American Genetic Association

Evolutionary, Ecological, or Conservation Genomics (EECG) Research Award Application Form

Deadline 15 January 2026
Awards announced 10 April 2025

The American Genetic Association grants EECG Research Awards to graduate and post-doctoral researchers who are at a critical point in their research, where additional funds would allow them to conclude their research project and prepare it for publication.

These awards are open to graduate students and postdocs who are members of the American Genetic Association at the time of application (visit http://www.theaga.org/ for membership details). Awards will only be dispersed to applicants who have not yet started an independent research position (e.g., tenure-track faculty) at the time of the award announcement.

The program is not intended to fund an entire research project, to initiate new research projects, or to provide salary support. Priority for funding will be given to proposals that address genome-scale questions, or ecological, evolutionary, and conservation genetics questions that are best addressed using genomic approaches in a hypothesis-testing framework. While we will accept applications to work on any organism or group of organisms, we are most interested in projects that will generate results and conclusions that are broadly applicable, with the potential to move the field forward. Funds are awarded to a maximum of $6,000, awarded to the PI or institution (no overhead is provided).

Successful applications meet these criteria:
- genomic in scope
- novel question within ecology, evolution, and conservation
- likely to achieve results
- clearly written
- broadly applicable result
- appropriate final project within research program

Awardees will be required to complete a blog post for the AGA website describing their planned research before the award is dispersed, and to complete an annual report for three years. In addition to the research funding, awardees will have access to additional benefits within three years from the date of award disbursement: (1) a second blog post with a $250 honorarium, (2) paid travel and registration for a poster or oral presentation at one AGA presidential symposium, (3) a formal mentorship connection with AGA members, and (4) one free Open Access publication at the *Journal of Heredity*. Accepted Original Articles (not Genome Resources) will be eligible to compete for an additional $2,000 through the Outstanding Student-Authored Paper Award, if the first author is a student.

Due to the large number of applications received and evaluated, there will be no individual feedback for unsuccessful proposals.

Guidelines
Prepare your application using the attached format, and save as one PDF file. Replace the header identifier "EECG2025_LASTNAME_Descriptor" with your last name and a one-word project descriptor (e.g., EECG2025_SMITH_Fruitbats). The completed application will include a one-to-two page cover section with applicant details and the two summaries, one budget page with anticipated expenses and budget justification, and a one-to-three-page proposal (i.e., total application no more than six pages). The main proposal text is limited to 1,000 words, using 12-pt font. References and figure captions are not included in the 1,000-word limit, and may be in 10-pt font. The proposal should include a project description and expected results. Funds may be used to provide research expenses; however, no overhead or salary support will be provided.

Save your application to the SAME NAME as the header title (e.g., EECG2025_SMITH_Fruitbats). Please use this name in all correspondence. Expand boxes as needed. Submit your completed application online no later than midnight EST (New York time) on Jan 15, 2026.

Cover: one-to-two pages only

Applicant details: Name: Email: Dept: Institute:	AGA Member #: (See your profile at https://members.theaga.org/member for Member #) Grad student or Post-doc? Expected project completion month/year: $ Amount requested:

Please indicate if you wish to be considered for the Robert K. Wayne Conservation Scholarship & Research Fund (https://www.theaga.org/donate): _X_Yes

Principal Investigator/Faculty Supervisor:

Research project title:

Research summary (limit 200 words):

Summary of how this award will provide a critical bridge to conclude your project and prepare it for publication (limit 200 words):

Please comment on how AGA support for the research or the applicant might contribute to a more inclusive, diverse, and equitable discipline (limit 200 words):

Budget: one page only

ITEM	AMOUNT	NOTES

Please use this space for any justification/clarity about budget items, and to report any additional sources of funding for this project.

Project description and expected results (limit 1000 words; expand up to 3 pages)

