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**The 2023 Dan M. DiGiacomo FCSal Small Grant Application and Guidelines**

**The Foundation for the Conservation of Salamanders will consider proposals for its small grant program for amounts up to $5,000.**

**FUNDING PRIORITIES:**

**The Foundation for the Conservation of Salamanders will support research, education, or conservation efforts towards salamanders and their habitats, particularly species that are locally or regionally listed.**

* Field conservation of species and their habitats or mitigation of threats
* Innovative education initiatives to benefit species at risk and their habitats
* Research that has direct application to the health or recovery of species at risk
* Zoo and aquarium partnerships and permits must be approved and demonstrated

**The following are ineligible expenses/costs which are not supported:**

* Salaries, except for graduate student stipends or technicians
* Administrative costs, including institutional overhead
* Travel unrelated to completion of the project
* General institutional support, projects considered to be normal institutional operating expenses, or shortfalls in budgets
* Grants may not be used for political lobbying, litigation, or travel funds for attending or presenting at conferences
* Grants will not be provided to fund projects that are already completed

**APPLICATION PROCEDURE AND DEADLINE**

The proposal must be submitted as a PDF or Microsoft Word document to the FCSal Grant Committee (grants@fcsal.org) by January 15, 2023.  Should your project receive funding, we will disburse funds as specified in the award letter. Recipients will be notified by March 1, 2023.

**GRANT PERIOD**

Ideally, grants must be spent within 12 months after the grant is awarded. However, exceptions can be made; please provide a detailed timeline in your application. Additionally, FCSal requires a progress report mid-way through the duration of the project and a final report within 2 months of the completion of the project.  FCSal reserves the right to display and promote this research on their website and other social media pages.

**THE APPLICATION**

**Only complete applications will be considered** for review and possible funding. Separate mailing of materials will not be accepted.The application contains a budget (see below) and must include the following:

* Support letters from the CEO/Director of the Primary Investigator(s) and collaborating institution(s)
* Copies of permits or letters of approval by the appropriate regulatory agencies or recovery team, and/or Institutional Animal Care and Use Committee (IACUC) approvals
* *Curriculum vitae* of Primary Investigator(s); maximum one page per investigator

Format must not deviate from the following form. Total application length may not exceed seven typewritten pages. Appendices are permitted, but may only *clarify*, and not *supplement*,information in the narrative (i.e., photos/diagrams would be acceptable, but not videos/publications).

**The Dan M. DiGiacomo FCSal Small Grant 2023**

1. **TITLE PAGE (Page 1; single page)**

|  |  |
| --- | --- |
| Project Title: | You can’t protect what you can’t see: harnessing next generation sequencing to identify unique lineages within the threatened Cascade torrent salamander, *Rhyacotriton cascadae* |
| Principal Investigator (PI) name:  Job title:  Institution:  Address:  Phone:  Email address: | Christopher Cousins  PhD Graduate Student  Oregon State University  Nash Hall, 2820 SW Campus Way, Corvallis, OR, 97331  5417374531  Christopher.Cousins@oregonstate.edu |
| Name and contact information to whom check is payable, or method of fund transfer: | Dr. Tiffany Garcia, Oregon State University  See below for contact information |
| Amount of Grant Request: | $3977 |
| Collaborator name:  Job title:  Institution:  Address:  Phone:  Email address: | Dr. Brian Sidlauskas  Professor  Oregon State University  Nash Hall, 2820 SW Campus Way, Corvallis, OR, 97331  5417374531  Brian.Sidlauskas@oregonstate.edu |
| Collaborator name:  Job title:  Institution:  Address:  Phone:  Email address: | Dr. Tiffany Garcia  Professor  Oregon State University  Nash Hall, 2820 SW Campus Way, Corvallis, OR, 97331  5417374531  Tiffany.Garcia@oregonstate.edu |

