Sutton	PhD Advisee, New York University 2004
Andrew Burrell	PhD Advisee, New York University 2007
Kate Detwiler	PhD Advisee, New York University 2009
Morgan Chaney	PhD Candidate, Kent State University
Cody Ruiz	MA Candidate, Kent State University

ANDREW BURRELL

Collaborators and Co-editors

Christina Bergey	New York University
Tara Clarke	Duke University
Kate Detwiler	Florida Atlantic University
Todd Disotell	New York University
John Hart	TL2 project (D. R. Congo)
Terese Hart	TL2 project (D. R. Congo)
James Higham	New York University
Jason Hodgson	Imperial College
Clifford Jolly	New York University
Jane Phillips-Conroy	Washington University, St. Louis
Luca Pozzi	University of Texas, San Antonio
Ryan Raaum	Lehman College, City University of New York
Jeff Rogers	Baylor College of Medicine
Eric Sargis	Yale University
Kirstin Sterner	University of Oregon
Nelson Ting	University of Oregon
Anthony Tosi	Kent State University

Collaborators & Other Affiliations
Christina M. Bergey

Department of Anthropology, Pennsylvania State University, e-mail: cxb585@psu.edu,

Collaborators & Other Affiliations

Collaborators and Co-Editors:

Paramjit Arora, New York University;
Mary E. Blair, American Museum of Natural History;
Andrew S. Burrell, New York University;
Angelo P. Canedo;
Kenneth L. Chiou, Washington University in St. Louis;
Anthony F. Di Fiore, University of Texas - Austin;
Todd R. Disotell, New York University;
Sarah Haueisen;
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Evelyn Jagoda, Harvard University;
Clifford J. Jolly, New York University;
Eileen Larney, Stony Brook University;
Minh D. Le, American Museum of Natural History;
Elora H. López, American Museum of Natural History;
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Erik R. Patel, Duke University;
Jane E. Phillips-Conroy, Washington University in St. Louis;
Sarah B. Pickett, University of Washington;
Luca Pozzi, German Primate Center;
Ryan L. Raaum, Lehman College, CUNY;
Jeffrey Rogers, Baylor College of Medicine;
Eleanor J. Sterling, American Museum of Natural History;
Anthony J. Tosi, Kent State University;
Andrew Watkins, New York University;

Graduate Advisers and Postdoctoral Sponsors:

New York University:
Todd R. Disotell;
Clifford J. Jolly;
University of Notre Dame:
Nora J. Besansky
Pennsylvania State University:
George H. Perry

Thesis Adviser and Postgraduate-Scholar Sponsor:

Total graduate students: 0; Total postgraduate scholars: 0.

COVER SHEET FOR PROPOSAL TO THE NATIONAL SCIENCE FOUNDATION

PROGRAM ANNOUNCEMENT/SOLICITATION NO./DUE DATE PD 98-1392 11/16/16		<input type="checkbox"/> Special Exception to Deadline Date Policy		FOR NSF USE ONLY NSF PROPOSAL NUMBER 1718715	
FOR CONSIDERATION BY NSF ORGANIZATION UNIT(S) (Indicate the most specific unit known, i.e. program, division, etc.) BCS - Biological Anthropology					
DATE RECEIVED	NUMBER OF COPIES	DIVISION ASSIGNED	FUND CODE	DUNS# (Data Universal Numbering System)	FILE LOCATION
11/16/2016	1	04040000 BCS	1392	041071101	08/29/2017 2:09pm S
EMPLOYER IDENTIFICATION NUMBER (EIN) OR TAXPAYER IDENTIFICATION NUMBER (TIN) 316402079		SHOW PREVIOUS AWARD NO. IF THIS IS <input type="checkbox"/> A RENEWAL <input type="checkbox"/> AN ACCOMPLISHMENT-BASED RENEWAL		IS THIS PROPOSAL BEING SUBMITTED TO ANOTHER FEDERAL AGENCY? YES <input type="checkbox"/> NO <input checked="" type="checkbox"/> IF YES, LIST ACRONYM(S)	
NAME OF ORGANIZATION TO WHICH AWARD SHOULD BE MADE Kent State University		ADDRESS OF AWARDEE ORGANIZATION, INCLUDING 9 DIGIT ZIP CODE Kent State University Office of the Comptroller Kent, OH. 442420001			
AWARDEE ORGANIZATION CODE (IF KNOWN) 0030510000					
NAME OF PRIMARY PLACE OF PERF Kent State University		ADDRESS OF PRIMARY PLACE OF PERF, INCLUDING 9 DIGIT ZIP CODE Kent State University Kent ,OH ,442420001 ,US.			
IS AWARDEE ORGANIZATION (Check All That Apply) (See GPG II.C For Definitions)		<input type="checkbox"/> SMALL BUSINESS <input type="checkbox"/> FOR-PROFIT ORGANIZATION		<input type="checkbox"/> MINORITY BUSINESS <input type="checkbox"/> WOMAN-OWNED BUSINESS <input type="checkbox"/> IF THIS IS A PRELIMINARY PROPOSAL THEN CHECK HERE	
TITLE OF PROPOSED PROJECT Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini					
REQUESTED AMOUNT \$ 208,990	PROPOSED DURATION (1-60 MONTHS) 36 months	REQUESTED STARTING DATE 06/01/17	SHOW RELATED PRELIMINARY PROPOSAL NO. IF APPLICABLE		
THIS PROPOSAL INCLUDES ANY OF THE ITEMS LISTED BELOW <input type="checkbox"/> BEGINNING INVESTIGATOR (GPG I.G.2) <input type="checkbox"/> DISCLOSURE OF LOBBYING ACTIVITIES (GPG II.C.1.e) <input type="checkbox"/> PROPRIETARY & PRIVILEGED INFORMATION (GPG I.D, II.C.1.d) <input type="checkbox"/> HISTORIC PLACES (GPG II.C.2.j) <input checked="" type="checkbox"/> VERTEBRATE ANIMALS (GPG II.D.6) IACUC App. Date Pending PHS Animal Welfare Assurance Number A3571-01 <input checked="" type="checkbox"/> FUNDING MECHANISM Research - other than RAPID or EAGER					
<input type="checkbox"/> HUMAN SUBJECTS (GPG II.D.7) Human Subjects Assurance Number _____ Exemption Subsection _____ or IRB App. Date _____ <input checked="" type="checkbox"/> INTERNATIONAL ACTIVITIES: COUNTRY/COUNTRIES INVOLVED (GPG II.C.2.j) BE FR UK XJ <input checked="" type="checkbox"/> COLLABORATIVE STATUS A collaborative proposal from multiple organizations (GPG II.D.4.b)					
PI/PD DEPARTMENT Anthropology		PI/PD POSTAL ADDRESS 750 Hilltop Drive Lowry Hall 238 Kent, OH 44242 United States			
PI/PD FAX NUMBER					
NAMES (TYPED)	High Degree	Yr of Degree	Telephone Number	Email Address	
PI/PD NAME Anthony J Tosi	PhD	2000	330-672-5121	atosi@kent.edu	
CO-PI/PD					
CO-PI/PD					
CO-PI/PD					
CO-PI/PD					

CERTIFICATION PAGE

Certification for Authorized Organizational Representative (or Equivalent) or Individual Applicant

By electronically signing and submitting this proposal, the Authorized Organizational Representative (AOR) or Individual Applicant is: (1) certifying that statements made herein are true and complete to the best of his/her knowledge; and (2) agreeing to accept the obligation to comply with NSF award terms and conditions if an award is made as a result of this application. Further, the applicant is hereby providing certifications regarding conflict of interest (when applicable), drug-free workplace, debarment and suspension, lobbying activities (see below), nondiscrimination, flood hazard insurance (when applicable), responsible conduct of research, organizational support, Federal tax obligations, unpaid Federal tax liability, and criminal convictions as set forth in the NSF Proposal & Award Policies & Procedures Guide, Part I: the Grant Proposal Guide (GPG). Willful provision of false information in this application and its supporting documents or in reports required under an ensuing award is a criminal offense (U.S. Code, Title 18, Section 1001).

Certification Regarding Conflict of Interest

The AOR is required to complete certifications stating that the organization has implemented and is enforcing a written policy on conflicts of interest (COI), consistent with the provisions of AAG Chapter IV.A.; that, to the best of his/her knowledge, all financial disclosures required by the conflict of interest policy were made; and that conflicts of interest, if any, were, or prior to the organization's expenditure of any funds under the award, will be, satisfactorily managed, reduced or eliminated in accordance with the organization's conflict of interest policy. Conflicts that cannot be satisfactorily managed, reduced or eliminated and research that proceeds without the imposition of conditions or restrictions when a conflict of interest exists, must be disclosed to NSF via use of the Notifications and Requests Module in FastLane.

Drug Free Work Place Certification

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent), is providing the Drug Free Work Place Certification contained in Exhibit II-3 of the Grant Proposal Guide.

Debarment and Suspension Certification

(If answer "yes", please provide explanation.)

Is the organization or its principals presently debarred, suspended, proposed for debarment, declared ineligible, or voluntarily excluded from covered transactions by any Federal department or agency?

Yes ☐

No ☒

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) or Individual Applicant is providing the Debarment and Suspension Certification contained in Exhibit II-4 of the Grant Proposal Guide.

Certification Regarding Lobbying

This certification is required for an award of a Federal contract, grant, or cooperative agreement exceeding \$100,000 and for an award of a Federal loan or a commitment providing for the United States to insure or guarantee a loan exceeding \$150,000.

Certification for Contracts, Grants, Loans and Cooperative Agreements

The undersigned certifies, to the best of his or her knowledge and belief, that:

- (1) No Federal appropriated funds have been paid or will be paid, by or on behalf of the undersigned, to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with the awarding of any Federal contract, the making of any Federal grant, the making of any Federal loan, the entering into of any cooperative agreement, and the extension, continuation, renewal, amendment, or modification of any Federal contract, grant, loan, or cooperative agreement.
- (2) If any funds other than Federal appropriated funds have been paid or will be paid to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with this Federal contract, grant, loan, or cooperative agreement, the undersigned shall complete and submit Standard Form-LLL, "Disclosure of Lobbying Activities," in accordance with its instructions.
- (3) The undersigned shall require that the language of this certification be included in the award documents for all subawards at all tiers including subcontracts, subgrants, and contracts under grants, loans, and cooperative agreements and that all subrecipients shall certify and disclose accordingly.

This certification is a material representation of fact upon which reliance was placed when this transaction was made or entered into. Submission of this certification is a prerequisite for making or entering into this transaction imposed by section 1352, Title 31, U.S. Code. Any person who fails to file the required certification shall be subject to a civil penalty of not less than \$10,000 and not more than \$100,000 for each such failure.

Certification Regarding Nondiscrimination

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is providing the Certification Regarding Nondiscrimination contained in Exhibit II-6 of the Grant Proposal Guide.

Certification Regarding Flood Hazard Insurance

Two sections of the National Flood Insurance Act of 1968 (42 USC §4012a and §4106) bar Federal agencies from giving financial assistance for acquisition or construction purposes in any area identified by the Federal Emergency Management Agency (FEMA) as having special flood hazards unless the:

- (1) community in which that area is located participates in the national flood insurance program; and
- (2) building (and any related equipment) is covered by adequate flood insurance.

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) or Individual Applicant located in FEMA-designated special flood hazard areas is certifying that adequate flood insurance has been or will be obtained in the following situations:

- (1) for NSF grants for the construction of a building or facility, regardless of the dollar amount of the grant; and
- (2) for other NSF grants when more than \$25,000 has been budgeted in the proposal for repair, alteration or improvement (construction) of a building or facility.

Certification Regarding Responsible Conduct of Research (RCR)

(This certification is not applicable to proposals for conferences, symposia, and workshops.)

By electronically signing the Certification Pages, the Authorized Organizational Representative is certifying that, in accordance with the NSF Proposal & Award Policies & Procedures Guide, Part II, Award & Administration Guide (AAG) Chapter IV.B., the institution has a plan in place to provide appropriate training and oversight in the responsible and ethical conduct of research to undergraduates, graduate students and postdoctoral researchers who will be supported by NSF to conduct research. The AOR shall require that the language of this certification be included in any award documents for all subawards at all tiers.

CERTIFICATION PAGE - CONTINUED**Certification Regarding Organizational Support**

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is certifying that there is organizational support for the proposal as required by Section 526 of the America COMPETES Reauthorization Act of 2010. This support extends to the portion of the proposal developed to satisfy the Broader Impacts Review Criterion as well as the Intellectual Merit Review Criterion, and any additional review criteria specified in the solicitation. Organizational support will be made available, as described in the proposal, in order to address the broader impacts and intellectual merit activities to be undertaken.

Certification Regarding Federal Tax Obligations

When the proposal exceeds \$5,000,000, the Authorized Organizational Representative (or equivalent) is required to complete the following certification regarding Federal tax obligations. By electronically signing the Certification pages, the Authorized Organizational Representative is certifying that, to the best of their knowledge and belief, the proposing organization:

- (1) has filed all Federal tax returns required during the three years preceding this certification;
- (2) has not been convicted of a criminal offense under the Internal Revenue Code of 1986; and
- (3) has not, more than 90 days prior to this certification, been notified of any unpaid Federal tax assessment for which the liability remains unsatisfied, unless the assessment is the subject of an installment agreement or offer in compromise that has been approved by the Internal Revenue Service and is not in default, or the assessment is the subject of a non-frivolous administrative or judicial proceeding.

Certification Regarding Unpaid Federal Tax Liability

When the proposing organization is a corporation, the Authorized Organizational Representative (or equivalent) is required to complete the following certification regarding Federal Tax Liability:

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is certifying that the corporation has no unpaid Federal tax liability that has been assessed, for which all judicial and administrative remedies have been exhausted or lapsed, and that is not being paid in a timely manner pursuant to an agreement with the authority responsible for collecting the tax liability.

Certification Regarding Criminal Convictions

When the proposing organization is a corporation, the Authorized Organizational Representative (or equivalent) is required to complete the following certification regarding Criminal Convictions:

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is certifying that the corporation has not been convicted of a felony criminal violation under any Federal law within the 24 months preceding the date on which the certification is signed.

Certification Dual Use Research of Concern

By electronically signing the certification pages, the Authorized Organizational Representative is certifying that the organization will be or is in compliance with all aspects of the United States Government Policy for Institutional Oversight of Life Sciences Dual Use Research of Concern.

AUTHORIZED ORGANIZATIONAL REPRESENTATIVE		SIGNATURE		DATE
NAME Susan Tribuzzo		Electronic Signature		Nov 16 2016 4:42PM
TELEPHONE NUMBER	EMAIL ADDRESS stribuzz@kent.edu		FAX NUMBER	

COVER SHEET FOR PROPOSAL TO THE NATIONAL SCIENCE FOUNDATION

PROGRAM ANNOUNCEMENT/SOLICITATION NO./DUE DATE PD 98-1392 11/16/16		<input type="checkbox"/> Special Exception to Deadline Date Policy		FOR NSF USE ONLY NSF PROPOSAL NUMBER 1718339	
FOR CONSIDERATION BY NSF ORGANIZATION UNIT(S) (Indicate the most specific unit known, i.e. program, division, etc.) BCS - Biological Anthropology					
DATE RECEIVED	NUMBER OF COPIES	DIVISION ASSIGNED	FUND CODE	DUNS# (Data Universal Numbering System)	FILE LOCATION
11/16/2016	1	04040000 BCS	1392	041968306	08/29/2017 2:09pm S
EMPLOYER IDENTIFICATION NUMBER (EIN) OR TAXPAYER IDENTIFICATION NUMBER (TIN) 135562308		SHOW PREVIOUS AWARD NO. IF THIS IS <input type="checkbox"/> A RENEWAL <input type="checkbox"/> AN ACCOMPLISHMENT-BASED RENEWAL		IS THIS PROPOSAL BEING SUBMITTED TO ANOTHER FEDERAL AGENCY? YES <input type="checkbox"/> NO <input checked="" type="checkbox"/> IF YES, LIST ACRONYM(S)	
NAME OF ORGANIZATION TO WHICH AWARD SHOULD BE MADE New York University		ADDRESS OF Awardee ORGANIZATION, INCLUDING 9 DIGIT ZIP CODE New York University 70 Washington Square S New York, NY. 100121019			
AWARDEE ORGANIZATION CODE (IF KNOWN) 0027854000					
NAME OF PRIMARY PLACE OF PERF Molecular Anthropology Laboratory		ADDRESS OF PRIMARY PLACE OF PERF, INCLUDING 9 DIGIT ZIP CODE Molecular Anthropology Laboratory 25 Waverly Place New York ,NY ,100036701 ,US.			
IS Awardee ORGANIZATION (Check All That Apply) (See GPG II.C For Definitions)		<input type="checkbox"/> SMALL BUSINESS <input type="checkbox"/> FOR-PROFIT ORGANIZATION		<input type="checkbox"/> MINORITY BUSINESS <input type="checkbox"/> WOMAN-OWNED BUSINESS <input type="checkbox"/> IF THIS IS A PRELIMINARY PROPOSAL THEN CHECK HERE	
TITLE OF PROPOSED PROJECT Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini					
REQUESTED AMOUNT \$ 135,093	PROPOSED DURATION (1-60 MONTHS) 36 months	REQUESTED STARTING DATE 06/01/17	SHOW RELATED PRELIMINARY PROPOSAL NO. IF APPLICABLE		
THIS PROPOSAL INCLUDES ANY OF THE ITEMS LISTED BELOW <input type="checkbox"/> BEGINNING INVESTIGATOR (GPG I.G.2) <input type="checkbox"/> DISCLOSURE OF LOBBYING ACTIVITIES (GPG II.C.1.e) <input type="checkbox"/> PROPRIETARY & PRIVILEGED INFORMATION (GPG I.D, II.C.1.d) <input type="checkbox"/> HISTORIC PLACES (GPG II.C.2.j) <input type="checkbox"/> VERTEBRATE ANIMALS (GPG II.D.6) IACUC App. Date _____ PHS Animal Welfare Assurance Number _____ <input checked="" type="checkbox"/> FUNDING MECHANISM Research - other than RAPID or EAGER					
<input type="checkbox"/> HUMAN SUBJECTS (GPG II.D.7) Human Subjects Assurance Number _____ Exemption Subsection _____ or IRB App. Date _____ <input checked="" type="checkbox"/> INTERNATIONAL ACTIVITIES: COUNTRY/COUNTRIES INVOLVED (GPG II.C.2.j) BE FR UK <input checked="" type="checkbox"/> COLLABORATIVE STATUS A collaborative proposal from multiple organizations (GPG II.D.4.b)					
PI/PD DEPARTMENT Anthropology		PI/PD POSTAL ADDRESS 25 Waverly Place			
PI/PD FAX NUMBER		New York, NY 10003 United States			
NAMES (TYPED)	High Degree	Yr of Degree	Telephone Number	Email Address	
PI/PD NAME Andrew Burrell	PhD	2009	212-998-8578	asb224@nyu.edu	
CO-PI/PD					
CO-PI/PD					
CO-PI/PD					
CO-PI/PD					

CERTIFICATION PAGE

Certification for Authorized Organizational Representative (or Equivalent) or Individual Applicant

By electronically signing and submitting this proposal, the Authorized Organizational Representative (AOR) or Individual Applicant is: (1) certifying that statements made herein are true and complete to the best of his/her knowledge; and (2) agreeing to accept the obligation to comply with NSF award terms and conditions if an award is made as a result of this application. Further, the applicant is hereby providing certifications regarding conflict of interest (when applicable), drug-free workplace, debarment and suspension, lobbying activities (see below), nondiscrimination, flood hazard insurance (when applicable), responsible conduct of research, organizational support, Federal tax obligations, unpaid Federal tax liability, and criminal convictions as set forth in the NSF Proposal & Award Policies & Procedures Guide, Part I: the Grant Proposal Guide (GPG). Willful provision of false information in this application and its supporting documents or in reports required under an ensuing award is a criminal offense (U.S. Code, Title 18, Section 1001).