The hypothalamic-pituitary-adrenal (interrenal in fishes; HPA/I) axis mediates stress response in vertebrates, allowing organisms to withstand the challenges of their environments. This highly conserved physiological reaction functions by directing resources away from non-essential processes to endure the specific conditions imparted by a stressor, though long-term exposure to unpredictable stressors can make this reaction maladaptive. A stress response is initiated by activation of corticotropin-releasing hormone (CRH) neurons in the hypothalamus. This triggers a hormonal cascade, resulting in the release of glucocorticoid hormones (primarily cortisol in fishes) from the adrenal/interrenal glands. Glucocorticoids mobilize energy throughout the body to establish a temporary physiological equilibrium, or allostasis, but also inhibit further stress-related hormone release by negative feedback on hypothalamic CRH neurons. However, dysregulation due to exposure to unpredictable stressors over time can increase resistance to GR suppression signals, inducing chronic stress. This leads to extended inhibition of non-essential functions, such as range exploration and social behavior, which becomes deleterious. Further, dysregulated stress response is cumulatively taxing on body condition, immune response, and fecundity; this toll is described as an organism's allostatic load.
Chronic stress is typically only attributed to humans and captive animals because wild animals across taxa thrive throughout highly variable environments, where rapidly fluctuating conditions can impart unrelenting, unpredictable stressors. This suggests that these organisms must balance both the exogenous and endogenous covariates of stress through some adaptive regulatory mechanism of the HPA/I axis. Our understanding of these mechanisms has been limited by the challenges of quantifying both physiology and behavior in natural systems. However, recent advances in climatological remote sensing, deep learning models, and high throughput sequencing now allow us to link gene-expression profiles with behavioral phenotypes across ecological space and time. I seek to capitalize on these innovations by uncovering the neuromolecular underpinnings of stress response in variable environments. I will do this by monitoring social teleost fish populations via video drone across diverse field sites, integrating deep learning-based behavior tracking, combined with single nucleus RNA sequencing (snRNA-seq) of the hypothalamus. I will then raise offspring from a subset of populations for a common garden study to disentangle genetic and locally adaptive effects.
My first aim is to determine social behavior, space use, and hypothalamic single-cell gene expression patterns of the Rio Grande cichlid across Texas. The Rio Grande Cichlid (*Herichthys cyanoguttatus*) is a social species that exhibits biparental care in fiercely defended breeding territories. Originally endemic to the lower reaches of Rio Grande River, this species now thrives throughout most of Texas. My study sites were selected to both capture the environmental diversity of Texas's ecoregions and genetic diversity between populations. Decadal and seasonal climatological data from Texas Commission on Environmental Quality (TCEQ), NASA Power, and USGS, in combination with real-time data collected during site visits, will allow me to measure the variability of a site across multiple time scales. I hypothesize that behavioral phenotypes will not differ significantly across populations, while both stress response activation and inhibition genes will be more highly expressed in populations from higher variability sites. Though increased exposure to environmental stressors should upregulate HPA/I axis activation genes (e.g. CRH gene which encodes for CRH hormone), the fitness ramifications of chronic stress, such as reduced social behavior

and space use, should select for overexpressed inhibitory genes in these populations as well (e.g. NR3C1 which encodes for GR). Alternatively, H. cyanoguttatus may be resistant to the stressors of highly variable environments and not vary in gene expression profile or behavioral phenotype across populations.
At each site (N=21), I will make 30 min video drone (DJI Mavic Pro 4) observations of n=10 H. cyanoguttatus breeding pairs during the breeding season (April-July). I will track x-y coordinates and heading of each fish using the SLEAP video processing algorithm, to quantify kinematics and derive social network metrics of each fish. I will use BORIS to score social behaviors. This study will be a novel application of deep learning for multi-animal pose tracking and its potential in a natural setting.
I will then catch and euthanize n=10 individuals after video recording and harvest their blood (to measure circulating cortisol) and hypothalami (for single nucleus RNA-sequencing at the UT Austin Genetic Sequencing & Analysis Facility). Using the Cell Ranger 6.1.2 pipeline, I can map and annotate these reads to the Midas Cichlid (*Amphilophus citrinellus)* reference genome. I will then use the Seurat integrated analysis pipeline to normalize the snRNA-seq data infer cell clusters. Gene co-expression networks across metacells can be determined by performing an adapted Weighted Gene Co-expression Network Analysis. Lastly, I will infer the genetic population structure from single nucleotide polymorphisms in the RNA-seq data using ANGSD. This cutting-edge transcriptomic approach, in tandem with behavior and climatological data, will determine the physiology behind how H. cyanoguttatus withstands the exogenous and endogenous covariates of stress across environmental variation gradients.
Then I will experimentally disentangle genetic and locally adaptative effects on stress physiology across populations using a “Common Garden” design. I will catch and transport n=5 breeding pairs from the highest and lowest variability sites to the Hofmann aquaculture lab at the University of Texas, Austin. Here, I will isolate pairs under controlled conditions (26.7^{o}C, 7.0 pH, low flow) in 120-gallon mesocosms, until reproduction. I will then ID tag and relocate the F1 generation to a shared mesocosm. Once these individuals reach maturity, I will fluctuate water temperature ±5 ^{o}C over 24 hours for 7 days to impart a stress response (confirmed by blood assay of cortisol). During this period I will record and, followed by harvesting the blood and brains and performing

H1: I hypothesize that the offspring from different populations will have similar gene-expression profiles as their parents during a stressful event. This would indicate the differential gene-expression profiles found in Aim 1 contribute to a heritable strategy to withstand living in highly variable environments, not confounded by local adaption. Conversely, H0: all offspring across parentage having similar gene-expression profiles would mean H. cyanoguttatus thrives in highly variable environments via phenotypic plasticity. To test this, I will maintain the F1 generation mesocosm under controlled conditions until individuals reach sexual maturity. Then, I will fluctuate water temperature ±5 oC over 24 hours for 7 days to impart a stress response (confirmed by blood assay of cortisol). I will then use the behavioral and transcriptomic approaches outlined in Aim 1 and compare results between populations.