Type of project *(circle all that apply):*

Education Conservation Research

Abstract *(no more than 250 words):*

The Cascade torrent salamander (*Rhyacotriton cascadae)* is one of four species within the monogeneric family of Rhyacotritonidae, endemic to the Pacific Northwest. *Rhyacotriton* species are extremely sensitive to changes in their environment because of low thermal tolerances and high susceptibility to desiccation. The United States Fish and Wildlife Service (USFWS) is currently considering listing two of the four species (*R. cascadae* and *R. kezeri)* under the federal Endangered Species Act. In 2022, as part of a study with the goal of identifying genetically distinct populations within of *R. cascadae,* we sampled across the range of the species, using next generation sequencing techniques to assemble genetic markers. Our preliminary results putatively identified four populations, one of which showed an unexpected and surprising amount of differentiation between all others. Further investigation using phylogenetic tree building methods, and inclusion of congeners, has failed to explain the patterns we are seeing within the currently accepted taxonomy of Rhyacotritonidae. To better understand the evolutionary history of *R. cascadae* and Rhyacotritonidae, we will assemble a dataset of all four extant species of the family, as well as individual representatives of six other families within the order Caudata. Using phylogenetic analyses, this dataset will enable both a fine and broad scale examination of lineage diversification and speciation events within Rhyacotritonidae, critical for successful conservation of evolutionarily significant units. This research will also contribute to the taxonomical placement of Rhyacotritonidae within Caudata, an area of active research.

**B) NARRATIVE (Pages 2–5; no more than 4 pages in total).**

**1. Background (250 words maximum)**

**Please give a brief description of the project, its research/conservation/education goals, and why it is a priority.**

Due to its high sensitivity to environmental change, and predicted loss of habitat in future climate scenarios, the Cascade torrent salamander (Rhyacotriton cascadae), endemic to the western slopes of the Cascade Range of Oregon and Washington, is currently being assessed by the United States Fish and Wildlife Service (USFWS) for listing under the federal Endangered Species Act (ESA).The USFWS uses the concept of ‘distinct population segments’ (DPS’s) to spatially allocate conservation efforts, protecting unique evolutionary lineages identified by genetic studies. In 2022, we performed the first range wide population genomics study for *R. cascadae,* to support conservation efforts. Our preliminary results tentatively identified four to five distinct populations. Unexpectedly, one population showed markedly elevated levels of differentiation from the others. With the inclusion of two congeners in analyses, this divergent population appeared to be markedly different from all three species of the dataset. The goal of our study is to use a dataset of all extant species of Rhyacotritonidae, as well as representatives of six other salamander families, to investigate the evolutionary history of *R. cascadae.* Our study will elucidate lineage diversification and speciation events within the family and contribute to our current understanding of taxonomy within Caudata. Our research is a priority, as the species is under assessed for ESA listing, and our preliminary results suggest that currently accepted species boundaries may be incorrect, which may lead to a misallocation of conservation efforts for *R. cascadae.*

**2. Project Description (1000 words maximum)**

**Please provide a detailed account of the project methodologies and why they are appropriate, conservation significance of the specific outcomes, project evaluation methods, and partnerships involved (specify roles of all partners). If proposal is an education project, explain how the educational impact of the program will be measured (i.e., changes in knowledge, attitudes, and behaviors)?**

Our phylogenetic project has its beginnings in unexpected preliminary results of an ongoing population genomics project study of *R. cascadae*. The goal of our ongoing study is to identify genetically distinct populations, and reservoirs of genetic diversity within the species. As the impacts of climate change accelerate, populations with higher genetic diversity, and thus, higher adaptive potential, will have higher likelihoods of persistence. This necessitates identification of these unique evolutionary lineages, which in turn helps to identify DPS’s, the units used by the USFWS to allocate conservation efforts for ESA species. To examine population structure across the species, we collected a total of 144 tail tips from individuals at 28 sites across the range of R. cascadae to perform a population genomics study using double digest restriction-site associated DNA sequencing (ddRADseq) to assemble markers across the genome.

As salamanders have genomes which are larger than most other vertebrates by an order of magnitude, we increased the amount of starting DNA per sample, and used a narrow fragment size selection window to ensure that we would have sufficient sequencing depth and coverage. We submitted tissue to the Center for Quantitative Life Sciences (CQLS) at Oregon State University (OSU) for DNA extraction, library preparation, and next-generation sequencing on an Illumina NextSeq 2000 using a 150 base pair paired end P2 flow cell. We chose to use ddRADseq to identify genetic markers, as multiple studies have found that this method produces higher numbers of markers than microsatellites, mitochondrial DNA, and other molecular techniques, allowing for detection of genetic differentiation between populations that might go otherwise undetected. We also used these methods with previously collected tissue of ESA candidate species R. kezeri and R. variegatus (two of the other three species within the monogenetic family). We performed quality control and filtering using the STACKS pipeline, identifying the optimal parameters by examining the total number of single nucleotide polymorphisms (SNPs), total number of loci within 80% of all samples, individual heterozygosity, and cumulative variance of PCA’s within subsets of the dataset ran with varying parameters. We used optimal parameters to assemble a dataset from a subset of samples (112 samples and twenty sites) for preliminary analyses.