Certification Regarding Conflict of Interest

The AOR is required to complete certifications stating that the organization has implemented and is enforcing a written policy on conflicts of interest (COI), consistent with the provisions of AAG Chapter IV.A.; that, to the best of his/her knowledge, all financial disclosures required by the conflict of interest policy were made; and that conflicts of interest, if any, were, or prior to the organization's expenditure of any funds under the award, will be, satisfactorily managed, reduced or eliminated in accordance with the organization's conflict of interest policy. Conflicts that cannot be satisfactorily managed, reduced or eliminated and research that proceeds without the imposition of conditions or restrictions when a conflict of interest exists, must be disclosed to NSF via use of the Notifications and Requests Module in FastLane.

Drug Free Work Place Certification

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent), is providing the Drug Free Work Place Certification contained in Exhibit II-3 of the Grant Proposal Guide.

Debarment and Suspension Certification

(If answer "yes", please provide explanation.)

Is the organization or its principals presently debarred, suspended, proposed for debarment, declared ineligible, or voluntarily excluded from covered transactions by any Federal department or agency?

Yes ☐

No ☒

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) or Individual Applicant is providing the Debarment and Suspension Certification contained in Exhibit II-4 of the Grant Proposal Guide.

Certification Regarding Lobbying

This certification is required for an award of a Federal contract, grant, or cooperative agreement exceeding \$100,000 and for an award of a Federal loan or a commitment providing for the United States to insure or guarantee a loan exceeding \$150,000.

Certification for Contracts, Grants, Loans and Cooperative Agreements

The undersigned certifies, to the best of his or her knowledge and belief, that:

- (1) No Federal appropriated funds have been paid or will be paid, by or on behalf of the undersigned, to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with the awarding of any Federal contract, the making of any Federal grant, the making of any Federal loan, the entering into of any cooperative agreement, and the extension, continuation, renewal, amendment, or modification of any Federal contract, grant, loan, or cooperative agreement.
- (2) If any funds other than Federal appropriated funds have been paid or will be paid to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with this Federal contract, grant, loan, or cooperative agreement, the undersigned shall complete and submit Standard Form-LLL, "Disclosure of Lobbying Activities," in accordance with its instructions.
- (3) The undersigned shall require that the language of this certification be included in the award documents for all subawards at all tiers including subcontracts, subgrants, and contracts under grants, loans, and cooperative agreements and that all subrecipients shall certify and disclose accordingly.

This certification is a material representation of fact upon which reliance was placed when this transaction was made or entered into. Submission of this certification is a prerequisite for making or entering into this transaction imposed by section 1352, Title 31, U.S. Code. Any person who fails to file the required certification shall be subject to a civil penalty of not less than \$10,000 and not more than \$100,000 for each such failure.

Certification Regarding Nondiscrimination

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is providing the Certification Regarding Nondiscrimination contained in Exhibit II-6 of the Grant Proposal Guide.

Certification Regarding Flood Hazard Insurance

Two sections of the National Flood Insurance Act of 1968 (42 USC §4012a and §4106) bar Federal agencies from giving financial assistance for acquisition or construction purposes in any area identified by the Federal Emergency Management Agency (FEMA) as having special flood hazards unless the:

- (1) community in which that area is located participates in the national flood insurance program; and
- (2) building (and any related equipment) is covered by adequate flood insurance.

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) or Individual Applicant located in FEMA-designated special flood hazard areas is certifying that adequate flood insurance has been or will be obtained in the following situations:

- (1) for NSF grants for the construction of a building or facility, regardless of the dollar amount of the grant; and
- (2) for other NSF grants when more than \$25,000 has been budgeted in the proposal for repair, alteration or improvement (construction) of a building or facility.

Certification Regarding Responsible Conduct of Research (RCR)

(This certification is not applicable to proposals for conferences, symposia, and workshops.)

By electronically signing the Certification Pages, the Authorized Organizational Representative is certifying that, in accordance with the NSF Proposal & Award Policies & Procedures Guide, Part II, Award & Administration Guide (AAG) Chapter IV.B., the institution has a plan in place to provide appropriate training and oversight in the responsible and ethical conduct of research to undergraduates, graduate students and postdoctoral researchers who will be supported by NSF to conduct research. The AOR shall require that the language of this certification be included in any award documents for all subawards at all tiers.

CERTIFICATION PAGE - CONTINUED**Certification Regarding Organizational Support**

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is certifying that there is organizational support for the proposal as required by Section 526 of the America COMPETES Reauthorization Act of 2010. This support extends to the portion of the proposal developed to satisfy the Broader Impacts Review Criterion as well as the Intellectual Merit Review Criterion, and any additional review criteria specified in the solicitation. Organizational support will be made available, as described in the proposal, in order to address the broader impacts and intellectual merit activities to be undertaken.

Certification Regarding Federal Tax Obligations

When the proposal exceeds \$5,000,000, the Authorized Organizational Representative (or equivalent) is required to complete the following certification regarding Federal tax obligations. By electronically signing the Certification pages, the Authorized Organizational Representative is certifying that, to the best of their knowledge and belief, the proposing organization:

- (1) has filed all Federal tax returns required during the three years preceding this certification;
- (2) has not been convicted of a criminal offense under the Internal Revenue Code of 1986; and
- (3) has not, more than 90 days prior to this certification, been notified of any unpaid Federal tax assessment for which the liability remains unsatisfied, unless the assessment is the subject of an installment agreement or offer in compromise that has been approved by the Internal Revenue Service and is not in default, or the assessment is the subject of a non-frivolous administrative or judicial proceeding.

Certification Regarding Unpaid Federal Tax Liability

When the proposing organization is a corporation, the Authorized Organizational Representative (or equivalent) is required to complete the following certification regarding Federal Tax Liability:

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is certifying that the corporation has no unpaid Federal tax liability that has been assessed, for which all judicial and administrative remedies have been exhausted or lapsed, and that is not being paid in a timely manner pursuant to an agreement with the authority responsible for collecting the tax liability.

Certification Regarding Criminal Convictions

When the proposing organization is a corporation, the Authorized Organizational Representative (or equivalent) is required to complete the following certification regarding Criminal Convictions:

By electronically signing the Certification Pages, the Authorized Organizational Representative (or equivalent) is certifying that the corporation has not been convicted of a felony criminal violation under any Federal law within the 24 months preceding the date on which the certification is signed.

Certification Dual Use Research of Concern

By electronically signing the certification pages, the Authorized Organizational Representative is certifying that the organization will be or is in compliance with all aspects of the United States Government Policy for Institutional Oversight of Life Sciences Dual Use Research of Concern.

AUTHORIZED ORGANIZATIONAL REPRESENTATIVE		SIGNATURE		DATE
NAME Nancy S Daneau		Electronic Signature		Nov 16 2016 3:51PM
TELEPHONE NUMBER 212-998-2121	EMAIL ADDRESS osp.agency@nyu.edu		FAX NUMBER 212-995-4029	

COVER SHEET FOR PROPOSAL TO THE NATIONAL SCIENCE FOUNDATION

PROGRAM ANNOUNCEMENT/SOLICITATION NO./DUE DATE PD 98-1392 11/16/16		<input type="checkbox"/> Special Exception to Deadline Date Policy		FOR NSF USE ONLY NSF PROPOSAL NUMBER 1717188	
FOR CONSIDERATION BY NSF ORGANIZATION UNIT(S) (Indicate the most specific unit known, i.e. program, division, etc.) BCS - Biological Anthropology					
DATE RECEIVED	NUMBER OF COPIES	DIVISION ASSIGNED	FUND CODE	DUNS# (Data Universal Numbering System)	FILE LOCATION
11/16/2016	1	04040000 BCS	1392	003403953	08/29/2017 2:10pm S
EMPLOYER IDENTIFICATION NUMBER (EIN) OR TAXPAYER IDENTIFICATION NUMBER (TIN) 246000376		SHOW PREVIOUS AWARD NO. IF THIS IS <input type="checkbox"/> A RENEWAL <input type="checkbox"/> AN ACCOMPLISHMENT-BASED RENEWAL		IS THIS PROPOSAL BEING SUBMITTED TO ANOTHER FEDERAL AGENCY? YES <input type="checkbox"/> NO <input checked="" type="checkbox"/> IF YES, LIST ACRONYM(S)	
NAME OF ORGANIZATION TO WHICH AWARD SHOULD BE MADE Pennsylvania State Univ University Park		ADDRESS OF Awardee Organization, including 9 digit ZIP CODE Pennsylvania State Univ University Park 110 Technology Center Building University Park, PA. 168027000			
AWARDEE ORGANIZATION CODE (IF KNOWN) 0033290000					
NAME OF PRIMARY PLACE OF PERF The Pennsylvania State University		ADDRESS OF PRIMARY PLACE OF PERF, INCLUDING 9 DIGIT ZIP CODE The Pennsylvania State University 110 Technology Center University Drive ,PA ,168027000 ,US.			
IS AWARDEE ORGANIZATION (Check All That Apply) (See GPG II.C For Definitions)		<input type="checkbox"/> SMALL BUSINESS <input type="checkbox"/> FOR-PROFIT ORGANIZATION		<input type="checkbox"/> MINORITY BUSINESS <input type="checkbox"/> WOMAN-OWNED BUSINESS <input type="checkbox"/> IF THIS IS A PRELIMINARY PROPOSAL THEN CHECK HERE	
TITLE OF PROPOSED PROJECT Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini					
REQUESTED AMOUNT \$ 43,411	PROPOSED DURATION (1-60 MONTHS) 36 months	REQUESTED STARTING DATE 06/01/17	SHOW RELATED PRELIMINARY PROPOSAL NO. IF APPLICABLE		
THIS PROPOSAL INCLUDES ANY OF THE ITEMS LISTED BELOW <input checked="" type="checkbox"/> BEGINNING INVESTIGATOR (GPG I.G.2) <input type="checkbox"/> DISCLOSURE OF LOBBYING ACTIVITIES (GPG II.C.1.e) <input type="checkbox"/> PROPRIETARY & PRIVILEGED INFORMATION (GPG I.D, II.C.1.d) <input type="checkbox"/> HISTORIC PLACES (GPG II.C.2.j) <input type="checkbox"/> VERTEBRATE ANIMALS (GPG II.D.6) IACUC App. Date _____ PHS Animal Welfare Assurance Number _____ <input checked="" type="checkbox"/> FUNDING MECHANISM Research - other than RAPID or EAGER					
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PI/PD DEPARTMENT Anthropology		PI/PD POSTAL ADDRESS 116 Sparks Building			
PI/PD FAX NUMBER		University Park, PA 16802			
		United States			
NAMES (TYPED)	High Degree	Yr of Degree	Telephone Number	Email Address	
PI/PD NAME Christina M Bergey	PhD	2015	[REDACTED]	[REDACTED]	
CO-PI/PD					
CO-PI/PD					
CO-PI/PD					
CO-PI/PD					

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- (1) No Federal appropriated funds have been paid or will be paid, by or on behalf of the undersigned, to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with the awarding of any Federal contract, the making of any Federal grant, the making of any Federal loan, the entering into of any cooperative agreement, and the extension, continuation, renewal, amendment, or modification of any Federal contract, grant, loan, or cooperative agreement.
- (2) If any funds other than Federal appropriated funds have been paid or will be paid to any person for influencing or attempting to influence an officer or employee of any agency, a Member of Congress, an officer or employee of Congress, or an employee of a Member of Congress in connection with this Federal contract, grant, loan, or cooperative agreement, the undersigned shall complete and submit Standard Form-LLL, "Disclosure of Lobbying Activities," in accordance with its instructions.
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AUTHORIZED ORGANIZATIONAL REPRESENTATIVE		SIGNATURE		DATE
NAME Rocco Zinobile		Electronic Signature		Nov 16 2016 10:47AM
TELEPHONE NUMBER 814-865-7135	EMAIL ADDRESS raz11@psu.edu		FAX NUMBER 814-865-2805	

PROJECT SUMMARY

Overview:

Introggressive hybridization is a significant evolutionary force that has been documented or detected in groups throughout the primate order, including contemporaneous populations of Neandertals, Denisovans, and modern humans. The proposed study uses the very speciose tribe Cercopithecini ("guenons") to model the mechanics of introgressive hybridization through a primate radiation. Whole genome sequences will be collected for every species in the tribe. Noncoding regions - the majority of the genome - will be used to infer the overall species phylogeny, and subsequent analyses will compare this phylogeny against evolutionary trees constructed for individual genes/coding regions. Genes with incongruent patterns will be further analyzed to separate episodes of true introgressive hybridization from processes of lineage sorting or evolutionary convergence. Two main questions will be addressed: (1) Are greater levels of genetic exchange to be found between more closely related (e.g. congeneric) or more distantly related (e.g. intergeneric) forms? and (2) Are introgressed alleles likely to represent 'random' functional genes, or will many fall into distinct functional classes?

Intellectual Merit:

The proposed project is among the first to examine the effects of introgressive hybridization in primates through phylogenetic time. This work is the beginning of a planned series of investigations to search for commonalities in adaptive exchange through multiple primate radiations (stages 2 and 3 will focus on macaques and gibbons, respectively). Ultimately, patterns revealed among this and similar studies will speak to broader truths regarding the nature and importance of reticulation in the evolutionary process. For example, if the same sets of genes are found to be exchanged within multiple primate groups, such genes would by definition serve important roles as the adaptive engines of primate evolution. The analyses employed in this project will also yield the first empirical estimate of the proportion of a species' genome that may be an amalgamation of introgressed elements accumulated over evolutionary time. Another notable outcome of this study is the determination of a robust guenon phylogeny. A strongly-supported guenon tree provides an essential foundation to other studies, including evolutionary analysis of visual species recognition systems (i.e. the wide variety of facial coloration patterns among the guenons) and studies of the simian immunodeficiency virus (SIV), for which guenons are one of the main reservoirs.

Broader Impacts:

This project has a number of broader impacts as defined by the mission of the National Science Foundation. It broadens the participation of groups under-represented in science through a partnership with the McNair Scholars Program at Kent State (a program that identifies promising undergraduates who are first-generation, low-income and/or under-represented in PhD programs) and by working with other organizations that focus on similar groups of high school students, such as the Harlem Children's Society, BridgeUp:STEM, and ARISE in New York City. This project enhances infrastructure for research by making all analytical pipelines and software freely available under an open source license. Two other outcomes are more directly related to the project itself. First, the sequences gathered will add to the online database of diagnostic guenon molecular markers and thereby help to identify zoo hybrids and assist in captive management decisions. Second, the bioinformatics framework created for this study will be presented in a workshop at the annual conference of H3ABioNet, a pan-African bioinformatics group. The workshop, and associated "breakout sessions," will add to the bio-analytical capacity of the African based research network.

TABLE OF CONTENTS

For font size and page formatting specifications, see PAPPG section II.B.2.

	Total No. of Pages	Page No.* (Optional)*
Cover Sheet for Proposal to the National Science Foundation		
Project Summary (not to exceed 1 page)	1	_____
Table of Contents	1	_____
Project Description (Including Results from Prior NSF Support) (not to exceed 15 pages) (Exceed only if allowed by a specific program announcement/solicitation or if approved in advance by the appropriate NSF Assistant Director or designee)	15	_____
References Cited	8	_____
Biographical Sketches (Not to exceed 2 pages each)	2	_____
Budget (Plus up to 3 pages of budget justification)	6	_____
Current and Pending Support	1	_____
Facilities, Equipment and Other Resources	1	_____
Special Information/Supplementary Documents (Data Management Plan, Mentoring Plan and Other Supplementary Documents)	1	_____
Appendix (List below.) (Include only if allowed by a specific program announcement/ solicitation or if approved in advance by the appropriate NSF Assistant Director or designee)	_____	_____
Appendix Items:		

*Proposers may select any numbering mechanism for the proposal. The entire proposal however, must be paginated. Complete both columns only if the proposal is numbered consecutively.

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Budget (Plus up to 3 pages of budget justification)	5	_____
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Facilities, Equipment and Other Resources	1	_____
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Table of Contents	1	_____
Project Description (Including Results from Prior NSF Support) (not to exceed 15 pages) (Exceed only if allowed by a specific program announcement/solicitation or if approved in advance by the appropriate NSF Assistant Director or designee)	0	_____
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Title: Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini.

PROJECT DESCRIPTION

Note on resubmission

This is a twice-revised version of a proposal previously submitted to the NSF Biological Anthropology program, first in July 2015 and then March 2016. We made significant revisions in the earlier (second) submission, which included (1) operationalization of hypotheses into more clearly testable predictions, (2) justification of sample size and use of museum skins, and (3) expanded description of the broader impacts. The reviewers praised the improvements and noted, again, the transformative potential of a study that tracks genetic exchange through the evolutionary history of a primate radiation. The reviewers also made positive note of our comprehensive collection of guenon biomaterials and our very recent discovery of Y-chromosomal introgression between two species. The proposal was elevated to “Competitive B,” and the panel encouraged a few additional modifications and resubmission. We have addressed the remaining concerns and summarize our revisions below.

Expanded analyses of genetic exchange

In this submission, we have added methods such as the partitioned D test to determine the direction of gene flow between lineages. We include the use of the R package HybridCheck to detect and date introgression events, and to distinguish such events from those resulting from incomplete lineage sorting. We also more fully describe our approach for detecting “recent hybrid ancestry” (e.g. captive/zoo hybridization) – if any exists – through searches for large linkage blocks which would be hallmarks of a very recently admixed genome.

Revised stylistic elements of the writing

The components of proposal have been tied together with better transitioning. We have provided more detail in the explanation of methods. Redundant comments were removed without sacrificing the clarity of the independent proposal sections.

