

1. RESEARCH PLAN

The panel rated the proposal in Highly Meritorious. Reviewers were enthusiastic about the collaborative nature of the team and the potential of the project to identify alleles in wild populations that may provide abiotic stress resistance. Several questions were raised during the review as itemized below. Please consider these comments and address each concern.

- **Collection of wild ecotypes:** Reviewers considered whether there was a need to characterize the ecology of the habitat particularly soil chemistry. Please comment.

Response: We consider analyses of soil chemistry to be a critically important component of our population genomic analyses, especially to the extent that they provide insight into soil fertility and salinity (low nutrient and salt stress are two of our three focal stresses). As described in the proposal, we will collect representative soil samples from all wild populations surveyed (3 species x 50 populations/species = 150 populations total) for subsequent analysis. These analyses are currently budgeted in year 2 of the project (150 samples x \$20/sample = \$3,000 total) with all work being carried out at facilities on the UGA campus. The resulting data will then be used in downstream analyses aimed at identifying locally adapted alleles. In short, this will involve searching for correlations between SNP genotypes and spatially explicit environmental variables, including the soil data from each site and climatic variables from the WorldClim database and the CGIAR Global Aridity and PET database. Unusually strong correlations (as compared to the neutral expectation) between SNP allele frequencies at a given locus and one or more of these ecological variables will not only provide evidence that variation at that locus has been shaped by natural selection, but also the nature of the selection pressure. In the absence of the soil chemistry data, we would be much less likely to identify alleles contributing to salt and low nutrient stress.

- **Method of using PEG to mimic drought stress:** The panel discussed some methodological details, many of which will likely be resolved through the experimental process. One question of concern was about the use of PEG as an osmoticum to simulate drought stress. Several reviewers noted it could be problematic for several reasons: 1) Osmotic stress induced by PEG may not be an accurate measure of the complex trait of drought, and 2) There is some evidence that PEG 6000 can be incorporated into plant tissues when used for drought induction. Please consider and address.

Response: The reviewers are correct that osmotic regulators such as PEG yield an osmotic stress as opposed to a traditional drought. However, PEG has been shown to effectively simulate low water potentials that reflect the type of stress imposed by drying soil. We are aware of the other caveats associated with the use of an osmoticum such as PEG to simulate drought stress and agree that care must be used when implementing this “physiological” drought treatment. The most prevalent of these concerns are hypoxia and toxicity via root microfractures that increase with root age. To avoid hypoxia, we apply the PEG solution to a soil substrate that allows airflow to the root system of each seedling. To avoid toxicity, we use a large molecular weight osmotic regulator (PEG-6000) that does not naturally enter the cytoplasm of a cell, and limit the application of these treatments to the seedling stage in order to minimize the occurrence of root microfractures. Given the scope of this aspect of the proposed research and the challenges associated with the alternatives (e.g., the implementation of a simultaneous, controlled dry down for hundreds of individual pots), we believe that the protocol outlined in the proposal is the best approach to achieving our goals.

- **Sample size for GWAS:** One reviewer noted: *The SAM population of 288 inbred lines represents a somewhat modest sample size for GWAS. It should be acknowledged that many genes of minor effect will likely be missed. How important are these to the genetics of stress resistance?*

Response: The reviewer is correct that the power of association mapping approaches is limited by sample size, and we do recognize that the size of the SAM population will limit our ability to identify genes of minor effect. It should be noted, however, that we are most interested in the identification of major effect loci, as these are likely to be of the greatest utility in downstream breeding programs. In this light, it

is worth noting that we have successfully used the SAM population to map loci of moderate to large effect for a variety of morphological traits (e.g., Mandel et al. 2013, PLoS Genetics 9: e1003378; Nambeesan et al. 2015, BMC Plant Biology, in press). Our preliminary analyses of traits related to drought and salt stress tolerance have resulted in the identification of loci with effect sizes as small as 2% (Mandel et al., unpublished; Ishibashi et al. unpublished), and are thus similarly promising.