Our preliminary results have putatively identified 4-5 distinct populations within the species, and evidence of little to no gene flow between populations. Unexpectedly, we found surprising levels of genetic differentiation between the two identified populations at the northern extent of the species range boundary. When including both *R. kezeri* and *R. variegatus* along with *R. cascadae* in RAXML and other phylogenetic analyses, results suggest that the divergences between these populations could be at similar magnitudes to those between the congeneric species. To better understand the phylogenetic structure within the family, we will construct a dataset with R. olympicus, in addition to representatives of six other families within the order Caudata. This dataset will contain all current species of Rhyacotritonidae, and seven of the ten currently recognized families of salamanders (Rhyacotritonidae, Ambystomatidae, Cryptobranchidae, Dicamptodontidae, Plethodontidae, Proteidae, and Sirenidae). We have intentionally chosen families that (with our current taxonomical knowledge) are either close relatives to, or sufficiently distant from Rhyacotritonidae, to allow for a broad temporal scale of diversification within the family. The breadth of the dataset will allow us to compare interspecific levels of divergence within R. cascadae to interfamilial levels of divergence within Rhyacotritonidae, and infraorder levels of divergence and speciation within Caudata.

To ensure that we have sufficient genetic markers to allow for examining phylogenetic relationships within the species, we will use library preparation and sequencing methods proven with our population genomics study, as well as tailored loci filtering methods. This study will contribute to the efforts of our ongoing population genomics work to identify distinct population segments within R. cascadae, adding a broader lens to our investigations. Our work will elucidate the evolutionary history and speciation events within Rhyacotritonidae and ensure that future conservation efforts take distinct genetic lineages into account. As the USFWS is currently considering listing *R. cascadae* under the ESA, timely and accurate delimitation of both species and genetically distinct populations is critical for supporting efforts to ensure the long-term persistence of the species. These results will also contribute to the active research in amphibian taxonomy. The evolutionary history of salamander families within the order Caudata is an area of debate, and our study will help support efforts to trace the evolutionary history of Caudata.

**3. If request involves a multi-year project, please outline the funding strategy for subsequent years (50 words maximum).**

N/A

**4. Have all the necessary permits or letters of approval by the appropriate regulatory agencies or recovery team been obtained for the project? (Y/N)**

Yes

**Have Institutional Animal Care and Use Committee (IACUC) approvals been obtained, if necessary? (Y/N)**

Yes

**If yes to either question, attach copies of related permits and approvals to this proposal. Proposals cannot be considered unless proof of permits or support letters from the permitting authority is provided.**

**5. Project timeline:**

**We will complete the data collection and analysis for this project in 2023, with a draft manuscript completed by early 2024.**

**6. Is the project underway? (Y/N)**

Yes, we are in the process of obtaining the needed tissue from multiple sources, including collaborators at state agencies, zoos, and scientific museum collections.

**C) PROJECT BUDGET FOR ONE YEAR (add additional lines as necessary; not to exceed 1 page)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Budget Category** | **Item/Amount** | **Amount Requested from FCSal** | **Other Funding Sources;**  **Identify Pending, In-Kind, or Other Support** |
| Sequencing | **Nextseq 2000 150 bp x 2 PE P2 Sequencing: $3977** | **$3977** | **0** |
| Sequencing | **Library Preparation: $1288** | **0** | **$1288, In-Kind** |
| Sequencing | **Fragment Size Selection: $176** | **0** | **$176, In-Kind** |
| Sequencing | **qPCR: $34** | **0** | **$34, In-Kind** |
|  |  |  |  |
| **Total** | **$5475.00** | **$3977** | **$1498, In-Kind** |

**D) ATTACHMENTS (digital submissions only)**

**1. Letters of support from the CEO/Director of the Primary Investigator(s) and collaborating institution(s)**

**2. Copies of appropriate permits and/or IACUC approvals**

**3. *Curriculum vitae* of Primary Investigator(s); maximum one page per investigator**