10X Chromium Genome library preparation for better assemblies

Though not a suggestion of the reviewers, we have updated the methods to take advantage of 10X Genomics’ new Chromium Genome library preparation, which allows for the sequencing of long strands of DNA (>10kb). This will allow us to assemble reads into much longer contigs, greatly improving our whole genome sequences.

INTRODUCTION

The evolutionary significance of introgressive hybridization

The ubiquity of hybridization between animal species is increasingly recognized, but its importance as an evolutionary force remains debated. Theory predicts that occasional mating between closely-related species can serve as a conduit for the exchange of beneficial alleles that have been “preadapted” when subject to natural selection in the original gene pool. Hybridization thus has the potential to increase the fitness of the recipient species via “adaptive introgression,” the transfer of beneficial alleles between species. In other situations, the alleles may lose their benefit when among the genetic background of the recipient population (*i.e.* negative epistasis),

making hybridization a dead-end (Arnold & Meyer 2006; Abott *et al.* 2013). Hybridization may also be a mechanism that cements the speciation process, as natural selection against less fit hybrid offspring spurs the evolution of prezygotic barriers between the incipient species (Abott *et al.* 2013). The relative importance of hybridization as a source of adaptive variation versus the final step in the speciation process remains debated in the post-genomic age.

Though botanists have long appreciated the pervasiveness of hybridization (Anderson 1949; Stebbins 1959), zoologists have only recently begun to consider hybridization anything more than an aberrant evolutionary dead-end. It is only with the recent sequencing of Neanderthal (Green *et al.* 2010; Prüfer *et al.* 2014) and Denisovan genomes (Reich *et al.* 2010) – revealing evidence of genetic exchange among these lineages and modern humans – that the majority of molecular anthropologists now give serious consideration to introgressive hybridization as a factor in the hominin radiation. The past few years have seen several publications that provide evidence for adaptive introgression of genomic regions related to skin and hair (Sankararaman *et al.* 2014; Vernot & Akey 2014) and immunity (Deschamps *et al.* 2016; Dannemann *et al.* 2016) from archaic hominin populations into the modern human gene pool. Despite the massive insight gained from recent studies of archaic hominin introgression, compelling questions remain concerning the mechanics of hybridization through a primate radiation:

- **Question 1: Are greater levels of genetic exchange to be found between more closely related or more distantly related forms?** Though the capacity for gene flow is greatest among most closely related forms (e.g. congeneric taxa), more deeply divergent taxa (e.g. different genera) are more genetically distinct and may therefore offer a wider pool of novel, potentially “pre-adapted” alleles which could be pulled through the contact zone via adaptive introgression. This greater evolutionary distance, however, also means a higher probability of incompatibilities with genetic background and greater potential for lowered fitness of hybrid offspring. Yet, as long as the progeny are not sterile they represent a potentially significant opportunity for the transfer of highly differentiated alleles. On the rare occasion that one of these alleles is beneficial, it might be very much so because it could represent a different adaptive peak in the evolutionary landscape of a genetic lineage (Wright 1932).
- **Question 2: Are introgressed alleles likely to represent “random” functional genes, possibly unique to each hybridization event, or will patterns of genes with similar functions be found to commonly cross between pairs of taxa?** After a hybridization event, deleterious variation is predicted to be eliminated, neutral variation will generally be lost to drift, and only adaptive variation is expected to introgress and spread to fixation. A functional *category* of genic regions that successfully introgresses likely has played an important role in the evolution of the radiation as it colonized new niches. In this way, such a radiation-wide analysis of the function of introgressed alleles allows insight into selection pressures. In guenons, some predictions for categories under ecological selection include those such as metabolic enzymes and regions of the genome involved in response to pathogens. Conversely, entire functional categories that show levels of introgression far below expectations from the rest of the genome may be resistant to introgression due to epistasis: the coadapted gene complexes lose their benefit when reshuffled by hybridization. Such epistatic complexes that co-evolved in a single genomic background and are resistant to interspecific transfer could be predicted to include neuroactive genes. Finally, genes underlying traits involved in species recognition, such as those for pelage patterns, would be expected to show very little introgression as these may be involved in reproductive isolation and reinforcement of speciation between close taxa.

The Cercopithecini as a Model System

The tribe Cercopithecini, also known as the “guenons,” is a remarkably diverse radiation of African monkeys that includes six genera: *Allenopithecus* (swamp monkeys), *Miopithecus* (talapoin), *Erythrocebus* (patas monkeys), *Chlorocebus* (vervets), *Allochrocebus* (the *preussi* superspecies), and *Cercopithecus* (a highly speciose group of arboreal monkeys) (Hart *et al.* 2012). They represent an excellent surrogate for testing the mechanics of introgressive hybridization in primates for several reasons.

The evolutionary depth and taxonomic diversity of the extant guenons provides an ideal framework for investigating the effects of divergence time on adaptive genetic exchange (**Question 1**). Indeed, the high level of exchange predicted among the guenons is likely near the upper limit for primates in general. Though uncommon, guenon genera that have been divergent for over 6 million years have produced hybrid offspring in captivity (Matsubayashi *et al.* 1978; Erhart *et al.* 2005) and in the wild (Galat *et al.* 1993; de Jong & Butynski 2010; Mekonnen *et al.* 2012). Guschanski *et al.* (2013) also argue from their recent study of guenon mitochondrial genomes that multiple episodes of ancestral hybridization occurred between lineages that are today recognized at the genus level. By comparison, interspecific hybrids representing different (congeneric) guenon species groups divergent at 3 to 5 million years (Tosi *et al.* 2005a; Hart *et al.* 2012) have been frequently observed across the *Cercopithecus* range (Detwiler *et al.* 2005 and references therein). The relative significance of hybridization between lineages at different divergence levels remains to be tested. Based on the widespread reports of interbreeding between members of different species groups, **we predict that whole genome comparisons of guenon species will reveal that the peak number of adaptive exchanges throughout the guenon radiation has occurred between lineages when they were at divergence depths of 3 to 5 million years.** If this same yardstick is applicable to the hominin radiation, it would suggest that all contemporaneous lineages from *Ardipithecus* through *Homo* were capable of adaptive introgression. Even the strictest interpretation of this argument would suggest that all contemporaneous forms of *Homo* were likely to have experienced some level of genetic exchange, ultimately leading to the question of how ‘admixed’ is the modern human genome.

A second reason the guenons are a useful model system is that the numerous species groups display considerable phenotypic, behavioral, and ecological diversity – variables that are thought to mediate levels of introgression. Many members of the genus *Cercopithecus* frequently travel and forage in polyspecific troops (Gautier-Hion 1988; Jaffe & Isbell 2011) making them a group of primates perpetually “poised” for interbreeding. The prevalence of opportunities for hybridization coupled with the vast diversity seen in the guenons leads to an important consequence with relevance to all primate radiations: a large number of interspecies exchanges will yield a broad distribution of introgressed genes by which to assess whether such genes are a random sample from the genome, or whether they fall into clusters with similar functions (**Question 2**). In other words, the adaptive divergence between guenon species groups leads to opportunities for adaptive introgression. This would provide important analogs to, for example, skin color divergence and subsequent introgression between modern humans and Neandertals and elimination by natural selection of other introgressed regions.

Evidence for such a phenomenon may have already been found in the guenons: early protein analyses (Ruvolo 1988) find that animals belonging to different species groups (*cephus* vs. *nictitans*) share electrophoretic variants of 6-phosphogluconate dehydrogenase and phosphoglucomutase-2, enzymes involved in glucose storage and harvest (Figure 1). While one cannot absolutely rule out convergence or differential lineage sorting, the fact the four species sharing these unique allozymes represent pairs of taxa known to hybridize – *C. cephus* x *C. nictitans* (Tutin 1999) and *C. ascanius* x *C. mitis* (Struhsaker *et al.* 1988; Detwiler 2002) – strongly suggests that introgression is the underlying explanation for such enzyme similarities. **Overall, we predict that (i) particular functional classes, rather than random genes, are important (frequent) categories of genomic elements exchanged, and (ii) these categories include genes associated with metabolism and immunity.**

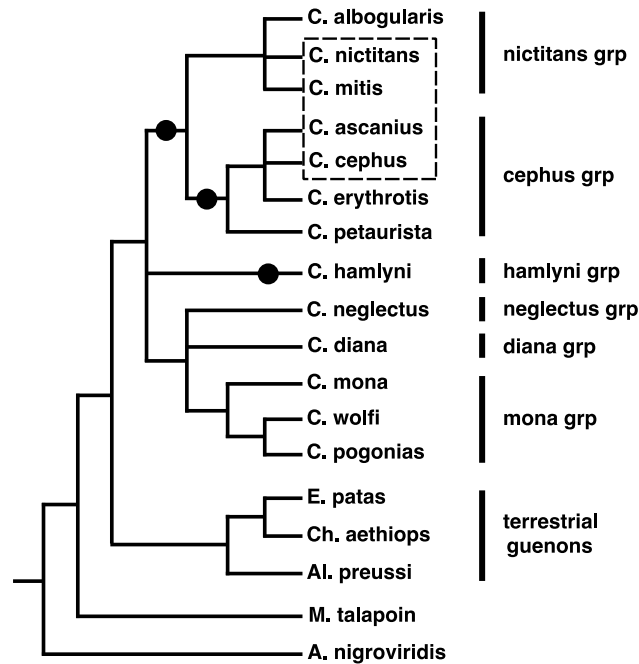


Figure 1. Guenon phylogeny depicting the relationships most commonly recovered from molecular analyses. The “terrestrial guenons” clade is supported by karyotype, autosomal, and X- and Y-chromosomal DNA research; however, analyses of complete mtDNA genomes (Guschanski *et al.* 2013) breaks this clade and adjoins the terrestrial forms to three separate internodes (black dots), highlighting possible episodes of ancestral introgression. Protein studies (Ruvolo 1988) cluster members of the *nictitans* and *cepus* species groups (dashed box) to the exclusion of other taxa within their respective groups – a pattern that may represent more recent introgression.

The third reason why guenons are an excellent system for modeling the possible effects of hybridization among primates is that strong evidence of introgression already exists. Beyond the enzyme patterns described above, there is another study even more robust. Members of the *nictitans* and *mona* groups are found to be reciprocally monophyletic in all genetic and blood protein studies, except one: widespread Y-chromosomal introgression has very recently been uncovered between *C. mitis* (*nictitans* group) and *C. denti* (*mona* group) in Central Africa (Tosi *et al.*, in prep.). This pattern cannot be attributed to differential lineage sorting; the small effective population size of the Y-chromosome (which is exacerbated by the wide variance in reproductive success among males) and the fact that it has high mobility due to male migration, means that it is very likely to reach fixation in the internodes between species divergences (Tosi *et al.* 2002, 2003a). Observational reports of guenon hybridization, coupled with these blood protein and Y-chromosome studies lead to strong predictions of reticulation between specific lineages. **We predict to find evidence of adaptive introgression between, at least: (1) *C. mitis* and *C. ascanius*, (2) *C. cephus* and *C. nictitans*, and (3) *C. mitis* and *C. denti*.** If the full mitochondrial tree published from museum skins is representative of the species tree (Guschanski *et al.* 2012), we also predict to find additional episodes of introgression between deep internodes that today represent distinct genera: specifically, introgression of early *Cercopithecus* with early members of each of *Chlorocebus*, *Allochrocebus*, and *Erythrocebus*.

Intellectual Merit

The proposed project will use guenons as a model to investigate the mechanics of introgressive hybridization in primates, including issues such as (i) the evolutionary depth at which the greatest amount of genetic exchange is expected and (ii) the functional categories of genes most likely to introgress. The results will, in turn, offer insight into the potential for introgressive hybridization across other groups, including the hominin radiation. However, the significance of this work reaches far beyond guenons and hominins. It is one of the earliest primate studies to examine genetic exchange through phylogenetic time and will therefore be the foundation for later such studies, potentially transformative for the field of primate phylogenomics. If investigations of other primate groups reveal common patterns – for example, if the same sets of functional genes are found to be exchanged through multiple radiations – this research will have identified much broader truths, including some key adaptive complexes driving the evolution of primates. With this in mind, our future goals include studies of other speciose groups: stage 2 will be an analysis of *Macaca*, and stage 3 will focus on the hylobatid radiation. Samples are already in hand for the former, and we are actively building a collection for the latter.

The collection of whole genome sequences as a foundation for this study will also provide the first empirical estimate of the proportion of a genome that may have evolved “*ex situ*.” In other words, assuming adaptive introgression occurs occasionally over evolutionary time, many lineages will have an accumulation of DNA sequence blocks that have integrated into their broader genomic background through a series of widely temporally spaced horizontal transfers. It is possible that such a ‘chimeric’ state of the genome is more the norm than the exception. **Such an investigation was impossible to undertake until now – when the sequencing of entire genomes across a species complex is technologically feasible.**

The proposed project benefits other branches of research by recovering the general species relationships among the tribe Cercopithecini, the largest catarrhine clade for which a robust phylogeny remains elusive. Despite overlapping ecologies and occasional hybridization, sympatric guenons maintain distinct phenotypes; with only one known exception (Detwiler 2002, Detwiler *et al.* 2005), persistent hybrid zones do not develop. Many researchers believe that the wide variety of facial coloration patterns in the guenons is one major mechanism maintaining this species integrity and, further, that it has evolved in response to potential hybridization among closely-related forms (Kingdon 1988; Allen *et al.* 2014; Allen & Higham 2015), putting the guenons among the strongest evidence supporting the controversial idea of “reinforcement.” To test this hypothesis, one must first know the phylogenetic relationships of the sympatric forms (Allen *et al.* 2014). Likewise, **a detailed understanding of guenon relationships is essential to studies of SIV**, the simian form of HIV. Guenons are one of the main reservoirs for the virus, and their evolutionary relationships are often invoked as the template on which to trace mutational changes in the virus. Furthermore, the *Cercopithecus* SIV phylogeny does not match the best estimates for that of the host guenons, suggesting that SIV strains did not coevolve with their hosts as they speciated, but were transmitted between species (Bibollet-Ruche *et al.* 2004). Again, a more robust understanding of guenon relationships allow for more accurate investigation of the evolution of this important zoonotic pathogen.

This is a potentially transformative project using cutting-edge techniques and an unprecedented collection of biomaterials to examine an under-represented evolutionary phenomenon that has affected many lineages, including hominins.

We consider the process of hybridization as a potentially significant creative force in evolution. To better understand its impacts, we will analyze a library of high-quality guenon biomaterials that is matched by few, if any, other research groups. Not only do we have high-quality materials from nearly every species in the tribe Cercopithecini, we are the only group with the extremely rare *C. sclateri*. We test our broad hypotheses on the nature of primate hybridization, as well as specific predictions on the guenon radiation, from a genomic viewpoint, using the latest sequencing technology and computational methodologies.

Broader Impacts

The proposed project meets several of the goals described in the mission of the National Science Foundation. Broader impacts of the proposal include (i) increasing the participation of under-represented groups, (ii) training high school, undergraduate, and graduate students in some of the latest scientific methods, (iii) holding bioinformatics workshops in countries that are home to guenon populations, (iv) expanding the database of diagnostic molecular markers across the guenon radiation, and (v) rapidly disseminating data and novel software.

This project will open new training opportunities for McNair Scholars at KSU. The McNair Scholars program is a federal TRIO program, and its purpose is to prepare undergraduates who are first-generation, low-income and/or underrepresented in science for entrance into graduate school. At KSU, one of the main components is an eight-week Summer Research Institute in which the students conduct original research under the guidance of a Faculty Mentor. Two McNair scholars would be invited into the Tosi laboratory as summer researchers and thereby learn some of the latest genomic techniques. NYU has similar outreach programs; several are designed to bring New York City high school students from underrepresented groups into active research laboratories to acquire hands-on training. Partner organizations involved in such efforts include the Harlem Children's Society, BridgeUP:STEM, and ARISE. Burrell would accept 3-5 students each summer and train them in laboratory techniques related to the proposed project. (Burrell has trained over a dozen high school students in the last 4 years.) He will also invite NYU undergraduate interns to join this project. The NYU Molecular Anthropology Laboratory has a long-standing, and competitive (<10% acceptance) internship program, and several of its participants have published peer-reviewed papers based on their research and continued on to graduate programs in anthropology, genetics, and medicine. (Bergey is, in fact, an alumnus of the program.) This project also includes support for one PhD student at KSU.

Upon completion of the research, we will hold a workshop at the annual meeting of H3ABioNet, a pan-African bioinformatics group. Demonstration of the statistical approaches and analytical pipelines used in our work will add to the scientific capacity of this research network. We will also hold "breakout sessions" in which we provide more directed training to interested African colleagues. We have already contacted Dr. Nicola Mulder, head of the H3ABioNet central node at the University of Cape Town and received approval to direct such training sessions.

The sequence data collected, research results, and newly-created bioinformatic tools will all be made publicly available through a combination of databases (e.g. NCBI Short Read Archive), publications, open source software repositories, and university websites. For example, Tosi has compiled on his laboratory website a list of diagnostic mutations of various guenon species, and this dataset has already led to the discovery of a hybrid zoo animal. The proposed research will expand the dataset, making it an increasingly useful tool for the detection and management of hybrids created in captivity. All analytical pipelines and software designed for this project will be made freely available under an open source license (GNU General Public License v3.0) in public repositories hosted on GitHub, as has been done previously by Bergey. Other scientific findings will be presented at professional meetings and in the popular media. Our past research uncovering the new species *C. lomamiensis*, for example, was featured by CNN, the BBC, and MSNBC. The complete genomes gathered in this project will be valuable to biomedical research, especially AIDs studies because many of these animals are natural hosts for SIV, the simian version of HIV.

Collaboration Components

The investigators are well qualified to undertake the proposed research on the basis of their combined background in guenon evolution, phylogenetics, and computational genomics, as evidenced by their many publications on these subjects. Components of this unique collaboration include Tosi's extensive research on guenons; Bergey and Burrell's extensive work with high throughput sequencing analysis; Bergey's bioinformatics skills and pre-built analytical pipelines;

Tosi's large collection of high quality guenon samples; Burrell's access to NYU Langone Medical Center's sequencing facilities, where sequencing can be done under cost; Bergery's access to High Performance Computing clusters; and Burrell's experience with museum skin processing.

