



NATIONAL SCIENCE FOUNDATION
4201 WILSON BOULEVARD
ARLINGTON, VIRGINIA 22230

NSF 17-052

Dear Colleague Letter: Programmatic Changes to the Systematics and Biodiversity Science Cluster in the Division of Environmental Biology, Directorate for Biological Sciences

February 6, 2017

Dear Colleagues:

The Systematics and Biodiversity Science (SBS) cluster will be reorganized to have one core program — named "Systematics and Biodiversity Science" (SBS) — which will now support all research proposals that were formerly submitted to the Phylogenetic Systematics (PS), Biodiversity: Discovery and Analysis (BDA) and Genealogy of Life (GoLife) programs. **This change will be effective for preliminary and full proposals submitted to the 2018 deadlines for the DEB Core Programs solicitation.** The revised core program will encompass all expeditionary and exploratory research, tree-based approaches to studies of organismal evolution, and proposals that advance systematics theory and/or development of new methods for phylogenetic or biodiversity analysis. Further, to recognize a growing interest in macroevolutionary questions within the systematics research community, the revised SBS core program will now consider projects that look to test comparative research questions by collecting and integrating various data layers (e.g., genomic, phenotypic, spatial, ecological, geological, and temporal data) within a phylogenetic context.

CONTEXT

In the past, the Systematics and Biodiversity Science (SBS) cluster has accepted proposals submitted to two core programs — Phylogenetic Systematics (PS) and Biodiversity: Discovery and Analysis (BDA). Research proposals submitted to the PS and BDA core programs, however, have become increasingly integrative in recent years, with most having both collection/discovery and phylogenetic tree/analysis components. This new combination of approaches has created some confusion within the research community as to whether PS or BDA is more appropriate for a proposal containing elements supported by both programs.

Since 2014, the Division of Environmental Biology (DEB) has also supported the Genealogy of Life (GoLife) special program focused on poorly known areas of the Tree of Life with a goal of producing an open access, comprehensive Genealogy of Life that would provide the framework for data-layer integration necessary for testing comparative questions in systematics, evolutionary biology, ecology,

paleontology, and other fields. GoLife awards continue to significantly advance our understanding of the phylogenetic relationships and evolution of poorly sampled clades, or dark areas, of the Tree of Life. However, the number of proposal submissions to GoLife have been decreasing, and few proposals have focused on pivotal dark areas of the Tree of Life. Additionally, although GoLife proposals required researchers to provide compelling hypotheses justifying the use of data layers, the rationale for choosing particular data layers were primarily provided for better known groups and not for poorly sampled areas of the Tree of Life.

In response to these observations, the GoLife program and the SBS programs will be re-aligned and simplified to reflect the NSF's continued commitment to engage the entire systematics community at large. **All research proposals that were previously submitted to the PS, BDA and GoLife programs should now be submitted to the Systematics and Biodiversity Science (SBS) core program according to the requirements in the DEB Core Programs solicitation.** This change recognizes the increasingly integrative nature of SBS proposals and the breadth of research questions being asked within the research community. **The SBS cluster will continue to emphasize efforts to produce a comprehensive Tree of Life and support biodiversity discovery.**

Note that the **ARTS** category (Advancing Revisionary Taxonomy and Systematics) will continue to accept revisionary taxonomic-focused proposals (see [Dear Colleague Letter NSF 11-037](#)).

Lastly, in order to encourage proposals focused on advancing biodiversity discovery and description of extinct and/or extant organisms in poorly known/dark areas of the Tree of Life, a new proposal category (described below) is created within the SBS core program: Poorly Sampled and Unknown Taxa (*PurSUiT*).

NEW SBS PROGRAM PROPOSAL CATEGORY: POORLY SAMPLED AND UNKNOWN TAXA (*PurSUiT*)

The evolution of life on Earth began over 3.5 billion years ago, is ongoing today, and will continue as long as life exists on the planet. Discovering the world's biota underpins the study of the origins, evolution, and maintenance of biodiversity. Yet despite centuries of exploration, our knowledge of the diversity of life is still temporally and spatially biased, and critical areas of extant and extinct biodiversity remain undiscovered or undocumented. This restricts our ability to develop a comprehensive and comparative evolutionary framework for all life and hinders our understanding of the mechanisms and processes of evolution.