- **Potential for SNP bias:** One reviewer noted: *For the 200K Affy SNP array, these SNPs are obviously chosen from resequencing data on one or more discovery panels, but little info on the*

Response: The reviewer is correct that the SNPs including on the genotyping array will be derived from resequencing data, and will thus be subject to potential ascertainment bias. In addition to the extensive WGS resequencing data that we have for genotypes spanning the diversity of the cultivated sunflower gene pool, which has resulted in the identification of over 70 million high quality SNPs, including a subset of 4.1 million SNPs with minimal missing data and minor allele frequency (MAF) > 10%, we also have extensive re-sequencing data from numerous wild species. We will thus minimize the impact of ascertainment bias by ensuring that our SNP discovery panel includes multiple representatives of all focal species, and that any targeted loci are present in a single copy in all species under consideration.

2. BROADER IMPACTS

The panel was enthusiastic about the broader impacts plan, and considered it to be a multi-faceted program. Please address the following issues raised during programmatic review:

- The Program questions the use of a senior graduate student as an "Outreach Coordinator" for the project. Please describe how this role fits in with the training and mentoring plan for the student.

Response: In our graduate program, graduate students are encouraged to develop outreach activities as part of their professional development, under the guidance of their advisors. For this project, one of the senior graduate students will receive partial support to oversee the outreach activities here at UGA, including the following: training junior graduate students in best practices of mentoring high school and undergraduate students, coordinating the logistics of different activities (Hilsman Middle School, Young Dawgs, UGA undergraduate interns), and serving as a liaison for the CWU students visiting UGA for two weeks in the summer as part of the CWU Science Research Leadership Internship. In all of these efforts, the graduate student coordinator will be guided by Burke and Donovan. Serving as the "outreach coordinator" will facilitate professional of a senior graduate student through the enhancement of mentoring skills and a development of a portfolio of outreach activities. Please note that these activities will be incorporated into the overall responsibilities of this individual, as opposed to being simply added on top of their research workload.

- The proposal mentions that UGA educational experts will be involved but it is not clear how. Please clarify.

Response: At UGA, the Center for Teaching and Learning (CTL; <http://t.uga.edu/1sM>) is a University-wide resource center that provides pedagogical training. Graduate students interested in developing teaching expertise have access to the educational experts at the center via instructional seminars, workshops, classes, and one-on-one mentoring. Participation in the activities will facilitate endeavors such as the completion of a Teaching portfolio (<http://t.uga.edu/1sL>) and/or an Interdisciplinary Teaching Certificate (<http://t.uga.edu/1sN>) through the UGA Graduate School. These activities are particularly valuable for students wishing to pursue a career with a greater emphasis on instruction.

- Are there prior relationships established between UGA and the middle school involved? If not, how will these be established? And most importantly, how does the project plan to engage with teachers to ensure that activities are consistent with state standards and fulfill the particular needs for science learning in the targeted classroom?

Response: The relationship between the UGA Department of Plant Biology and Hilsman Middle School is well established, with a five-year track record of successful interactions. The lesson plans that underlie this program were developed in collaboration with the teachers, and the fact that they have already been incorporated into the middle school curriculum demonstrates that they meet the state standards as well as the targeted needs of these classrooms. The new lessons will be developed within the same collaborative framework and implemented within the timeline of the grant.

3. BUDGET & BUDGET JUSTIFICATION

An updated Current & Pending Support form for each funded PI and collaborator should be submitted to me by email.

Response: The requested documents have been included as e-mail attachments.

NSF limits salary support to a maximum of 2-months total per year over all NSF grants. Consequently, please also verify that you will not be receiving over 2 month's salary support over all NSF grants.

Response: No senior personnel (PI, co-PIs, senior personnel) will receive more than 2 month's salary support over all NSF grants.

Other budget issues that need some explanation and correction are as follows:

UGA budget

- Personnel – Explain and delineate the roles of the senior personnel included in the project.

Response: We have provided additional information on roles of the senior personnel (Burke and Donovan) in the Budget Justification.