METHODS

To answer our questions regarding the evolutionary mechanics of adaptive exchange, we will collect and analyze three datasets from an unprecedentedly thorough sampling of guenon taxa. The datasets include: (i) whole genome sequences, (ii) the protein-coding portion of genome ("exome"), and (iii) long-noncoding and putatively neutral stretches of orthologous DNA ("neutral loci"). The whole genome data will act as a backbone for the assembly of the exome and neutral datasets. For **Question 1** on the extent and timing of hybridization between species, orthologous loci from all three datasets will be aligned for phylogeny-based inference of introgression. The introgression analyses involve 1) inferring gene trees for coding and neutral loci; 2) "gene trees" from neutral loci to infer the "species tree"; and 3) using D and f statistics and extensions of these statistics with the inferred species tree to identify likely introgressed loci. To answer **Question 2** on the function of introgressed alleles, we will test if any loci from the exome sequences show outlier patterns of introgression. Statistical overrepresentation tests will be used to identify any functional classes of genes that are unexpectedly common among the inferred introgressed loci. The application of the analyses outlined below frequently overlaps for the three datasets, but each provides a unique window into the evolution of the Cercopithecini.

Samples

Given our phylogenetic approach to finding potentially introgressed areas of the genome, we do not need to have large sample sizes in order to find fixed or high-frequency alleles. Therefore, we will generate one whole genome sequence and three "exome-plus" datasets per species. "Exome-plus" refers to commercially-available kits (e.g., Roche SeqCap EZ Exome Plus Kit) that allow the capture of DNA from coding regions and untranslated regions (~64Mb) as well as custom specified neutral regions of the genome (up to 200Mb). We have selected the exome-plus approach, rather than whole genome sequencing because it is an inexpensive method to capture the genic regions whose possible transfer between species is most interesting. *We already have high quality biomaterials for at least one individual from 23 of the 26 guenon species* (Table I), and the majority are from wild or wild-born captive animals. The remaining three species will be collected from museum skins. In total, we will gather 23 whole genome sequences from high quality samples (three other genomes are already near completion) and roughly 80 exomes-plus, mainly from museum skins (three per species, with additional samples included for wide-ranging taxa such as *C. mitis* and *Ch. aethiops*.) The addition of the museum skin samples greatly enhances the project; however, **even if a significant percentage fail to yield usable DNA, we will still be able to complete the basic set of analyses with the data gathered from the high quality samples.** For museum specimens, we will select individuals from as wide a geographic spread as possible as a further measurement of fixation. We will collect samples from more than three museum specimens per species in order to maximize the number of samples yielding usable DNA. While no single museum contains samples of every guenon species, various combinations of the following six institutions have samples covering the entire radiation: American Museum of Natural History (USA), British Museum of Natural History (UK), National Museum of Natural History (USA), Royal Museum for Central Africa (Belgium), Field Museum of Natural History (USA), Museum National d'Histoire Naturelle (France). However, to maximize the taxonomic and geographic spread of our samples, we will attempt to visit all six institutions.

Table I. Guenon taxonomy following Grubb <i>et al.</i> (2003) ^a . High-quality biomaterials (blood and/or tissue) are already in hand for 23 of 26 taxa.	
<i>Allenopithecus nigroviridis</i>	<i>Cercopithecus mona</i> species group
<i>Allochocebus preussi</i>	<i>C. campbelli</i>
<i>Allochocebus l'hoesti</i>	<i>C. denti</i> ^{b,d}
<i>Allochocebus solatus</i>	<i>C. mona</i>
<i>Cercopithecus cephus</i> species group	<i>C. pogonias</i>
<i>C. ascanius</i>	<i>C. wolfi</i>
<i>C. cephus</i>	<i>Cercopithecus neglectus</i>
<i>C. erythrogaster</i> ^b	<i>Cercopithecus nictitans</i> species group
<i>C. erythrotis</i>	<i>C. albogularis</i>
<i>C. petaurista</i>	<i>C. mitis</i>
<i>C. sclateri</i> ^c	<i>C. nictitans</i>
<i>Cercopithecus diana</i>	<i>Chlorocebus aethiops</i>
<i>Cercopithecus dryas</i> ^b	<i>Erythrocebus patas</i>
<i>Cercopithecus hamlyni</i> species group	<i>Miopithecus talapoin</i>
<i>C. hamlyni</i>	<i>Miopithecus ogouensis</i>
<i>C. lomamiensis</i> ^{c,d}	

^a Exceptions to taxonomy of Grubb *et al.* (2003) include the addition of *C. lomamiensis* (discovered 2012), and the treatment of *C. albogularis*, *C. wolfi*, and *C. denti* as full species based on genetic studies (Tosi *et al.* 2005a; Tosi 2008; Hart *et al.* 2012; Tosi *et al.*, in prep).

^b Not represented in our high-quality biomaterials collection, but available as museum skins.

^c Rare samples. *C. sclateri* has not previously been included in any genetic analysis, and *C. lomamiensis* has been surveyed only once (Hart *et al.* 2012).

^d Sample potentially available from collaborators who have shared samples in the past.

Extraction, Library Preparation, and Sequencing

DNA extraction

High quality DNA will be extracted using MagAttract HWM DNA Kits (Qiagen) with modifications recommended by 10X Genomics (10X Genomics Manual CG00016). We require high molecular weight DNA for the 10X Genomics' Chromium library preparation (see "Library Preparation" below). DNA will be extracted from museum specimens following protocols outlined in Burrell *et al.* (2015). DNA quantity and quality will be verified using a Qubit 2.0 DNA fluorometer and an Agilent 2100 Bioanalyzer or TapeStation.

We do not anticipate contamination being a major problem with museum skins, for several reasons. First, we follow common, basic protocols during sample collection and DNA extraction to avoid cross contamination and to exclude exogenous DNA (such as that of human handlers on the surface of museum skins) (Burrell *et al.* 2015). Second, a major advantage of high-throughput sequencing of short reads is that there is no initial PCR amplification step which, when using Sanger sequencing, could easily lead to the mistaken amplification and sequencing of exogenous DNA (Burrell *et al.* 2015). Third, unlike ancient DNA recovered from biomaterials exposed to the environment, museum specimens will yield DNA that – while highly fragmented – is overwhelmingly from the targeted specimen (Rowe *et al.* 2011, Burrell *et al.* 2015). Fourth, our analyses are based on relatively long assemblies of individual short reads, not single nucleotide polymorphisms, making it easier to identify and filter out exogenous sequences.

Library Preparation

Whole Genome Library Preparation

All samples used for whole genome shotgun sequencing are at NYU or Kent State and are of high quality (*i.e.* blood or tissue). In order to generate better genome assemblies, we will use 10X Genomics' Chromium Genome library preparation to sequence relatively long blocks of DNA. Briefly, the Chromium Genome method involves isolating and then uniquely barcoding individual DNA molecules prior to Illumina short-read sequencing. This allows short reads to be assigned to relatively long stretches of DNA (possibly up to 1Mb, but we expect more like 10kb-50kb). The output is analogous to PacBio single molecule sequencing, although much less expensive and with lower error rates. We will outsource Chromium Genome library preparation to NYU Langone Medical Center's Genome Technology Center (GTC) which uses a Biomek SPRIWorks HT for automated library preparation.

Exome 'Plus' Library Preparation

In addition to whole genome sequencing, we propose to capture and sequence the "exome," the protein coding ~1% of the genome. Exome capture allows high coverage of unbiased sequence data, making it a promising technique for demographic inference that may represent a "sweet spot" between SNP arrays and whole genome resequencing (Teer & Mullikin 2010; Tennessen *et al.* 2011). Exomes may be a particularly fruitful compromise to whole genome sequencing for non-model organisms, since cross-species capture can yield sufficient coverage yet still be generated extremely cheaply and quickly. The human exome capture kit, for instance, has been successfully used to enrich the exomes of closely related primates (Vallender 2011; George *et al.* 2011; Jin *et al.* 2012; Bergey & Raaum 2012).

The protocol for exome capture first requires samples to be prepared as if for shotgun sequencing as above. After this, we will follow Roche's protocol for exome capture and enrichment. This targeted enrichment uses oligonucleotide baits, to 'fish' the protein-coding regions out of the 'pool' of genomic DNA (Ng *et al.* 2009; Choi *et al.* 2009). Briefly, this involves 1) hybridizing our sequencing library to exome probes; 2) pulling down hybridized exome probes/library DNA with capture beads; 3) washing away unbound library fragments; 4) amplifying the enriched fragment pool via PCR; and 5) quality control of amplified enriched library prior to sequencing.

The SeqCap EZ Exome Plus Kit (Roche) also allows researchers to include up to 100 Mb of custom target oligonucleotide baits. We will utilize that additional 100 million basepairs in two ways. First, we will add baits specific to the vervet genome (the only publicly available guenon) for exons that differ substantially from the human sequence. Though human exome capture kits have been used in catarrhines as well as platyrrhines with success even in regions of high divergence from humans (Vallender 2011; George *et al.* 2011; Jin *et al.* 2012; Bergey & Raaum 2012), we nonetheless will add in cercopithecine baits to minimize possible capture biases. To do this, we will bioinformatically compare the existing vervet genome sequence to the human and locate regions in the exome kit targets with high diversity ($> 5\%$). A subset of our custom bait allocation will be used to cover such regions with baits designed to match the vervet genome sequence, which will likely be within 5% of other members of the tribe Cercopithecini. Second, we will augment our dataset by designing tiled baits to capture long (~10 kb) non-coding regions. As described below, we will use these putatively neutral regions to infer phylogeny using "gene tree-species tree methods," minimizing the confounding impact of selection. Design of these baits will use the draft vervet genome as well as the first rounds of genomes we sequence to identify regions ideal for phylogenetic inference at the desired scale.

In the case of museum samples, we will modify library preparation protocols to follow Bi *et al.* (2013) and Burrell *et al.* (2015). The basic adaptation for library preparation using museum samples is to carefully assess the quality and quantity of the DNA extracted from museum

specimens. Two to three times more initial DNA may be needed compared to library preparation using high-quality sequences to offset the highly fragmented and damaged nature of DNA from museum specimens (Burrell *et al.* 2015).

Sequencing

We will be using the Illumina HiSeq 4000 High Output platform with 2x100bp paired-end sequencing and TruSeq v4 chemistry, which is capable of generating over ~100 Gb per lane. We will sequence a whole genome in 1 lane for ~45x sequence depth coverage after filtration. Exomes (~100 Mb of capture probes) will be multiplexed (6 per lane) for an average sequenced depth of 40-50x. All sequencing and library quality control (QC) will be done at the NYU Langone Medical Center's GTC.

Bioinformatic Methods Common to All Datasets

The following bioinformatic analyses are common to all three datasets: whole genome sequences, exome sequences, and long non-coding stretches.

Read Mapping and Variant Identification

Reads will be mapped to the closest reference genome or to whole genomes generated as part of this study using BWA mem with default parameters (Li & Durbin 2009). Based on the mapping locations, we will then assemble overlapping reads using ABySS (Simpson *et al.* 2009), and then remap the reads to these assembled contigs. After realignment around indels using GATK (DePristo *et al.* 2011), variants will be called for all individuals mapped to a given genome simultaneously using GATK's UnifiedGenotyper, which uses a Bayesian genotype likelihood model to estimate genotypes and their frequencies in one or multiple samples and filtered with GATK's VariantFiltration based on several criteria to reduce the impact of sequencing errors or repetitive regions (DePristo *et al.* 2011). The steps for mapping and variant calling are encapsulated in the NGS-map pipeline, developed in the NYU Molecular Anthropology Laboratory and available online. This pipeline has successfully analyzed whole genome as well as exome sequences on both NYU's High Performance Computing Cluster and AWS cloud, most recently analyzing over 500 mosquito genomes (*Anopheles gambiae*) in addition to previous primate sequences.

Quality Filtration

We will perform both stringent and relaxed filtering to ensure our results are robust to methodological biases. These will include: excluding sequences that are known to be parts of segmental duplications in humans and other primates, excluding genes that we suspect of being duplicates given high levels of heterozygosity and the results of copy number prediction from the exome sequences themselves, removing of sequences that are orthologs of suspected copy number variants in the whole genome sequences generated in this study, and excluding sequences with aberrantly high or low coverage. Sequences of orthologous loci will be assembled for use in phylogeny and analyses of selection. Quality scores will be retained to allow similar variable filtration when inferring gene trees.

Whole Genome Sequence and Exome Analysis

Introgression analyses

A major goal of the project is to detect and quantify introgression between closely related members of the Cercopithecini radiation and determine if the transferred alleles have known functional associations. As hybridization results in a mosaic genome with heterogeneous levels of gene flow across the genome, introgression or incomplete sorting of ancestral variation can be inferred from incongruences in phylogenetic “gene trees” based on disparate parts of the genome. If these hybridization events are between deeply divergent taxa, they are easily detected using phylogenetic methods, by noting incongruences in gene trees. We will do so, as described in the section below. Such an approach has already been fruitfully applied in the guenons (Tosi *et al.* 2005a; Tosi *et al.* 2005b; Tosi *et al.* 2003a) and the proposed study would infer guenon phylogeny using long blocks of noncoding DNA (as described in later section).

Though hybridization between distant species is easily detected by [major] discordance between trees from different parts of the genome, detecting introgression between closely related species, which still may share polymorphism from their recent common ancestor, is more difficult. This has led to the development of a class of simple tests for introgression. Such methods are powerful despite their simplicity and have been used to infer introgression in various taxa, most famously, hominins (Green *et al.* 2010). In the present study, we propose to apply these statistics to detect and quantify introgression among the more closely related members of tribe Cercopithecini. To date the introgression events and distinguish between shared variation due to introgression and that due to retention of ancestral polymorphism, we will use estimates of the size of introgressed tracts and the divergence therein.

D statistic

One of the easiest methods for detecting possible introgression is to test for an excess of shared derived alleles in an alignment of four taxa (Kulathinal *et al.* 2009; Green *et al.* 2010). Sequences from two populations, P_1 and P_2 , are compared to a third, P_3 , using a fourth, P_4 , as an outgroup. For each taxon in the phylogeny, alleles are determined to be ancestral (“A”) or derived (“B”) and the proportion of sites which show the “ABBA” pattern and which show the “BABA” pattern in the four taxa are computed. In the absence of gene flow, the ABBA and BABA patterns should be of equal frequency. Patterson’s D statistic is used to test for deviation from that null hypothesis, or asymmetry, with D expected to be 0 if no introgression is detected and $E(D) > 0$ if admixture from P_3 to P_2 has occurred (Green *et al.* 2010; Durand *et al.* 2011). Block jackknifing can then be used to compute a standard error for the D statistic (Green *et al.* 2010).

We propose to compute the D statistic for quartets of guenons in the inferred overall species-level phylogeny with the highest support, excluding the comparison of pairs of taxa which diverged long enough ago to allow polymorphic variation to fix and for which we will use phylogenetic methods as described below. This will give us an overall view of the presence and directionality of gene flow. Such information on the presence or absence of introgression will then be interpreted within the context of guenon range overlap, ecological preference, and divergence times, allowing us to answer **Question 1** concerning the relationship between levels of genetic exchange and the evolutionary distance between guenon taxa. The D statistic is implemented in software such as ADMIXTOOLS (Patterson *et al.* 2012) and ANGSD (Korneliussen *et al.* 2014).

Though the D -statistic as originally conceived is a simple, yet powerful technique for detecting introgression, a positive value only denotes that introgression occurred and can say nothing of its directionality. We will also use an extension of the original D statistic, the partitioned D statistic, which uses five taxa to compare counts of the following configurations: ABBA vs. BABAA and ABBBA vs. BABBA (Eaton and Ree 2013). With the original D statistic, these three comparisons will allow us to control for shared ancestry among the guenons to improve phylogenetic resolution and to use the introgression of shared ancestral alleles to infer

directionality in gene flow between guenon species.

***f* estimators**

The *D* statistic is able to detect genome-wide introgression but is considerably biased when erroneously used to quantify amount of introgression or identify introgressed alleles (Martin *et al.* 2014). *D* is unreliable when computed in small sliding windows across the genome. Since it is inflated when the effective population size (N_e) is low, *D* outliers tend to fall in regions with overall low diversity (d_{xy}) (Martin *et al.* 2014). Several more robust statistics have been proposed to estimate *f*, the proportion of the genome shared between species, including \hat{f}_d (Green *et al.* 2010; Martin *et al.* 2014). \hat{f}_d can identify specific introgressed alleles.

We will compute \hat{f} statistics to quantify the amount of gene flow between guenon species at specific loci. Again, such results will be interpreted within the context of guenon range overlap, ecological preference, and divergence times. The estimator is implemented in ADMIXTOOLS (Patterson *et al.* 2012). We will compare the magnitude of introgression to evolutionary divergence between taxa, further exploring **Question 1**.

Additionally, we will annotate SNPs with known functional information gathered from other cercopithecine primate reference genomes such as that of the rhesus macaque and vervet using the database of functional annotations, PANTHER, (Mi *et al.* 2013) and a custom script that has been written by C.B. We will then do enrichment tests to determine if various functional categories are enriched for high or low levels of introgression (Mann-Whitney *U*). Doing so will allow us to answer **Question 2** on whether introgressing alleles or those that do not cross species boundaries are biased towards certain functional classes.

Recombination

Hybridization is expected to result in large, mosaic linkage blocks in F1 individuals. These linkage blocks will then be broken up over time by recombination. Therefore, genomic scans for linkage can shed light on the occurrence and timing of past episodes of admixture, at least until recombination thoroughly breaks down the linkage blocks. We will use the R package HybridCheck (Ward and van Oosterhout 2016) to detect, date, and visualize any recent or moderately old admixture events. Here, we are interested in HybridCheck's inference of linkage blocks. It detects these via a sliding window analysis of nucleotide variation in sets of aligned sequence triplets. The probability that a linkage block is introgressed is estimated via a binomial mass equation that determines whether nucleotide similarity within a linkage block shared by two individuals is significantly higher than the genome-wide average. HybridCheck infers the timing of introgression of a linked block by counting mutations within the block and assuming a mutation rate. In addition to the gene tree divergence dating detailed below, HybridCheck will allow us to detect and date possible introgression events using our whole genome dataset. For samples from individuals who were not wild-born, such methods will also permit our identification and exclusion of individuals with recent hybridization that occurred in artificial, captive environments.

Gene Tree Inference and Divergence Dating

Reliable phylogenetic trees are necessary for comparative evolutionary studies. The systematics of the anthropoids is still not completely resolved, and the **guenons represent the largest catarrhine clade for which a robust phylogeny remains elusive**. We have much combined experience inferring phylogenies and divergence dates (Tosi *et al.* 2000; Tosi *et al.* 2003a; Tosi *et al.* 2003b; Tosi *et al.* 2004; Tosi *et al.* 2005a; Tosi *et al.* 2005b; Tosi & Coke 2007; Tosi 2008; Burrell *et al.* 2009; Hodgson *et al.* 2009; Hart *et al.* 2012; Pozzi *et al.* 2014a; Pozzi *et al.* 2014b), which we will apply to estimating phylogenies for genes and their surrounding regions captured as part of the exome.