To address this issue the Systematics and Biodiversity Sciences (SBS) cluster (https://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503666) encourages the submission of proposals to support research on Poorly Sampled and Unknown Taxa (*PurSUiT*). The *PurSUiT* category is meant to encourage biodiversity discovery and description in poorly known, or dark areas, of the Tree of Life. This emphasis was previously included in the Genealogy of Life (GoLife) Program, and its incorporation as a special category within the SBS core program reflects a renewed effort to close significant gaps in biodiversity knowledge.

Proposals submitted with this category should address expeditionary and exploratory research on organismal diversity that occurs, or used to occur, in natural environments and should aim to advance

the discovery, identification, description, classification, and cataloguing of the world's unknown extant and extinct biodiversity. Research projects must address compelling biodiversity discovery questions and must entail a primarily clade- or guild-based approach (e.g., regional, global, or planetary inventories). Priority will be given to innovative projects that fill **significant gaps in biodiversity knowledge** and **integrate taxon information within an evolutionary or taxonomic framework**.

RESEARCH

Investigations will be focused at the organismal level, and must concentrate on pivotal areas of the Tree of Life for which biodiversity is very poorly known or undescribed. Proposals may target any such extant or extinct group of organisms from any habitat. Successful proposals will make a compelling case demonstrating that lack of knowledge, and they will describe how filling this gap will significantly advance our understanding of organismal evolution. Biodiversity documented in the proposed effort must be placed within a phylogenetic context (either by creating new trees or incorporating new data within existing trees such as from the Open Tree of Life) or taxonomic framework using cutting-edge approaches.

Projects that do not focus on biodiversity discovery in poorly explored areas of the Tree of Life or projects that generate biodiversity data without integration within a phylogenetic and/or taxonomic framework are not appropriate for the PurSUIT category.

Projects on poorly known groups that include fieldwork or work in existing collections are appropriate in this program. *PurSUIT* proposals must include well-documented plans for fieldwork coordination and permitting, sample or specimen vouchering, data sharing and storage, and taxon delimitation and description. When appropriate, collaboration and integration with other ongoing biodiversity efforts is encouraged. Successful proposals will document plans for long term sample storage or specimen deposition in a permanent and publicly accessible storage facility/collection, and describe a strategy for the rapid dissemination and sharing of data into public biodiversity databases (e.g., specimen data through iDigBio/GBIF). Any phylogenies and associated organismal data generated through this effort must be deposited in a format that allows easy integration with existing databases. Shared data should include sample numbers, specimen voucher and collections information with associated metadata, as well as morphological/genetic data for Dryad, GenBank, and other public resources, and, if applicable, should include source code for data pipelines/programs.

TRAINING

Student training that focuses on producing broad research competence in all areas of systematics and evolutionary biology is encouraged in *PurSUIT* proposals. Training should promote intellectual and methodological interaction and encourage an integrative perspective to understanding taxonomy, systematics, and biodiversity. *PurSUIT* seeks to enhance organismal, phylogenomic, bioinformatics, phenotypic, and biodiversity analytical expertise. Proposals that provide specific examples of how it will broaden the skill set of PIs, students, or postdocs (particularly with respect to researchers from traditionally underrepresented groups) are encouraged. Partnerships with undergraduate institutions, community colleges, high schools, museums, and other institutions are highly encouraged.

Titles of proposals submitted to this category should be prefaced with "PurSUIT:". *PurSUIT* proposals

must conform to all requirements in the DEB Core Programs solicitation, including initial submission of a preliminary proposal (https://www.nsf.gov/publications/pub_summ.jsp?ods_key=nsf17512).

Investigators with questions about *PurSUiT* proposals are encouraged to contact the SBS cluster program officers listed on the program page at: https://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503666. Lists of PurSUiT awards with links to their FastLane Award Abstracts will be posted on the BIO website at <https://www.nsf.gov/bio/pubs/awards/pursuit.htm>.

James L. Olds
Assistant Director
Directorate for Biological Sciences