- Travel – The travel budget of \$32,500 / year needs reduction. Travel should be for personnel to travel to conferences to give talks and posters, one per year per personnel.

Response: We have reduced the travel budget as requested. The travel for UGA personnel for conference presentations has been reduced to one per year per personnel and is combined with travel to the annual project meeting, which will be held in conjunction with a major scientific meeting. There are also travel funds for the PI to attend the annual NSF PGRP Awardees meeting. The remainder of the travel support for UGA personnel is directly related to our research activities. UGA personnel need to travel to the Desert Research and Extension Center (DREC) in Holtville, CA, to carry out portions of the phenotyping of the large-scale screens and ensure integration of measurements across scales and research groups from different institutions. The success of this project is contingent on the participation of UGA personnel in these aspects of the proposed research.

- Other Direct Costs – Program Fees. Unless otherwise negotiated, costs to cover program fees associated with the Young Dawgs high school internship program (6 students per year x 4 years x \$600/student = \$14,400 total) should be allocated to PSC.

Response: The program fees associated with the Young Dawgs high school internship program (\$14,400 total) have been moved to PSC.

- Other Direct Costs – G6 Other. Please provide additional information about the costs allocated to line G6 Other for all years.

Response: All costs in this category (\$258,000 total) are for SNP genotyping. This has been clarified in

the budget justification.

Central Washington University subaward budget

· Participant Support Costs – Tuition and Travel for CWU students. Unless otherwise negotiated, these costs should not be allocated to PSC which is usually for costs associated with individuals not associated with CWU. Please consult with the UGA and CWU SPOs for guidance.

Response: These costs have been moved out of PSC and into the appropriate categories.

Indiana University subaward budget

· Costs associated with years 2-4. Please provide a letter or a plan should planned funding for coPI Rieseberg not be available to support activities in years 2-4.

University of Arizona subaward budget

· Salary (Other Professional) – Please confirm that John Heun is not a USDA ARS federal employee (can be Temporary Fed).

Response: John Heun is exclusively a University of Arizona employee. He is in a non-tenure track position that is partially supported by soft money.

· Equipment – Please provide more detailed explanation of the use of the hydraulic lift for the tractor, with respect to its specific needs of this project.

Response: The current phenotyping platform needs to be upgraded with a frame lift system in order to increase the tractor clearance, as required by the height of sunflower plants.

University of California subaward budget

· Other Direct Costs – Unless otherwise negotiated, costs associated with the high school interns (see below) should be allocated to PSC:

Response: This change has been made.

· "a budget of \$1,200, \$2,400, and \$3,600 will be used to printing handouts and purchase bags, water, and food items for 300, 600, and 900 high school student visitors in the first, second, and third year to learn about drought tolerance, water conservation, irrigation, sunflower and other crops";

Response: Budget Justification has been modified.

· A budget of \$1,500, \$3,000, \$4,500 will be used as travel grants to assist 300, 600, and 900 high schools to bring their students in the first, second, and third year.

Response: Budget justification has been modified.

Please send a revised budget and budget justification in NSF format by email for Program review.

4. DATA AND MATERIALS RELEASE/SHARING POLICY (required of all proposals recommended for funding): For this section, data and materials would include all sequences and other such datasets, biological materials such as seeds, computational products, educational materials, etc.

· What is to be shared, when and how? What are the short- and long-term plans for release?

Response: We will produce and share both germplasm and data resources. The germplasm resources will include seeds from 50 wild populations of three *Helianthus* species as well as the lines comprising the multi-species MAGIC population. We are coordinating with Dr. Laura Marek, who manages the sunflower germplasm repository at USDA. Seeds of both the wild-collected populations and the MAGIC lines will be deposited into the USDA sunflower germplasm collection for future maintenance and public distribution, as we have already done for the SAM population. In our original application, Dr. Marek provided a letter of collaboration documenting her willingness to accept and maintain these materials. To assist in this process, we have budgeted for a one-time increase to provide sufficient seed for immediate distribution once the MAGIC lines have been produced and characterized. We anticipate making these available as soon as the lines have been increased and passed our internal quality checks.