We plan to infer phylogenies from long, phylogenetically informative putatively neutral loci as well as from individual coding loci. For the putatively neutral loci, we will select >2,000 non-

genic loci from the nuclear genome following a strategy similar to Carbone *et al.* (2014) but with the intent of obtaining longer non-genic loci for better tree inference. The non-genic loci will be at least 50 kb away from the nearest exon with at least 5 kb of sequence fully called in all individuals.

We will infer phylogenies for each locus using MrBayes (Ronquist *et al.* 2012) with an appropriate model of evolution and model parameters estimated using MrModeltest (Nylander 2004). A pipeline for model selection, parameter estimation, and Bayesian tree inference with MrBayes has already been established on NYU's High Performance Computing Cluster.

In addition to inferring phylogenies for individual loci, we plan to use phylogenetic trees ('gene trees') from many loci to infer the overall guenon 'species tree.' Each locus has its own evolutionary history, which—due largely to gene flow or differential sorting—may or may not coincide with other loci in the genome. Individual gene tree incongruence with the species tree is more likely in recent radiations like the guenons (Degnan & Rosenberg 2009). As multilocus datasets have become more easily available, methods have been developed to take trees inferred from multiple, independent datasets and infer an overall species tree that best represents the evolutionary history of a set of organisms (Knowles 2009). No coalescent-based gene tree–species tree program yet explicitly incorporates genetic exchange between lineages as well as differential lineage sorting, unfortunately. However, one gene tree-species tree program, BUCKY (Larget *et al.* 2010), does Bayesian concordance analyses of sets of trees to estimate what proportion of the genome supports each possible node in the species tree without assumptions as to the cause of tree incongruence. This approach is appropriate for the guenons.

Divergence dates will be estimated for a series of trees whose topology follows that of the species tree identified in the gene tree-species tree analysis using the software BEAST (Drummond *et al.* 2012). Orthologous outgroup taxa will be included in the analyses. Branch lengths will be calibrated using a series of fossil constraints as identified in (Pozzi *et al.* 2014c).

TIMELINE OF ACTIVITY

Expected duration: three years (June 2017-May 2020).

Phase I: Sample collection. Obtain samples from museums. Begins June 2017; likely end: early 2018.

Phase II: Data collection. Extract DNA, create libraries, DNA sequencing. This would extend between years one and two (early 2018 to fall 2018).

Phase III: Data analysis & dissemination of results. Initial bioinformatic processing of data (mapping, SNP calling, etc) would occur immediately in order to judge data quality. After bioinformatic screening, we expect data analysis to occur primarily in years two and three (fall 2018-May 2020), with publications and other dissemination (conferences, media) primarily occurring in year three and after.

RESULTS OF PRIOR NSF SUPPORT

ANTHONY TOSI:

(a) Award #BCS 0715281, \$209,814 effective August 1, 2007 and expired July 31, 2011, co-PI with Todd Disotell (PI), New York University

(b) Title: Molecular Systematics of the Mangabeys (*Cercocebus* and *Lophocebus*)

(c) Summary of the Results

Intellectual Merit:

This project inferred the diphyletic origin of the mangabeys with strong statistical support in almost all datasets. Conflicting signals from different regions of the genome suggested that *Cercocebus* was polyphyletic grouping *Mandrillus* with *C. galeritus* and *C. sanjei* for some loci suggesting a complex evolutionary history within the *Cercocebus-Mandrillus* clade.

Broader Impacts:

A high school student took part in this project which also produced 3 Masters theses. This project resulted in a number of publications, conference papers, and a peer-reviewed software package freely available to the public. (Note that Andrew Burrell and Christina Bergey also contributed to this project, see bold text below.)

(d) Publications resulting from the NSF award

-Burrell AS, Jolly CJ, **Tosi AJ**, Disotell TR. 2009. Genetic data suggest the kipunji mangabey (*Rungwecebus kipunji*) is hybrid in origin. *Am J Phys Anthropol* Suppl:99.

-Burrell AS, Jolly CJ, **Tosi AJ**, Disotell TR. 2009. Mitochondrial evidence for the hybrid origin of the kipunji, *Rungwecebus kipunji* (Primates: Papionini). *Mol Phylogenet Evol* 51:340-348.

-Burrell AS, Jolly CJ, Phillips-Conroy JE, Disotell TR. 2010. Conflicting mitochondrial and Y-chromosomal phylogenies indicate complex evolutionary history of *Papio* baboons. *Am J Phys Anthropol* Suppl 5:74.

-Canedo AP, **Burrell AS**, Jagoda E, Bergey CM, **Tosi AJ**, Disotell TR. 2010. Phylogenetic relationships of the mangabeys inferred from analyses of multiple independent loci. *Am J Phys Anthropol* Suppl: 76.

-Bergey CM. 2011. *AluHunter*: a database of potentially polymorphic *Alu* insertions for use in primate phylogeny and population genetics. *Bioinformatics* 27:2924-2925.

(e) Results have been presented at the American Association of Physical Anthropologists annual meetings, and in scientific talks at New York University, Yale University, Kyoto University, and CUNY. All code written for the project is available in a public repository.

CHRISTINA BERGEY:

(a) Award #1260816, \$31,226.00 effective March 1, 2013 and expired February 28, 2015

(b) Title: Doctoral Dissertation Improvement: The Effect of Interspecific Hybridization on MHC Diversity in Wild Baboons

(c) Summary of the Results

Intellectual merit:

The project characterized the nature of the hybrid zone found between two species of baboons (genus *Papio*) in Ethiopia and tested whether specific portions of the genome are preferentially introgressing across the species boundary and whether regions that differ markedly between the species may underlie their specific traits. We sequenced hundreds of individuals at thousands of locations spread randomly throughout the genome and found loci that differ from the neutral background which could be candidates for adaptive introgression or associated with reproductive isolation. Some such functional categories are biomedically important, such as pathways related to neurotransmitters that are known to influence behavior in humans and other animals. For instance, the dopamine mediated signaling pathway was enriched for regions of high differentiation between the parental species. Various pathways related to serotonin were found to be outliers for biased introgression among the hybrids; such pathways are worthy of further study to better understand the evolutionary impact of hybridization. Additionally, they are of interest for their connection to various human disorders, such as Parkinson's Disease.

Broader impacts:

The work on the project, both laboratory and computational, resulted in the training of several female undergraduates some of whom have decided to pursue a degree in genomics or a related field. The computational pipeline will be made freely available and published under an open source license.

(d) Publications resulting from the NSF award

- **Bergey CM**, Phillips-Conroy JE, Disotell TR, & Jolly CJ. (2016). A dopamine pathway is highly diverged in primate species that differ markedly in social behavior. *Proceedings of the National Academy of Sciences*, 113:22, 6178–6181.
- **Bergey CM**, Phillips-Conroy JE, Disotell TR, & Jolly CJ (2014). Hybrid zone genomics: The structure of a baboon contact zone inferred from RAD tags. (Abstract). *American Journal of Physical Anthropology*, 153, Supplement 58, 76-77.
- **Bergey, CM**. Dissertation: Population genomics of a baboon hybrid zone. (2015). New York University.

(e) The results of the study have been presented at several professional conferences. Associated manuscripts have been submitted for publication. All code written for the project is being made available in a public repository under an open source license.

Andy Burrell: No NSF Support within the previous five years

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- Tosi AJ, Morales JC & Melnick DJ. (2000). Comparison of Y chromosome and mtDNA phylogenies leads to unique inferences of macaque evolutionary history. *Molecular Phylogenetics and Evolution*. **17**:133-144.
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- Tosi AJ, Melnick DJ & Disotell TR. (2004). Sex chromosome phylogenetics indicate a single transition to terrestriality in the guenons (tribe *Cercopithecini*). *Journal of Human Evolution*. **46**:223–237.
- Tosi AJ, Detwiler KM & Disotell TR. (2005a). X-chromosomal window into the evolutionary history of the guenons. *Molecular Phylogenetics and Evolution*. **36**:58-66.
- Tosi AJ, Detwiler KM & Disotell TR. (2005b). Y-chromosomal Markers Suitable for Noninvasive Studies of Guenon Hybridization. *International Journal of Primatology*. **26**:685–696.
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- Wright S. (1932). The roles of mutation, inbreeding, crossbreeding, and selection in evolution. *Proceedings of the Sixth International Conference on Genetics*. pp. 355-366.

ANTHONY J. TOSI

PROFESSIONAL PREPARATION

Beloit College	Beloit, WI	Molecular Biology	B.Sc. 1994
Columbia University	New York, NY	Biological Anthropology	M.A, M.Phil, Ph.D 1995, 1997, 2000

APPOINTMENTS

2014-present	Assistant Professor , Department of Anthropology, Kent State University
2008-2014	Criminalist III , Low-Copy DNA Group, Department of Forensic Biology, Office of Chief Medical Examiner, New York City
2001-2008	Research Scientist , Center for the Study of Human Origins, Department of Anthropology, New York University
2000-2001	Research Scientist , Primate Research Institute, Department of Cellular & Molecular Biology, Kyoto University (Japan)

PUBLICATIONS MOST CLOSELY RELATED TO PROJECT

2012	Hart JA, Detwiler KM, Gilbert CC, Burrell AS, Fuller JL, Emetshu M, Hart TB, Vosper A, Sargis EJ, & Tosi AJ . Lesula: A new species of <i>Cercopithecus</i> monkey endemic to the Democratic Republic of Congo and implications for conservation of Congo's Central Basin. <i>PLoS ONE</i> . 7 : e44271.
2009	Kamilar JM, Martin SK, & Tosi AJ . Combining biogeographic and phylogenetic data to examine primate speciation: an example using cercopithecine monkeys. <i>Biotropica</i> . 41 :514-519.
2008	Tosi AJ . Forest monkeys and Pleistocene refugia: a phylogeographic window onto the disjunct distribution of the <i>Chlorocebus lhoesti</i> species group. <i>Zoological Journal of the Linnean Society</i> . 154 :408-418.
2007	Xing J, Wang H, Zhang Y, Ray DA, Tosi AJ , Disotell TR, & Batzer MA. A mobile element-based evolutionary history of guenons (tribe Cercopithecini). <i>BMC Biology</i> . 5 :5.
2005	Tosi AJ , Detwiler KM, & Disotell TR. X-chromosomal window onto the evolutionary history of the guenons (Primates: Cercopithecini). <i>Molecular Phylogenetics and Evolution</i> . 36 :58-66.

OTHER PUBLICATIONS / MANUSCRIPTS

2016	Tosi AJ & Detwiler KM. The efficacy of sex chromosomal markers in studies of <i>Cercopithecus</i> hybridization: discovery of a captive hybrid and applications in wild populations. <i>Zoo Biology</i> . 35 :61-64.
2015	Liedigk R, Kolleck J, Böker KO, Meijaard E, Md-Zain BM, Abdul-Latiff MAB, Ampeng A, Lakim M, Abdul-Patah P, Tosi AJ , Brameier M, Zinner D, & Roos C. Mitogenomic phylogeny of the common long-tailed macaque (<i>Macaca fascicularis fascicularis</i>). <i>BMC Genomics</i> . 16 :222.

- 2009 Burrell AS, Jolly CJ, **Tosi AJ**, & Disotell TR. Mitochondrial evidence for the hybrid origin of the kipunji, *Rungwecebus kipunji* (Primates: Papionini). *Molecular Phylogenetics and Evolution*. **51**:340-348.
- 2006 **Tosi AJ**, Detwiler KM, & Clifford SL. X-chromosomal synapomorphies provide a non-invasive test for introgression among *Cercopithecus* monkeys. *Conservation Genetics*. **7**:803-805.
- 2005 **Tosi AJ**, Detwiler KM, & Disotell TR. Y-chromosomal markers suitable for non-invasive studies of guenon hybridization. *International Journal of Primatology*. **26**:683-694.

SYNERGISTIC ACTIVITIES

Expert Witness Testimony (Forensic Biology & DNA Analysis) – testified 23 times from 2009 to 2014 in New York City Supreme Court (assaults & homicides).

Guenon Synapomorphies Database – created a database of synapomorphies that define various evolutionary groups within the tribe Cercopithecini. These can be used to monitor allelic movement between interbreeding taxa from different clades (e.g. species groups), and to identify hybrid animals inadvertently created in captivity. Database can be accessed at <https://www.kent.edu/anthropology/tosi-laboratory/guenon-synapomorphies>.

International Scholars Program – presently developing a *graduate-level* visiting scholar program with the Primate Research Institute of Kyoto University (two students sent to Japan in summers 2015 and 2016).

Primate Conservation – performing genetic analyses to identify evolutionarily distinct taxa (e.g. new species such as *Cercopithecus lomamiensis*) in Central Africa, a collaborative effort with morphologists, behavioral scientists, and ecologists.

Forensic Anthropology Minor – presently developing a minor in Forensics at Kent State University in collaboration with colleagues in the Anthropology and Sociology departments.

ANDREW STEPHEN BURRELL

A. Professional Preparation

Amherst College	Biology	B. A.	1995
New York University	Anthropology	Ph. D.	2009
New York University	Anthropology	Postdoc	2009-present

B. Appointments

2009-present	<i>Research Scientist</i> , Anthropology Department, New York University
2002-3; 2008	<i>Research Assistant</i> , Anthropology Department, New York University
2001-2002	<i>Editorial Assistant</i> , Journal of Human Evolution
1996-1998	<i>Laboratory Technician</i> , Department of Anatomy, Physiology, and Genetics, Uniformed Services University of the Health Sciences

C. Products

i. Closely related to the project:

- 2015 **Burrell AS**, Disotell TR, Bergey CM. The use of museum specimens with high-throughput sequencers. *Journal of Human Evolution* 79: 35-44.
- 2014 Pozzi L, Bergey CM, **Burrell AS**. The use (and misuse) of phylogenetic trees in comparative behavioral analyses. *Int. Journal of Primatology*. 35: 32-54.
- 2012 Hart JA, Detwiler KM, Gilbert CC, **Burrell AS**, Fuller JL, Emetshu M, Hart TB, Vosper A, Sargis E, Tosi AJ. Lesula: a new species of *Cercopithecus* monkey endemic to the Democratic Republic of Congo and implications for conservation of Congo's Central Basin. *PLoS ONE* 7: e44271.
- 2009 **Burrell AS**, Jolly CJ, Tosi AJ, Disotell TR. Mitochondrial evidence for the hybrid origin of the kipunji, *Rungwecebus kipunji* (Primates: Papionini). *Molecular Phylogenetics and Evolution* 51: 340-348.
- 2005 Detwiler KM, **Burrell AS**, Jolly CJ. Conservation implications of hybridization in African cercopithecine monkeys. *International Journal of Primatology* 26: 661-684.

ii. Other products

- 2014 Pozzi L, Hodgson JA, **Burrell AS**, Sterner KN, Raaum RL, Disotell TR. Primate phylogenetic relationships and divergence dates inferred from complete mitochondrial genomes. *Molecular Phylogenetics and Evolution* 75: 15-183.
- 2013 Bergey CM, Pozzi L, Disotell TR, **Burrell AS**. A new method for genome-wide marker development and genotyping holds great promise for molecular primatology. *International Journal of Primatology* 34: 303-314.
- 2011 Pozzi L, Hodgson JA, **Burrell AS**, Disotell TR. *Saadanius*: stem fossils cannot date the origins of crown groups. *Journal of Human Evolution* 61: 209-210.

- 2011 Jolly CJ, **Burrell AS**, Phillips-Conroy JE, Bergey C, Rogers J. Kinda baboons (*Papio kindae*) and grayfoot chacma baboons (*P. ursinus griseipes*) hybridize in the Kafue River Valley, Zambia. *American Journal of Primatology* 73: 291-303.
- 2009 **Burrell AS**, Disotell TR. Panmixia postponed: ancestry-related assortative mating in contemporary human populations. Minireview in *Genome Biology* 10: 245.

D. Synergistic activities

NYU Molecular Anthropology Undergraduate Internship Program: developed a program at NYU to train undergraduates in molecular genetic laboratory techniques (DNA extraction, PCR amplification, gel electrophoresis, DNA library preparation for high-throughput sequencing), data analysis, and manuscript preparation (2012-present).

Database of baboon biogeography: reviewed archival and scientific literature to find provenienced references for baboon (*Papio* sp.) presence in Africa and Arabia in order to build accurate picture of past and present baboon distribution. Over 1300 georeferenced sites obtained. Will be unprecedented resource for baboon (or possibly primate) biogeography.

Elementary School Educational outreach: Career days in Manhattan Chinatown elementary school, Yung Wing Elementary School (PS 124): speak about biological anthropology – and science - as a career at a predominantly immigrant Chinese community school. (2011-2014); NYU program (2012)...., Golden Pond School kindergarten (2015)

High School Summer Research Training: ARISE program at NYU (summers 2015 - 2016). Take New York City and New York region high school students (4) into our lab to learn basic molecular genetic laboratory techniques and to develop a project using environmental DNA (eDNA) as biomarkers for assessing ecological conditions at various locations in New York City.

Biographical Sketch
Christina M. Bergey

Department of Anthropology, Pennsylvania State University, e-mail: cxb585@psu.edu,

(a) Professional Preparation

New York University, New York, NY; Anthropology; B.A., 2009

New York University, New York, NY; Anthropology; M.A., 2011

New York University, New York, NY; Anthropology; Ph.D., 2015

University of Notre Dame, Notre Dame, IN; Dept. of Bio. Sciences; Postdoctoral Researcher, 2015–2016

Pennsylvania State University, University Park, PA; Dept. of Anthropology; Postdoctoral Researcher, 2016–

(b) Appointments

2016–: **Postdoctoral Scholar**, Pennsylvania State University, University Park, PA

2015–2016: **Postdoctoral Scholar**, University of Notre Dame, Notre Dame, IN

(c) Publications

1. **Bergey CM**, Phillips-Conroy JE, Disotell TR, & Jolly CJ (2016). A dopamine pathway is diverged in primate species that differ markedly in social behavior. *Proceedings of the National Academy of Sciences*, 113 (22): 6178-6181.
2. **Bergey CM**, Pozzi L, Disotell TR, & Burrell AS (2013). A new method for genome-wide marker development and genotyping holds great promise for molecular primatology. *International Journal of Primatology*, 34 (2): 303-314.
3. **Bergey CM** & Raaum RL (2012). A test of cross-species exome sequencing in the rhesus macaque (*Macaca mulatta*). (Abstract). *American Journal Physical Anthropology*, 147, Supplement 54, 97.
4. Burrell AS, Disotell TR, & **Bergey CM** (2015). The use of museum specimens with high-throughput DNA sequencers. *Journal of Human Evolution*. 79, 35-44.
5. Pozzi L, **Bergey CM**, & Burrell AS (2013). The use (and misuse) of phylogenies in investigating primate behavior. *International Journal of Primatology*, 35 (1): 32-54.
1. Hodgson JA, **Bergey CM**, & Disotell TR (2010). Neandertal Genome: The Ins and Outs of African Genetic Diversity. *Current Biology*. 20 (12): R517-R519.
2. Jolly CJ, Burrell AS, Phillips-Conroy JE, **Bergey C**, & Rogers J (2011). Kinda baboons (*Papio kindae*) and grayfoot chacma baboons (*P. ursinus griseipes*) hybridize in the Kafue River valley, Zambia. *American Journal of Primatology*, 73: 291-303.
3. Burrell AS, Jolly CJ, **Bergey CM**, Phillips-Conroy J, Rogers J, & Disotell TR (2013). Kinda baboons in phylogenetic and paleogeographic perspective. (Abstract). *American Journal of Physical Anthropology*, 150, Supplement 56, 74.
4. Pickett SB, **Bergey CM**, & Di Fiore AF (2012). A metagenomic study of primate diet diversity. *American Journal of Primatology*, 74 (7):622-631.
5. **Bergey CM** (2011). AluHunter: a database of potentially polymorphic Alu insertions for use in primate phylogeny and population genetics. *Bioinformatics*, 27 (20): 2924-2925.

(d) Synergistic Activities

- 1. Community service:** (i) Curriculum developer for “BridgeUp: STEM” at the American Museum of Natural History, two courses for female low-income New York City youth to explore computer science and bioinformatics using the museum’s scientific datasets (ii) Contributor to open source projects, with all research analytical code released upon publication under an open source license.
- 2. Mentoring:** (i) Mentor to numerous graduate, undergraduate, and high school students, providing training in bioinformatic and laboratory analyses.
- 3. Teaching:** (i) Curriculum developer, Instructor for “Harlem Childrens Society Bioinformatics Class,” a summer-long course on bioinformatics computer programming for New York City public high school students. (ii) Course assistant for “Topical Seminar: Phylogenetic Methods.” Department of Anthropology, New York University. (iii) Teaching assistant for “Human Evolution.” Department of Anthropology, New York University.

SUMMARY PROPOSAL BUDGET

YEAR 1

ORGANIZATION Kent State University				FOR NSF USE ONLY			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Anthony Tosi				PROPOSAL NO.	DURATION (months)		
				AWARD NO.	Proposed	Granted	
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	Funds granted by NSF (if different)
	CAL	ACAD	SUMR				
1.	0.00	0.00	0.00				
2.							
3.							
4.							
5.							
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)	0.00	0.00	0.00		0		
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)	0.00	0.00	0.00		0		
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS	0.00	0.00	0.00		0		
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)	0.00	0.00	0.00		0		
3. (1) GRADUATE STUDENTS					16,995		
4. (0) UNDERGRADUATE STUDENTS					0		
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)					0		
6. (0) OTHER					0		
TOTAL SALARIES AND WAGES (A + B)					16,995		
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)					4,758		
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)					21,753		
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT					0		
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)					2,415		
2. INTERNATIONAL					6,374		
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$		0					
2. TRAVEL		0					
3. SUBSISTENCE		0					
4. OTHER		0					
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS					0		
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES					2,520		
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION					0		
3. CONSULTANT SERVICES					0		
4. COMPUTER SERVICES					0		
5. SUBAWARDS					0		
6. OTHER					0		
TOTAL OTHER DIRECT COSTS					2,520		
H. TOTAL DIRECT COSTS (A THROUGH G)					33,062		
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 50.0000, Base: 33062)							
TOTAL INDIRECT COSTS (F&A)					16,531		
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)					49,593		
K. SMALL BUSINESS FEE					0		
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)					49,593		
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$			
PI/PI NAME Anthony Tosi				FOR NSF USE ONLY			
ORG. REP. NAME* Susan Tribuzzo				INDIRECT COST RATE VERIFICATION			
				Date Checked	Date Of Rate Sheet	Initials - ORG	

SUMMARY PROPOSAL BUDGET

YEAR 2

ORGANIZATION Kent State University				FOR NSF USE ONLY				
				PROPOSAL NO.	DURATION (months)			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Anthony Tosi				AWARD NO.		Proposed	Granted	
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months			Funds Requested By proposer	Funds granted by NSF (if different)
				CAL	ACAD	SUMR		
1.				0.00	0.00	0.00		
2.								
3.								
4.								
5.								
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0	
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				0.00	0.00	0.00	0	
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)								
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0	
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0	
3. (1) GRADUATE STUDENTS							23,170	
4. (0) UNDERGRADUATE STUDENTS							0	
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0	
6. (0) OTHER							0	
TOTAL SALARIES AND WAGES (A + B)							23,170	
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							6,073	
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							29,243	
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)								
TOTAL EQUIPMENT							0	
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							0	
2. INTERNATIONAL							0	
F. PARTICIPANT SUPPORT COSTS								
1. STIPENDS \$ _____ 0								
2. TRAVEL _____ 0								
3. SUBSISTENCE _____ 0								
4. OTHER _____ 0								
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0	
G. OTHER DIRECT COSTS								
1. MATERIALS AND SUPPLIES							5,020	
2. PUBLICATION COSTS/DOCUMENTATION/DISSEMINATION							0	
3. CONSULTANT SERVICES							0	
4. COMPUTER SERVICES							0	
5. SUBAWARDS							0	
6. OTHER							25,650	
TOTAL OTHER DIRECT COSTS							30,670	
H. TOTAL DIRECT COSTS (A THROUGH G)							59,913	
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 50.0000, Base: 59913)								
TOTAL INDIRECT COSTS (F&A)							29,957	
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							89,870	
K. SMALL BUSINESS FEE							0	
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							89,870	
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$				
PI/PI NAME Anthony Tosi				FOR NSF USE ONLY				
ORG. REP. NAME* Susan Tribuzzo				INDIRECT COST RATE VERIFICATION				
				Date Checked	Date Of Rate Sheet	Initials - ORG		

2 *ELECTRONIC SIGNATURES REQUIRED FOR REVISED BUDGET

SUMMARY PROPOSAL BUDGET

YEAR 3

ORGANIZATION Kent State University				FOR NSF USE ONLY		
				PROPOSAL NO.	DURATION (months)	
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Anthony Tosi				AWARD NO.		
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer
				CAL	ACAD	SUMR
1.		0.00	0.00	0.00		
2.						
3.						
4.						
5.						
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)		0.00	0.00	0.00		0
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)		0.00	0.00	0.00		0
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)						
1. (0) POST DOCTORAL SCHOLARS		0.00	0.00	0.00		0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)		0.00	0.00	0.00		0
3. (1) GRADUATE STUDENTS						5,835
4. (0) UNDERGRADUATE STUDENTS						0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)						0
6. (0) OTHER						0
TOTAL SALARIES AND WAGES (A + B)						5,835
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)						846
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)						6,681
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)						
TOTAL EQUIPMENT						0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)						1,500
2. INTERNATIONAL						5,000
F. PARTICIPANT SUPPORT COSTS						
1. STIPENDS \$		0				
2. TRAVEL		0				
3. SUBSISTENCE		0				
4. OTHER		0				
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS						0
G. OTHER DIRECT COSTS						
1. MATERIALS AND SUPPLIES						5,020
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION						2,500
3. CONSULTANT SERVICES						0
4. COMPUTER SERVICES						0
5. SUBAWARDS						0
6. OTHER						25,650
TOTAL OTHER DIRECT COSTS						33,170
H. TOTAL DIRECT COSTS (A THROUGH G)						46,351
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 50.0000, Base: 46351)						
TOTAL INDIRECT COSTS (F&A)						23,176
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)						69,527
K. SMALL BUSINESS FEE						0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)						69,527
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$		
PI/PI NAME Anthony Tosi				FOR NSF USE ONLY		
ORG. REP. NAME* Susan Tribuzzo				INDIRECT COST RATE VERIFICATION		
		Date Checked	Date Of Rate Sheet	Initials - ORG		

SUMMARY PROPOSAL BUDGET

Cumulative

ORGANIZATION Kent State University				FOR NSF USE ONLY			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Anthony Tosi				PROPOSAL NO.	DURATION (months)		
				AWARD NO.	Proposed	Granted	
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	Funds granted by NSF (if different)
				CAL	ACAD	SUMR	
1.				0.00	0.00	0.00	
2.							
3.							
4.							
5.							
6. () OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0
7. (0) TOTAL SENIOR PERSONNEL (1 - 6)				0.00	0.00	0.00	0
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0
3. (3) GRADUATE STUDENTS							46,000
4. (0) UNDERGRADUATE STUDENTS							0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0
6. (0) OTHER							0
TOTAL SALARIES AND WAGES (A + B)							46,000
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							11,677
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							57,677
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT							0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							3,915
2. INTERNATIONAL							11,374
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$ 0							
2. TRAVEL 0							
3. SUBSISTENCE 0							
4. OTHER 0							
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES							12,560
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION							2,500
3. CONSULTANT SERVICES							0
4. COMPUTER SERVICES							0
5. SUBAWARDS							0
6. OTHER							51,300
TOTAL OTHER DIRECT COSTS							66,360
H. TOTAL DIRECT COSTS (A THROUGH G)							139,326
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE)							
TOTAL INDIRECT COSTS (F&A)							69,664
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							208,990
K. SMALL BUSINESS FEE							0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							208,990
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$			
PI/PI NAME Anthony Tosi				FOR NSF USE ONLY			
ORG. REP. NAME* Susan Tribuzzo				INDIRECT COST RATE VERIFICATION			
				Date Checked	Date Of Rate Sheet	Initials - ORG	

C *ELECTRONIC SIGNATURES REQUIRED FOR REVISED BUDGET

Kent State University Budget Justification

A. Senior Personnel:

Salary support is not requested for Anthony Tosi, Principal Investigator

B. Other Personnel:

ONE Graduate Assistant will be supported on this project. The graduate student will assist with wet-lab operations related to library prep (*e.g.* DNA extraction, quantitation)

(1) Graduate Student, PhD candidate, Biological Anthropology

Student will contribute:

9 Mo. AY Yr1

3 Mo. Sum Yr2 & 9 Mo. AY Yr2

3 Mo. Sum Yr3

C. Fringe Benefits:

Kent State University's fringe benefit rates are based on actual costs. Fringe benefits for Graduate Student academic appointments varies by pay rate and classification and includes retirement, worker's compensation, insurance and Medicare. GA AY appointment is projected to begin at 28% and includes insurance, retirement, worker's compensation and Medicare. GA summer appointment fringe rate is 14.5% and includes retirement, worker's compensation and Medicare. Benefits have been budgeted in accordance with Kent State University policy.

D. Equipment: No equipment is requested. \$0

E. Travel Costs: \$15,289

International

(Europe: UK, France, Belgium) \$6,374

Airfare for museum skin collection. (\$2,695)

Food & lodging (shared room), \$182.50 per day. Two weeks. (\$2,555)

Museum bench fees. \$75 per day. Twelve days total. (\$900)

Local travel. \$16 per day. Two weeks total. (\$224)

Travel to Africa to attend H3ABioNet Conference (location TBD) \$5000

Domestic

(Chicago, Boston, D.C.) \$2,415

Airfare for museum skin collection (3 trips, \$250/trip). (\$750)

Food & lodging (shared room), \$175 per day. Nine days. (\$1,575)

Local travel. \$10 per day. Nine days total. (\$90)

Academic Conferences \$1,500

F. Participant Support: No participant support is requested. \$0

G. Other Direct Costs

G1. Materials and Supplies: \$12,560

Consumables (\$210/month for 36 months) \$7,560

McNair Scholars \$5,000
(\$2,500 is requested for each of two summers)

G2. Publication Costs/Documentation/Dissemination \$2,500

G3. Consultant Services. \$0.

No funds are requested for consultant services.

G4. Computer Services. \$0

No funds are requested for computer services.

G5. Subcontracts. \$0

No funds are requested for subcontracts.

G6. Other Direct Costs: \$51,300

Other Professional Fees

ExomePlus Library Prep and Sequencing of 82 individuals: \$45,100
\$300 for library prep and \$250 for 128Mb per sample
(Split each – Yrs 2 & 3)

Data Storage: Local and long-term cloud storage: \$6,200
(\$3,100 each – Yrs 2 & 3)

I. Indirect Costs

Kent State University's indirect cost rate for organized research is 50.0% MTDC per DHHS negotiated agreement of 06/23/2014.

SUMMARY PROPOSAL BUDGET

YEAR 1

ORGANIZATION New York University				FOR NSF USE ONLY			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Andrew Burrell				PROPOSAL NO.	DURATION (months)		
				AWARD NO.	Proposed	Granted	
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	Funds granted by NSF (if different)
				CAL	ACAD	SUMR	
1. Andrew Burrell - Research Scientist				0.12	0.00	0.00	581
2.							
3.							
4.							
5.							
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				0.12	0.00	0.00	581
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0
3. (0) GRADUATE STUDENTS							0
4. (0) UNDERGRADUATE STUDENTS							0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0
6. (0) OTHER							0
TOTAL SALARIES AND WAGES (A + B)							581
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							0
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							581
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT							0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							2,415
2. INTERNATIONAL							11,374
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$ _____ 0							
2. TRAVEL _____ 0							
3. SUBSISTENCE _____ 0							
4. OTHER _____ 0							
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES							22,733
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION							0
3. CONSULTANT SERVICES							0
4. COMPUTER SERVICES							0
5. SUBAWARDS							0
6. OTHER							0
TOTAL OTHER DIRECT COSTS							22,733
H. TOTAL DIRECT COSTS (A THROUGH G)							37,103
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 58.5000, Base: 37103)							
TOTAL INDIRECT COSTS (F&A)							21,705
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							58,808
K. SMALL BUSINESS FEE							0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							58,808
M. COST SHARING PROPOSED LEVEL \$ 0 AGREED LEVEL IF DIFFERENT \$							
PI/PI NAME Andrew Burrell				FOR NSF USE ONLY			
ORG. REP. NAME* Nancy Daneau				INDIRECT COST RATE VERIFICATION			
				Date Checked	Date Of Rate Sheet	Initials - ORG	

SUMMARY PROPOSAL BUDGET

YEAR **2**

ORGANIZATION New York University				FOR NSF USE ONLY			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Andrew Burrell				PROPOSAL NO.	DURATION (months)		
				AWARD NO.	Proposed	Granted	
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	Funds granted by NSF (if different)
				CAL	ACAD	SUMR	
1. Andrew Burrell - Research Scientist				0.12	0.00	0.00	581
2.							
3.							
4.							
5.							
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				0.12	0.00	0.00	581
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0
3. (0) GRADUATE STUDENTS							0
4. (0) UNDERGRADUATE STUDENTS							0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0
6. (0) OTHER							0
TOTAL SALARIES AND WAGES (A + B)							581
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							0
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							581
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT							0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							750
2. INTERNATIONAL							0
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$ 0							
2. TRAVEL 0							
3. SUBSISTENCE 0							
4. OTHER 0							
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES							45,467
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION							0
3. CONSULTANT SERVICES							0
4. COMPUTER SERVICES							0
5. SUBAWARDS							0
6. OTHER							0
TOTAL OTHER DIRECT COSTS							45,467
H. TOTAL DIRECT COSTS (A THROUGH G)							46,798
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 58.5000, Base: 46798)							
TOTAL INDIRECT COSTS (F&A)							27,377
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							74,175
K. SMALL BUSINESS FEE							0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							74,175
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$			
PI/PI NAME Andrew Burrell				FOR NSF USE ONLY			
ORG. REP. NAME* Nancy Daneau				INDIRECT COST RATE VERIFICATION			
				Date Checked	Date Of Rate Sheet	Initials - ORG	

2 *ELECTRONIC SIGNATURES REQUIRED FOR REVISED BUDGET

SUMMARY PROPOSAL BUDGET

YEAR 3

ORGANIZATION New York University				FOR NSF USE ONLY			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Andrew Burrell				PROPOSAL NO.	DURATION (months)		
				AWARD NO.	Proposed	Granted	
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	Funds granted by NSF (if different)
				CAL	ACAD	SUMR	
1. Andrew Burrell - Research Scientist				0.12	0.00	0.00	581
2.							
3.							
4.							
5.							
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				0.12	0.00	0.00	581
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0
3. (0) GRADUATE STUDENTS							0
4. (0) UNDERGRADUATE STUDENTS							0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0
6. (0) OTHER							0
TOTAL SALARIES AND WAGES (A + B)							581
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							0
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							581
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT							0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							750
2. INTERNATIONAL							0
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$ _____ 0							
2. TRAVEL _____ 0							
3. SUBSISTENCE _____ 0							
4. OTHER _____ 0							
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES							0
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION							0
3. CONSULTANT SERVICES							0
4. COMPUTER SERVICES							0
5. SUBAWARDS							0
6. OTHER							0
TOTAL OTHER DIRECT COSTS							0
H. TOTAL DIRECT COSTS (A THROUGH G)							1,331
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 58.5000, Base: 1331)							
TOTAL INDIRECT COSTS (F&A)							779
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							2,110
K. SMALL BUSINESS FEE							0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							2,110
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$			
PI/PI NAME Andrew Burrell				FOR NSF USE ONLY			
ORG. REP. NAME* Nancy Daneau				INDIRECT COST RATE VERIFICATION			
				Date Checked	Date Of Rate Sheet	Initials - ORG	

SUMMARY PROPOSAL BUDGET

Cumulative

ORGANIZATION New York University				FOR NSF USE ONLY			
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Andrew Burrell				PROPOSAL NO.		DURATION (months)	
				AWARD NO.		Proposed	Granted
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	
				CAL	ACAD	SUMR	Funds granted by NSF (if different)
1. Andrew Burrell - Research Scientist				0.36	0.00	0.00	1,743
2.							
3.							
4.							
5.							
6. () OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				0.36	0.00	0.00	1,743
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0
3. (0) GRADUATE STUDENTS							0
4. (0) UNDERGRADUATE STUDENTS							0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0
6. (0) OTHER							0
TOTAL SALARIES AND WAGES (A + B)							1,743
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							0
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							1,743
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT							0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							3,915
2. INTERNATIONAL							11,374
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$ 0							
2. TRAVEL 0							
3. SUBSISTENCE 0							
4. OTHER 0							
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES							68,200
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION							0
3. CONSULTANT SERVICES							0
4. COMPUTER SERVICES							0
5. SUBAWARDS							0
6. OTHER							0
TOTAL OTHER DIRECT COSTS							68,200
H. TOTAL DIRECT COSTS (A THROUGH G)							85,232
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE)							
TOTAL INDIRECT COSTS (F&A)							49,861
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							135,093
K. SMALL BUSINESS FEE							0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							135,093
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$			
PI/PI NAME Andrew Burrell				FOR NSF USE ONLY			
ORG. REP. NAME* Nancy Daneau				INDIRECT COST RATE VERIFICATION			
				Date Checked	Date Of Rate Sheet	Initials - ORG	

C *ELECTRONIC SIGNATURES REQUIRED FOR REVISED BUDGET

Budget justification – NYU

Senior Personnel

\$1742

Andrew Burrell, Co-Investigator (0.12 person-months for years 1,2, and 3): Will be responsible for directing and participating in NYU wet-lab operations related to library prep; museum skin and sample acquisition; data analysis & interpretation; manuscript writing.