With respect to data, we disseminate information generated as part of this project as freely, widely, and rapidly as possible. We anticipate making our genotypic, sequence, and/or expression data available via deposition into appropriate public databases as soon as they have passed our filtering and quality controls. We anticipate making phenotypic data publicly available via deposition into relevant public databases at publication. Other data types, such as soil characteristics will be made available via deposition into Dryad (<http://datadryad.org/>) and via prompt publication. Project data will also be made accessible via the Sunflower Genome Database (<http://www.sunflowergenome.org/>, see below).

· Which community database(s) is(are) involved in the project? Where will the project materials be housed for maximum community access and longevity of the access?

Response: Information will be distributed to the general public and to our end users via the Sunflower Genome Database (<http://www.sunflowergenome.org/>). This decision was made in consultation with our primary stakeholders, who have already invested in the development of this database via an ongoing industry consortium, and who wish to see the results of our project presented in the context of the reference sunflower genome. Note that our industry collaborators view the sort of information being generated as part of this project as pre-competitive and have requested no limits on the availability of our data. Consistent with this view, all access controls have been removed from the Sunflower Genome Database, and all information housed there is completely freely available. Ongoing support from our industry consortium helps to ensure the longevity of this database, and the deposition of our data into other relevant public databases likewise ensures the longevity of the data generated in this project.

· For data release, explain the understanding between any database curators and the PI as to when and how transfer will occur, who will pay for it (if costs are involved), and long term maintenance plans and costs. Include a statement of projected release of the data.

Response: As noted above, we anticipate that our molecular datasets (i.e., genotypic, sequence, and/or expression data) will be made publicly available as soon as they have passed our filtering and quality controls, whereas phenotypic data will be made available upon publication. The Sunflower Genome Database is currently managed by the project PIs and personnel in their labs, so no special arrangements are required for data transfer. We do not anticipate any costs associated with data transfer. Long-term maintenance of these datasets (beyond the life of the project) will be funded by an ongoing industry consortium, and further ensured by deposition into relevant public databases.

· Elaborate on the nature of the collaboration with industry participants listed in Section A-3 of your proposal. Clarify data release issues that may arise from these collaborations. Explain any intellectual property issues that are associated with data release and sharing.

Response: We will build upon established collaborations with multiple public and private sunflower breeding programs, both within the USA and abroad. On the private side, our industry collaborators include Advanta Semillas, Biogemma, Dow AgroSciences, Pioneer Hi-Bred, and Soltis. On the public side, our partners include the USDA and INRA (France) sunflower breeding programs. These

collaborators have already provided us with valuable feedback on line selection for the establishment of our MAGIC population, and our industry partners will assist with the production of these populations. As described above, our industry partners consider these materials to be pre-competitive. As such, these materials will be made publicly available and we anticipate no intellectual property issues with their release. We are coordinating with Dr. Laura Marek to deposit these lines into the USDA sunflower germplasm collection for future maintenance and distribution.

5. PROJECTED TIMELINE (required of all proposals recommended for funding.) Provide detail about the project timeline in the following table format, including both research and education/outreach activities as goals and deliverables.

Response: See detailed timeline, below. Please note that this project was originally submitted with a four year timeline. However, due to unforeseen delays in the anticipated start date and the seasonal nature of various aspects of our work, we have extended timeline to five years. Without this change, we would have to forego the 4th field season (spanning years 4 and 5) during which we will perform detailed phenotypic characterization of lines from the MAGIC population that will be produced as part of this project. Also, because certain aspects of our educational activities are timed to coincide with our field seasons, this change will allow us to maintain all of the originally planned training activities. The longer timeline will also allow us to extend the middle school outreach program for an additional year, providing additional educational opportunities to local middle schoolers. From a budgetary standpoint, this timeline change was largely accommodated by re-allocating funds amongst years, though it did result in a modest (ca. 3.9%) increase in the overall budget.

Year(s)	Goals	Participant roles	Deliverables
1	Adapt high-throughput, sensor-based field phenotyping system for use in cultivated sunflower	Andrade-Sanchez	Field phenotyping system capable of collecting data from tall crops such as cultivated sunflower
1	Collect seeds and soil samples from across the natural range of three wild sunflower species	Rieseberg	Novel germplasm resources to be deposited into USDA-GRIN for maintenance and distribution
1	Train undergraduates, graduate students, and postdoctoral researchers	Bali, Burke, Dechaine, Donovan, Rieseberg	Training opportunities for 4 postdoctoral researchers, 3+ graduate students, and 8+ undergraduates
1	Middle school outreach in collaboration with Hilsman Middle School	Burke, Donovan	Educational opportunities for 40+ middle school students
1	Prepare manuscripts for publication; public presentation of results	Andrade-Sanchez, Bali, Burke, Dechaine, Donovan, Langlade, Rieseberg, White	Publications and public presentations of research results
1-2	Analyze WGS sequencing data of sunflower diversity panel for SNP and structural variants	Burke, Rieseberg	Dataset describing SNP and structural variants contained within the cultivated sunflower gene pool
1-2	Design 200k SNP genotyping array for population genomic analyses in sunflower and related species	Burke, Rieseberg	200k SNP genotyping array for use in sunflower and related species
1-2	Conduct first large-scale field screen of drought resistance in SAM population; GWAS based on the resulting data	Andrade-Sanchez, Bali, Burke, Donovan, Rieseberg, White	Identification of candidate genes/genetic variants underlying drought resistance in sunflower

1-2	Conduct growth room studies of drought resistance in SAM population; GWAS based on the resulting data	Burke, Donovan	Identification of candidate genes/genetic variants underlying drought resistance in sunflower
1-2	Conduct greenhouse studies of low nutrient resistance in SAM population; GWAS based on the resulting data	Burke, Donovan	Identification of candidate genes/genetic variants underlying low nutrient resistance in sunflower
1-4	Development of MAGIC population	Burke, Rieseberg	600 RILs derived from multiple cultivated and wild sunflower donors for sunflower research
2	Prepare manuscripts for publication; public presentation of results	Andrade-Sanchez, Bali, Burke, Dechaine, Donovan, Langlade, Rieseberg, White	Publications and public presentations of research results
2	Train undergraduates, graduate students, and postdoctoral researchers	Bali, Burke, Dechaine, Donovan	Training opportunities for 3 postdoctoral researchers, 4+ graduate students, and 8+ undergraduates
2	Middle school outreach in collaboration with Hilsman Middle School	Burke, Donovan	Educational opportunities for 40+ middle school students
2	Train high school interns via the Young Dawgs internship program	Burke, Donovan	Training opportunities for six high school students
2	K-12 outreach via the FARM SMART program at UC-DREC	Bali	Educational opportunities for 200 students (K-12)
2-3	Population genomic analyses of local adaptation to abiotic stress (drought, salt, low nutrient) in wild sunflower species; includes soil chemistry analyses	Burke, Rieseberg	SNP data for 1,500 wild sunflower samples and identification of candidate genes/genetic variants for abiotic stress resistance in the wild
2-3	Conduct second large-scale screen of drought resistance in SAM population; GWAS based on the resulting data	Andrade-Sanchez, Bali, Burke, Donovan, Rieseberg, White	Identification of candidate genes/genetic variants underlying drought resistance in sunflower
2-3	Greenhouse studies of resistance to salt stress in SAM population; GWAS based on the resulting data	Burke, Donovan	Identification of candidate genes/genetic variants underlying salt resistance in sunflower
2-3	Conduct field studies of low nutrient stress in select SAM lines at CWU	Dechaine	Identification and validation of cultivated sunflower lines that exhibit resistance to low nutrient stress for downstream breeding programs
2-4	Conduct detailed ecophysiological	Donovan	Mechanistic insights into the nature