Minor equipment **\$0**

No equipment is requested.

Travel

Domestic

\$3915

Two domestic meetings for Burrell (\$750 each) in Years 2 and 3. \$1500

Travel to 3 museums to sample specimens in Year 1.

Airfare for museum skin collection (3 trips, \$250/trip).	\$750
Food & lodging, \$175 per day. Nine days.	\$1575
Local travel, \$10 per day. Nine days.	\$90

International (Europe)

\$11374

Travel to London, Paris, and Brussels to sample museum specimens in Year 1.

Airfare for museum skin collection.	\$2695
Food & lodging, \$182.50 per day. Two weeks.	\$2555
Museum bench fees. \$75 per day. Twelve days.	\$900
Local travel, \$16 per day. Two weeks.	\$224

Travel to Africa to attend H3ABionet Conference (location TBD) \$5000

Materials and Supplies

Whole genome library preparation including Quality Control (NYU Medical School's Genome Technology Center, [GTC]) Years 1 and 2	\$68,200
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\$3100 for 10X Chromium Genome library prep and Illumina HiSeq 4000 sequencing per sample, x 22 samples

SUMMARY PROPOSAL BUDGET

YEAR 1

ORGANIZATION Pennsylvania State Univ University Park				FOR NSF USE ONLY		
				PROPOSAL NO.	DURATION (months)	
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Christina Bergey				AWARD NO.		
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer
	CAL	ACAD	SUMR			Funds granted by NSF (if different)
1.	0.00	0.00	0.00			
2.						
3.						
4.						
5.						
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)	0.00	0.00	0.00		0	
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)	0.00	0.00	0.00		0	
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)						
1. (0) POST DOCTORAL SCHOLARS	0.00	0.00	0.00		0	
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)	0.00	0.00	0.00		0	
3. (0) GRADUATE STUDENTS					0	
4. (0) UNDERGRADUATE STUDENTS					0	
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)					0	
6. (0) OTHER					0	
TOTAL SALARIES AND WAGES (A + B)					0	
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)					0	
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)					0	
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)						
TOTAL EQUIPMENT					0	
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)					0	
2. INTERNATIONAL					5,000	
F. PARTICIPANT SUPPORT COSTS						
1. STIPENDS \$		0				
2. TRAVEL		0				
3. SUBSISTENCE		0				
4. OTHER		0				
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS					0	
G. OTHER DIRECT COSTS						
1. MATERIALS AND SUPPLIES					0	
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION					0	
3. CONSULTANT SERVICES					0	
4. COMPUTER SERVICES					0	
5. SUBAWARDS					0	
6. OTHER					0	
TOTAL OTHER DIRECT COSTS					0	
H. TOTAL DIRECT COSTS (A THROUGH G)					5,000	
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE)						
MTDC (Rate: 57.2000, Base: 5000)						
TOTAL INDIRECT COSTS (F&A)					2,860	
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)					7,860	
K. SMALL BUSINESS FEE					0	
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)					7,860	
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$		
PI/PI NAME				FOR NSF USE ONLY		
Christina Bergey				INDIRECT COST RATE VERIFICATION		
ORG. REP. NAME*				Date Checked	Date Of Rate Sheet	Initials - ORG
Rocco Zinobile						

SUMMARY PROPOSAL BUDGET

YEAR 2

ORGANIZATION				FOR NSF USE ONLY			
Pennsylvania State Univ University Park				PROPOSAL NO.	DURATION (months)		
					Proposed	Granted	
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Christina Bergey				AWARD NO.			
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer	Funds granted by NSF (if different)
				CAL	ACAD	SUMR	
1. Christina M Bergey - PI				2.00	0.00	0.00	8,295
2.							
3.							
4.							
5.							
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				2.00	0.00	0.00	8,295
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)							
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0
3. (0) GRADUATE STUDENTS							0
4. (0) UNDERGRADUATE STUDENTS							0
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0
6. (0) OTHER							0
TOTAL SALARIES AND WAGES (A + B)							8,295
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							2,132
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							10,427
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)							
TOTAL EQUIPMENT							0
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							1,500
2. INTERNATIONAL							0
F. PARTICIPANT SUPPORT COSTS							
1. STIPENDS \$ _____ 0							
2. TRAVEL _____ 0							
3. SUBSISTENCE _____ 0							
4. OTHER _____ 0							
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0
G. OTHER DIRECT COSTS							
1. MATERIALS AND SUPPLIES							0
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION							0
3. CONSULTANT SERVICES							0
4. COMPUTER SERVICES							0
5. SUBAWARDS							0
6. OTHER							0
TOTAL OTHER DIRECT COSTS							0
H. TOTAL DIRECT COSTS (A THROUGH G)							11,927
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE) MTDC (Rate: 57.2000, Base: 11927)							
TOTAL INDIRECT COSTS (F&A)							6,822
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							18,749
K. SMALL BUSINESS FEE							0
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							18,749
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$			
PI/PI NAME Christina Bergey				FOR NSF USE ONLY			
ORG. REP. NAME*				INDIRECT COST RATE VERIFICATION			
Rocco Zinobile				Date Checked	Date Of Rate Sheet	Initials - ORG	

2 *ELECTRONIC SIGNATURES REQUIRED FOR REVISED BUDGET

SUMMARY PROPOSAL BUDGET

YEAR 3

ORGANIZATION				FOR NSF USE ONLY		
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR				PROPOSAL NO.		DURATION (months)
AWARD NO.				Proposed		Granted
Pennsylvania State Univ University Park Christina Bergey						
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer
				CAL	ACAD	SUMR
1. Christina M Bergey - PI				2.00	0.00	0.00
2.						
3.						
4.						
5.						
6. (0) OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				2.00	0.00	0.00
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)						
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00
3. (0) GRADUATE STUDENTS						
4. (0) UNDERGRADUATE STUDENTS						
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)						
6. (0) OTHER						
TOTAL SALARIES AND WAGES (A + B)						
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)						
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)						
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)						
TOTAL EQUIPMENT						
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)						
2. INTERNATIONAL						
F. PARTICIPANT SUPPORT COSTS						
1. STIPENDS \$ _____ 0						
2. TRAVEL _____ 0						
3. SUBSISTENCE _____ 0						
4. OTHER _____ 0						
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS						
G. OTHER DIRECT COSTS						
1. MATERIALS AND SUPPLIES						
2. PUBLICATION COSTS/DOCUMENTATION/DISEMINATION						
3. CONSULTANT SERVICES						
4. COMPUTER SERVICES						
5. SUBAWARDS						
6. OTHER						
TOTAL OTHER DIRECT COSTS						
H. TOTAL DIRECT COSTS (A THROUGH G)						
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE)						
MTDC (Rate: 57.2000, Base: 10688)						
TOTAL INDIRECT COSTS (F&A)						
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)						
K. SMALL BUSINESS FEE						
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)						
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$		
PI/PI NAME				FOR NSF USE ONLY		
Christina Bergey				INDIRECT COST RATE VERIFICATION		
ORG. REP. NAME*				Date Checked	Date Of Rate Sheet	Initials - ORG
Rocco Zinobile						

SUMMARY PROPOSAL BUDGET

Cumulative

ORGANIZATION Pennsylvania State Univ University Park				FOR NSF USE ONLY					
PRINCIPAL INVESTIGATOR / PROJECT DIRECTOR Christina Bergey				PROPOSAL NO.		DURATION (months)			
				AWARD NO.		Proposed	Granted		
A. SENIOR PERSONNEL: PI/PI, Co-PI's, Faculty and Other Senior Associates (List each separately with title, A.7. show number in brackets)				NSF Funded Person-months		Funds Requested By proposer		Funds granted by NSF (if different)	
				CAL	ACAD	SUMR			
1. Christina M Bergey - PI				4.00	0.00	0.00	16,798		
2.									
3.									
4.									
5.									
6. () OTHERS (LIST INDIVIDUALLY ON BUDGET JUSTIFICATION PAGE)				0.00	0.00	0.00	0		
7. (1) TOTAL SENIOR PERSONNEL (1 - 6)				4.00	0.00	0.00	16,798		
B. OTHER PERSONNEL (SHOW NUMBERS IN BRACKETS)									
1. (0) POST DOCTORAL SCHOLARS				0.00	0.00	0.00	0		
2. (0) OTHER PROFESSIONALS (TECHNICIAN, PROGRAMMER, ETC.)				0.00	0.00	0.00	0		
3. (0) GRADUATE STUDENTS							0		
4. (0) UNDERGRADUATE STUDENTS							0		
5. (0) SECRETARIAL - CLERICAL (IF CHARGED DIRECTLY)							0		
6. (0) OTHER							0		
TOTAL SALARIES AND WAGES (A + B)							16,798		
C. FRINGE BENEFITS (IF CHARGED AS DIRECT COSTS)							4,317		
TOTAL SALARIES, WAGES AND FRINGE BENEFITS (A + B + C)							21,115		
D. EQUIPMENT (LIST ITEM AND DOLLAR AMOUNT FOR EACH ITEM EXCEEDING \$5,000.)									
TOTAL EQUIPMENT							0		
E. TRAVEL 1. DOMESTIC (INCL. U.S. POSSESSIONS)							1,500		
2. INTERNATIONAL							5,000		
F. PARTICIPANT SUPPORT COSTS									
1. STIPENDS \$ 0									
2. TRAVEL 0									
3. SUBSISTENCE 0									
4. OTHER 0									
TOTAL NUMBER OF PARTICIPANTS (0) TOTAL PARTICIPANT COSTS							0		
G. OTHER DIRECT COSTS									
1. MATERIALS AND SUPPLIES							0		
2. PUBLICATION COSTS/DOCUMENTATION/DISSEMINATION							0		
3. CONSULTANT SERVICES							0		
4. COMPUTER SERVICES							0		
5. SUBAWARDS							0		
6. OTHER							0		
TOTAL OTHER DIRECT COSTS							0		
H. TOTAL DIRECT COSTS (A THROUGH G)							27,615		
I. INDIRECT COSTS (F&A)(SPECIFY RATE AND BASE)									
TOTAL INDIRECT COSTS (F&A)							15,796		
J. TOTAL DIRECT AND INDIRECT COSTS (H + I)							43,411		
K. SMALL BUSINESS FEE							0		
L. AMOUNT OF THIS REQUEST (J) OR (J MINUS K)							43,411		
M. COST SHARING PROPOSED LEVEL \$ 0				AGREED LEVEL IF DIFFERENT \$					
PI/PI NAME Christina Bergey				FOR NSF USE ONLY					
ORG. REP. NAME* Rocco Zinobile				INDIRECT COST RATE VERIFICATION					
				Date Checked		Date Of Rate Sheet		Initials - ORG	

C *ELECTRONIC SIGNATURES REQUIRED FOR REVISED BUDGET

Budget Justification

The Pennsylvania State University

Personnel

Christina Bergey, PI (2.0 months calendar, years 2 and 3) will be responsible for bioinformatic analyses of the datasets, along with PIs Tosi and Burrell. In particular, Bergey will be responsible for the early stages of data analysis using her computational expertise as well as her existing computational pipelines, which have been successfully used in other primates such as baboons. She will also assist PIs Tosi and Burrell on later phylogenetic analyses as well as contribute to the publication of the project's results.

For project time occurring after July 1 of any given year, the salaries have been adjusted at the University approved rate of 2.5%.

Fringe Benefits

Fringe benefits are computed using the fixed rates of 40.20% applicable to Category I Salaries, 15.40% applicable to Category II Graduate Assistants, 7.80% applicable to Category III Salaries and Wages, 0.10% applicable to Category IV Student Wages, and 25.70% for Category V, Postdoctoral Scholars and Fellows, for fiscal year 2017 (July 1, 2016, through June 30, 2017). If this proposal is funded, the rates quoted above shall, at the time of funding, be subject to adjustment for any period subsequent to June 30, 2017, if superseding Government approved rates have been established. Fringe benefit rates are negotiated and approved by the Office of Naval Research, Penn State's cognizant federal agency.

Travel

Academic conference travel \$1,500 (year 2) Results of the grant will be presented at academic conferences such as the meetings of the American Association of Physical Anthropologists, International Primatological Society, and the joint meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists. Requested funds are for travel to the meeting, lodging and food, and conference attendance.

International conference/workshop \$5,000 (year 1) Travel to Africa (location TBD) to attend H3ABioNet. Requested funds are for airfare, lodging and food, registration, and local transportation.

All travel will be in accordance with University travel regulations and mileage will be charged at the current rate on the date of travel.

Recovery of Facilities and Administrative Costs

F&A rates are negotiated and approved by the Office of Naval Research, Penn State's cognizant federal agency. Penn State's current provisional on-campus rate for research is 57.2% of MTDC from July 1, 2016, through June 30, 2017. New awards and new competitive segments with an effective date of July 1, 2016, or later shall be subject to adjustment when superseding Government approved rates are established. Per 2 CFR 200 (Appendix III, Section C.7), the actual F&A rates used will be fixed at the time of the initial award for the duration of the competitive segment.

CURRENT AND PENDING SUPPORT – Anthony J. Tosi

CURRENT:

Project Title: *The Molecular Signature of Sperm Competition: A Case Study in Macaque Monkeys*
Source of Support: Kent State University (Farris Family Innovation Award)
Total Award Amount: [REDACTED]
Total Award Period Covered: September 1, 2015 to August 31, 2018
Location of Project: Kent State University
Person-Months: 0.0 (expense only, no salary provided)

PENDING:

Project Title: **(This Proposal)** *Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini*
Source of Support: National Science Foundation
Total Award Amount: [REDACTED]
Total Award Period Covered: June 1, 2017 to May 31, 2020
Location of Project: Kent State University, New York University, Penn State University
Person-Months: 3.0

Project Title: *IRES: Insights into human evolution from genetic, morphological, and neuroscientific analyses at the Primate Research Institute of Kyoto University, Japan*
Source of Support: National Science Foundation
Total Award Amount: \$ [REDACTED]
Total Award Period Covered: March 1, 2017 to February 29, 2020
Location of Project: Kent State University (USA), Kyoto University (Japan)
Person-Months: 1.0

Project Title: *Establishing early-career research networks through summer internships at the Primate Research Institute of Kyoto University*
Source of Support: TOMODACHI Initiative, U.S.-Japan Council
Total Award Amount: \$ [REDACTED]
Total Award Period Covered: January 16, 2017 to December 31, 2017
Location of Project: Kent State University (USA), Kyoto University (Japan)
Person-Months: 1.0

Burrell current and pending support

Pending

Project title: Collaborative research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini

Source of support: NSF

Project location: Anthropology Dept., New York University

Total award amount: [REDACTED]

Starting date: 06/01/2017

Ending date: 05/31/2020

Person-months per year committed to the project: 0.12

Pending

Project title: The evolution of the anthropoid genome

Source of support: NSF

Project location: Anthropology Dept., New York University

Total award amount: [REDACTED]

Starting date: 01/01/2017

Ending date: 12/31/2019

Person-months per year committed to the project: 0.12

Current and Pending Support – Dr. Christina Bergey

Pending Support

Project/Proposal Title: Collaborative Research: The evolution of the anthropoid genome

Source of Support: National Science Foundation

Total Award Amount: [REDACTED]

Period of Performance: 01/01/2017-12/31/2019

Location of Project: The Pennsylvania State University

Person-Months per Year Committed to the Project: Cal: 0.00 Acad: 0.00 Sumr: 0.00

(This Proposal)

Project/Proposal Title: Collaborative Research: The evolutionary mechanics of hybridization across a primate radiation: a case study of the Cercopithecini

Source of Support: National Science Foundation

Total Award Amount: \$ [REDACTED]

Period of Performance: 06/01/2017-05/31/2020

Location of Project: The Pennsylvania State University

Person-Months per Year Committed to the Project: Cal: 0.00 Acad: 0.00 Sumr: 0.00

Facilities, Equipment, and Other Resources

Kent State University

Anthony Tosi (PI) will be responsible for directing and participating in KSU wet-lab operations related to library preparation; museum skin samples acquisition & processing; data analysis & interpretation; manuscript writing; and providing high-quality guenon biosamples for whole genome sequencing. One of his PhD students will assist with this project.

KSU's Molecular Anthropology Laboratory is equipped with a StepOnePlus Real-Time Quantitative PCR machine, two 96-well SimpliAmp gradient thermocyclers, QIAcube automated DNA extraction system, Purifier Logic Class II Biosafety Cabinet, chemical fume hood, -80 C freezer, -20 C freezer, 4 C refrigerator, Eppendorf ThermoMixer C, Qubit 3.0 DNA fluorometer, PCR workstation, high voltage power supplies, three electrophoresis units, UV-crosslinker, flake ice machine, incubators, 96-well plate centrifuge, two minicentrifuges, two microcentrifuges, analytical balance, pH meter, blue light transilluminator, 2 vortexes, microwave, and safety equipment. The laboratory also includes two desktop computers with phylogenetic, population genetic, and real-time PCR analysis software.

The laboratory biomaterials collection includes high-quality biosamples representing over 20 guenon species.

Tosi's office is one floor above his laboratory and is equipped with desks, bookshelves, file cabinets, and two computers.

NEW YORK UNIVERSITY

NYU's Molecular Anthropology Laboratory includes an ABI 3500 Automated DNA Analysis System, a QIAxtractor automated DNA extraction system, ten 96-well thermocyclers, Qubit 2.0 DNA fluorometer, high voltage power supplies, numerous freezers and refrigerators, UV-crosslinkers, ice machine, incubators, ovens, environmental shaker, centrifuges, various electrophoresis units, balances, pH meter, gel photography station, safety equipment and autoclave. A chemical fume hood and HEPA-filtered laminar flow hoods with UV-lighting are present. A DNA extraction room is located on the second floor of the Anthropology building with all necessary equipment listed above to allow the extraction of low copy number DNAs from exotic sources such as feces, bone, teeth, hair, museum skins and other biological detritus, so as to avoid DNA contamination from the main lab. All equipment necessary for DNA extraction, preparing libraries, high-throughput as well as any Sanger sequencing for the proposed project is available in our laboratory or in the NYU Langone School of Medicine Genome Technology Center.

The laboratory is well equipped with a dozen computers connected on a private server. Several NYU High Performance Computer clusters are available along with all necessary phylogenetic and population genetic software.

Burrell's office is in the laboratory and is equipped with desks, bookshelves, file cabinets, computers, and a printer.

Along with our laboratories ABI 3500 and NYU's High Performance Computing clusters we will utilize the DNA quantification and 2ndGen sequencing facilities available at the NYU Langone Medical Center's Genome Technology Center (GTC) and the Biology Department's Center for Genomics and Systems Biology. These include Illumina HiSeq 2500 and MiSeq DNA sequencing platforms with HiSeq v.4 reagents, and Agilent 2100 BioAnalyzers and an ABI 7900 HT SDS for quality control.

Facilities, Equipment & Other Resources
The Pennsylvania State University

Laboratory: N/A

Clinical: N/A

Animal: N/A

Computer: PSU provides computers for postdoctoral researchers as well as access to a high performance computing cluster (HPC) with over 16,000 processing cores and preinstalled bioinformatic software.

Office: PSU provides office space for postdoctoral researchers.

Other: N/A

Major Equipment: N/A

Other Resources:

Proposal Development and Grants Management: The Grants and Contracts Office in the College of the Liberal Arts offers an array of services to its faculty including, but not limited to, identifying funding sources, interpreting sponsor guidelines, proposal budget development, completion of forms, proposal editing, compiling the complete proposal, and obtaining the necessary university approvals.

When an award is received, the same grants and contracts staff assist faculty in the post-award administration of their projects by establishing grant accounts and overseeing the departmental budget clerks to process grant expenditures, provide updated reports to PIs, ensure that expenditures meet sponsor guidelines, and close out grant accounts.

DATA MANAGEMENT PLAN

Expected Data and Storage

Data acquired from the laboratory will consist of raw sequencing reads from the next-generation sequencing and SNP data. Prior to archival, all data will be stored redundantly on the drives of the NYU High Performance Computing cluster and on Amazon's cloud computing platform (AWS). Each kind of data will be submitted to the appropriate public database of the National Center for Biotechnology Information (NCBI) after publication. Raw sequencing reads will be submitted to the Short Reads Archive (SRA). Deposition of such data into public databases is common and often required in genetic studies published in many journals.

Any DNA alignments and phylogenetic trees that result from the analyses will be submitted to TreeBASE (<http://www.treebase.org/>) and made available for other researchers. TreeBASE is a repository of phylogenetic information, specifically user-submitted phylogenetic trees and the data used to generate them. Any custom scripts for the analysis will be released to the public under an open source license, allowing others to use and build upon the code. The pipeline for read mapping and variant identification has already been built, is available online, and is released under a GNU General Public License (GPL) version 3.

Period of Data Retention

All data generated will be made available to researchers and the public upon relevant publication. We estimate that all data generated will be available by the end of 2020.

Dissemination

Results of the study will be disseminated as oral and poster presentations at academic conferences (such as the meetings of the American Association of Physical Anthropologists and the International Primatological Society) and as publication in peer-reviewed scientific journals (such as the *International Journal of Primatology*, the *American Journal of Primatology*, *Molecular Biology and Evolution*, *Molecular Ecology*, and *Molecular Phylogenetics and Evolution*). In addition to academic channels, the project's findings will be shared to the public online.

Post-Award Monitoring

In compliance with the NSF Data Management Plan guidelines, we will submit annual reports to NSF to inform about relevant publications, conference proceedings, and other forms of data sharing. At the project's end, a final report will be submitted, detailing all data generated, an updated description of the data management and dissemination, and the location where all data are stored.

From: Andrew Burrell <[REDACTED]>
Sent: Tuesday, January 3, 2023 4:44 PM
To: Lamberson, Amanda M <amanda_lamberson@fws.gov>
Subject: Re: [EXTERNAL] Re: CITES and ESA permit application CS0082615

The fourth in the series: *C. lhoesti* (RMCA # 1988-047-M-001), *C. erythrotis* (RMCA #s 28426, 1974-032-M-0016).

I hope these got through satisfactorily, but if there are any problems or you need anything else, please let me know.

All the best wishes for the New Year!
Andy

On Tue, Jan 3, 2023 at 4:34 PM Andrew Burrell <[REDACTED]> wrote:
The third in the series: *C. diana* (RMCA #s 34971, 35699, 35778) and *C. lhoesti* (RMCA #s 9652, 9761).

On Tue, Jan 3, 2023 at 4:31 PM Andrew Burrell <[REDACTED]> wrote:
The next in the series: *C. diana* (RMCA #s 1977, 23726, 34973, and 36278).

On Tue, Jan 3, 2023 at 4:29 PM Andrew Burrell <[REDACTED]> wrote:
Hi Amanda,

I'm sending those photos in a series of emails, starting with this one.

These are *Cercopithecus lhoesti* (RMCA #s 1271, 2891, and 17673) and *C. diana* (RMCA #s 34964 and 34972).

On Fri, Dec 23, 2022 at 1:40 PM Andrew Burrell <[REDACTED]> wrote:
Hi Amanda,

OK, I totally understand and will send them as a series of (I think 3 to 4) separate emails, if that works.

Many thanks, and best wishes for the holidays!

Andrew

On Thu, Dec 22, 2022 at 1:46 PM Lamberson, Amanda M
<amanda_lamberson@fws.gov> wrote:

Hello Andrew,

Thank you for your reply and for the photos. Would you be able to upload the photos directly to the application file? Due to our stricter computer security measures I cannot directly download them from google drive. Or multiple emails with a photo or two attached would be fine also. Apologies for the inconvenience.

Kind regards,

Amanda

From: Andrew Burrell <[REDACTED]>
Sent: Monday, December 19, 2022 10:22 AM
To: Lamberson, Amanda M <amanda_lamberson@fws.gov>
Subject: Re: [EXTERNAL] Re: CITES and ESA permit application CS0082615

Good morning,

I'm sending the 17 photos as a zipped file that will be shared via a Google Drive link (below). If that doesn't work, just let me know and I'll send them some other way.

I've also attached the spreadsheet with the info about the 17 samples of *Cercopithecus diana* (9 samples), *C. erythrotis* (2 samples), and *C. lhoesti* (6 samples) for your convenience.

Many thanks for all your help with this!
Andrew

 **CS0082615_RMCA-Tervuren-specimen-photos.zip**

On Fri, Dec 16, 2022 at 4:59 PM Andrew Burrell <[REDACTED]> wrote:
Good afternoon!

Thank you for the follow-up email. I will have the photos of the ID tags for you first thing on this Monday, the 19th. I hope that is not too late!

All the best,
Andrew

On Thu, Dec 15, 2022 at 2:46 PM Lamberson, Amanda M
<amanda_lamberson@fws.gov> wrote:

Good afternoon Dr. Burrell,

I wanted to follow up with you regarding the photos of the ID tags. Do you have an estimated date of when you can send them? We are nearing the maximum amount of time I can allow for you to provide them. Thank you.

Kind regards,

Amanda Lamberson
Biologist
U.S. Fish and Wildlife Service
Division of Management Authority
Branch of Permits, MS: IA
5275 Leesburg Pike
Falls Church, VA 22041

From: Andrew Burrell <[REDACTED]>
Sent: Friday, September 30, 2022 4:45 PM
To: Lamberson, Amanda M <amanda_lamberson@fws.gov>
Cc: Andrew Burrell <aburrel4@kent.edu>
Subject: Re: [EXTERNAL] Re: CITES and ESA permit application CS0082615

Many thanks!

I will send you those photos of the specimens with ID tags next week.

And yes, we collected one skin sample per specimen listed on the excel sheet.

Please let me know if you require any additional information.

All the best,
Andrew

On Thu, Sep 29, 2022 at 2:08 PM Lamberson, Amanda M
<amanda_lamberson@fws.gov> wrote:

Good afternoon Dr. Burrell,

I apologize for the substantial delay. I have reviewed everything submitted including page 1 of the application that was mailed in at Kirstine's request. As you have indicated that there is no further information detailing the circumstances of the take of the 17 specimens and by whom, I am going to go ahead and ask for photographs of their ID tags so we have a copy of some form of original documentation for our records. Also, just to confirm, you collected one skin sample per specimen listed on the excel sheet provided by Dr. Gilissen, correct? Thank you.

In accordance with 50 CFR 13.11(e), if the requested information is not received by this office within 45 calendar days of the date of this email, your application will be abandoned and administratively closed. Once a file is closed, you will need to submit a new application, and all required fees, for the Service to consider your proposed activity.

Kind regards,

Amanda Lamberson
Biologist
U.S. Fish and Wildlife Service
Division of Management Authority
Branch of Permits, MS: IA
5275 Leesburg Pike
Falls Church, VA 22041

From: Andrew Burrell <[REDACTED]>
Sent: Thursday, July 28, 2022 3:54 PM

To: Lamberson, Amanda M <amanda_lamberson@fws.gov>

Subject: Re: [EXTERNAL] Re: CITES and ESA permit application CS0082615

Good afternoon!

I am just following up on your email from June 16 re: my CITES/ESA application CS0082615. Is there any additional information I can provide?

Thank you, and all the best wishes,
Andy

On Thu, Jun 16, 2022 at 2:17 PM Lamberson, Amanda M

<amanda_lamberson@fws.gov> wrote:

Good afternoon Dr. Burrell,

My name is Amanda Lamberson, your application has been re-assigned to me. I apologize for the delay in my response. Kirstine has forwarded me all the documentation and information that you submitted. I will review everything at the earliest opportunity and if I have any additional questions, I will email you directly. Thank you.

Kind regards,

Amanda Lamberson
Biologist
U.S. Fish and Wildlife Service
Division of Management Authority
Branch of Permits, MS: IA
5275 Leesburg Pike
Falls Church, VA 22041

From: Andrew Burrell [REDACTED]

Sent: Thursday, June 9, 2022 4:39 PM

To: Grab, Kirstine M <kirstine_grab@fws.gov>

Cc: Tosi, Anthony <atosi@kent.edu>; aburrel4@kent.edu

Subject: [EXTERNAL] Re: CITES and ESA permit application CS0082615

Importance: High

<p>This email has been received from outside of DOI - Use caution before clicking on links, opening attachments, or responding.</p>
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Dear Kirstine,

I'm checking in to make sure all is in order for our permit application. I'm listing below the information you asked for and our responses. We are aware that you set a

deadline of June 19 for our responses, so we just want to make sure we have everything you need. Below are your queries (in italics) with our responses in bold.

1. *Please complete and mail in page 1 of the attached application form filled out for the university you are affiliated with. The mailing address for this office is: Division of Management Authority, Branch of Permits, MS:IA 5275 Leesburg Pike, Falls Church, VA 22041-3803.* **We have sent a fully filled out and signed page 1 to the specified address.**
2. *The following species are listed under the ESA and prior authorization to import these specimens into the U.S. is required:*
 - a. *Ceropithecus diana*: CITES Appendix I and Endangered under the ESA
 - b. *Cercopithecus erythrotis*: CITES Appendix II and Endangered under the ESA
 - c. *Cercopithecus lhoesti*: CITES Appendix II and Endangered under the ESA
3. *Please provide documentation for when and how the museum acquired these specimens.* **We have sent (in previous emails from May 23 and June 3) all the information we have about who/how and when the specimens were collected for the Royal Museum for Central Africa.**
4. *The majority of the species listed in your application are protected under Appendix II of CITES and are not listed under the ESA. You will need to contact the management authority of the exporting country to obtain the necessary export documents (<http://cites.org/eng/cms/index.php/component/cp>). Therefore, an import permit from this office for the species listed below is not required.*
 - a. *Allenopithecus nigroviridis*,
 - b. *Cercopithecus albogularis*, *C. ascanius*, *C. cephyus*, *C. doggetti*, *C. hamlyni*, *C. kandi*, *C. mitis*, *C. mona*, *C. neglectus*, *C. nictitans*, *C. petaurista*, *C. pogonias*, *C. solatus*, and *C. wolffi*,
 - c. *Chlorocebus sabeus*, *Chlorocebus cynosurus*, *Chlorocebus pygerythrus*, *Chlorocebus tantalus*
 - d. *Erythrocebus patas*
 - e. *Miopithecus ogouensis* and *M. talapoin*.

I hope all is in order for our application. Please let us know if you need any further information and we will endeavor to get it.

All the best wishes,
Andy

On Thu, May 5, 2022 at 3:57 PM Grab, Kirstine M <kirstine_grab@fws.gov> wrote:

Dear Dr. Burrell,

We received your application for a Convention on International Trade in Endangered Species (CITES) and United States Endangered Species Act (ESA or Act) permit for the import of biological samples from primates. The processing of your application cannot be completed because of the following:

1. Please complete and mail in page 1 of the attached application form filled out for the university you are affiliated with. The mailing address for this office is:

Division of Management Authority, Branch of Permits, MS:IA 5275 Leesburg Pike,
Falls Church, VA 22041-3803.

2. The following species are listed under the ESA and prior authorization to import these specimens into the U.S. is required:
 - a. *Ceropithecus diana*: CITES Appendix I and Endangered under the ESA
 - b. *Cercopithecus erythrotis*: CITES Appendix II and Endangered under the ESA
 - c. *Cercopithecus lhoesti*: CITES Appendix II and Endangered under the ESA
3. Please provide documentation for when and how the museum acquired these specimens.
4. The majority of the species listed in your application are protected under Appendix II of CITES and are not listed under the ESA. You will need to contact the management authority of the exporting country to obtain the necessary export documents (<http://cites.org/eng/cms/index.php/component/cp>). Therefore, an import permit from this office for the species listed below is not required.
 - a. *Allenopithecus nigroviridis*,
 - b. *Cercopithecus albogularis*, *C. ascanius*, *C. cephus*, *C. doggetti*, *C. hamlyni*, *C. kandi*, *C. mitis*, *C. mona*, *C. neglectus*, *C. nictitans*, *C. petaurista*, *C. pogonias*, *C. solatus*, and *C. wolfe*,
 - c. *Chlorocebus sabeus*, *Chlorocebus cynosurus*, *Chlorocebus pygerythrus*, *Chlorocebus tantalus*
 - d. *Erythrocebus patas*
 - e. *Miopithecus ogouensis* and *M. talapoin*.

Please provide the information and documentation indicated. **Any response must be in written or email form.**

Pursuant to 50 CFR 13.11(e), if we do not receive **all** the information requested above within **45 days** from the date of this e-mail (**by June 19, 2022**), your application will be abandoned and administratively closed. Once the file is closed, you would need to submit a new application, supplemental documentation and all required fees.

If you have questions, you may contact me at kirstine_grab@fws.gov or at 5275 Leesburg Pike, MS: IA, Falls Church, VA 22041-3803. Please reference your file number CS0082615.

Sincerely,

Kirstine Grab (she/her)

Biologist | International Affairs | U.S. Fish and Wildlife Service

5275 Leesburg Pike, Falls Church, VA, 22041

kirstine_grab@fws.gov

<https://www.fws.gov/international/> | <https://cites.org/>

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Andrew Burrell

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Andrew Burrell



**IMPORT/EXPORT/RE-EXPORT OF BIOLOGICAL SPECIMENS (CITES/ESA) FOR
SCIENTIFIC RESEARCH**



☒ New ☐ Reissue/Renew ☐ Amendment

Complete Sections A or B, and C, D, and E of this application. U.S. address may be required in Section C."

A. Complete if applying as an individual			
1.a. Last name Burrell	1.b. First name Andrew	1.c. Middle name or initial S	1.d. Suffix
2. Date of birth (mm/dd/yyyy)	5.a. Telephone number	5.b. Alternate telephone number	6. E-mail address aburrel4@kent.edu,
			JUN 13 AM 11:44

B. Complete if applying on behalf of a business, corporation, public agency, Tribe, or institution			
1.a. Name of business, agency, Tribe, or institution Kent State University		1.b. Doing business as (dba)	
2. Tax identification no. 31-6402079	3.a. Description of business, agency, Tribe, or institution University		3.b. Website URL (if applicable)
4.a. Principal officer (P.O.) last name Burrell	4.b. P.O. first name Andrew	4.c. P.O. middle initial S	4.d. P.O. Title Affiliate Scientist
5. Primary contact name Andrew Burrell		6. Primary e-mail address aburrel4@kent.edu	
7.a. Business telephone number 330-672-4363		7.b. Alternate phone no.	8.a. Primary contact telephone no. 917-538-8646

C. All applicants complete address information					
1.a. Physical address (Street address; Apartment #, Suite #, or Room #; no P.O. Boxes) Lowry Hall, 750 Hilltop Drive, Kent State University					
1.b. City Kent	1.c. State OH	1.d. Zip code/Postal code 44242	1.e. County/Province	1.f. Country USA	
2.a. Mailing Address (include if different than physical address; include name of contact person if applicable) N/A					
2.b. City	2.c. State	2.d. Zip code/Postal code	2.e. County/Province	2.f. Country	

D. All applicants MUST complete	
1. Include a check or money order, payable to the U.S. FISH AND WILDLIFE SERVICE, a nonrefundable processing fee [50 CFR 13.11(d)(4)]. Federal, Tribal, State, and local government agencies, and those acting on behalf of such agencies, are exempt from the processing fee – attach documentation of fee exempt status as outlined in Instructions. (50 CFR 13.11(d))	
2. If you are requesting a reissue/renew/amendment, what is your permit/file number? N/A	
3. Certification: I hereby certify that I have read and am familiar with the regulations contained in Title 50, Part 13 of the Code of Federal Regulations and the other applicable parts in subchapter B of Chapter I of Title 50, and I certify that the information submitted in this application for a permit is complete and accurate to the best of my knowledge and belief. I understand that any false statement herein may subject me to	
The individual/principal officer of the business must print and sign this application. (No photocopied or stamped signatures)	
Date (mm/dd/yyyy) 06/05/2022	

** Further instructions for the above application may be found on our ePermits website. See the last page for information on the Privacy Act, Paperwork Reduction Act, Estimated Burden, and Freedom of Information Act aspects of this application form.

Mail your application(s) to Division of Management Authority, Branch of Permits, MS:IA 5275 Leesburg Pike, Falls Church, VA 22041-3803.



ANTHROPOLOGY

June 3, 2022

Dr. Andrew Burrell
Anthropology Department
Kent State University
Lowry Hall
Kent OH 44242
330-672-4363

RE: Permit application CS0082615

Dear CITES Permit Unit,

Enclosed is the first page of form 3-200-37e for CITES/ESA permit application CS0082615. I was asked by Kristine Grab to send this page to you by mail to with my university affiliation information.

I hope all is in order.

All the best,

A handwritten signature in black ink, appearing to read "A. Burrell".

Andrew Burrell, Ph. D.

226 LOWRY HALL ♦ P.O. BOX 5190 ♦ KENT, OHIO 44242-0001

PHONE: 330-672-4363 ♦ FAX: 330-672-2999 ♦ WEB SITE: <http://www.kent.edu/anthropology>

