	analyses of resistant and susceptible SAM lines		of abiotic stress resistance in cultivated sunflower
2-4	Conduct transcriptomic analyses of resistant and susceptible SAM lines	Burke, Donovan, Rieseberg	Identification of candidate genes/genetic variants, and/or expression networks involved in abiotic stress resistance
3	Design 50k SNP array using subset of markers from 200k array; genotypically characterize lines in MAGIC population; construct graphical genotypes	Burke, Rieseberg	50k genotyping sub-array for sunflower use in sunflower research; detailed genotypic dataset for MAGIC population; identification of MAGIC lines carrying putative abiotic stress resistance alleles
3	Prepare manuscripts for publication; public presentation of results	Andrade-Sanchez, Bali, Burke, Dechaine, Donovan, Langlade, Rieseberg, White	Publications and public presentations of research results
3	Train undergraduates, graduate students, and postdoctoral researchers	Bali, Burke, Dechaine, Donovan	Training opportunities for 3 postdoctoral researchers, 4+ graduate students, and 8+ undergraduates
3	Train Science Research Leadership Interns from CWU at UGA	Burke, Dechaine, Donovan	Training opportunities for 2-3 undergraduate interns who will take research knowledge back to a primarily undergraduate institution
3	Middle school outreach in collaboration with Hilsman Middle School	Burke, Donovan	Educational opportunities for 40+ middle school students
3	Train high school interns via the Young Dawgs internship program	Burke, Donovan	Training opportunities for six high school students
3	K-12 outreach via the FARM SMART program at UC-DREC	Bali	Educational opportunities for 400 students (K-12)
3-5	Conduct field trials and phenotypic characterization of MAGIC population at DREC; genetic map-based analyses based on the resulting data	Andrade-Sanchez, Bali, Burke, Donovan, Rieseberg, White	Identification of candidate genes/genetic variation underlying agriculturally important traits in MAGIC population
3-4	Conduct field studies of drought stress in select SAM lines at CWU	Dechaine	Identification and validation of cultivated sunflower lines that exhibit drought resistance for downstream breeding programs

3-4	Conduct Heliaphen analyses of drought stress in select SAM lines at INRA	Langlade	Identification and validation of cultivated sunflower lines that exhibit drought resistance for downstream breeding programs
3-5	Functional validation of the most promising candidate genes	Burke, Rieseberg	Validation of the effects of candidate genes for abiotic stress resistance; identification of beneficial variants from sunflower and related species for downstream breeding programs
3-5	Extend the sunflower genome database to provide access to project data in the context of the sunflower reference genome assembly	Burke, Rieseberg	Web-accessible, user-friendly interface for accessing the data from this project in the context of the reference sunflower genome
4	Prepare manuscripts for publication; public presentation of results	Andrade-Sanchez, Bali, Burke, Dechaine, Donovan, Langlade, Rieseberg, White	Publications and public presentations of research results
4	Train undergraduates, graduate students, and postdoctoral researchers	Bali, Burke, Dechaine, Donovan	Training opportunities for 3 postdoctoral researchers, 4+ graduate students, and 8+ undergraduates
4	Train Science Research Leadership Interns from CWU at UGA	Burke, Dechaine, Donovan	Training opportunities for 2-3 undergraduate interns who will take research knowledge back to a primarily undergraduate institution
4	Middle school outreach in collaboration with Hilsman Middle School	Burke, Donovan	Educational opportunities for 40+ middle school students
4	Train high school interns via the Young Dawgs internship program	Burke, Donovan	Training opportunities for six high school students
4	K-12 outreach via the FARM SMART program at UC-DREC	Bali	Educational opportunities for 600 students (K-12)
4-5	Conduct detailed ecophysiological analyses of putatively resistant/susceptible MAGIC lines	Donovan	Identification and validation of MAGIC lines exhibiting abiotic stress resistance for downstream breeding programs; mechanistic insights into the nature of abiotic stress resistance in sunflower and related species
4-5	Conduct field studies of drought/low	Dechaine	Identification and validation of

	nutrient stress resistance in select MAGIC lines at CWU		MAGIC lines exhibiting resistance to drought and low nutrient stress for downstream breeding programs
4-5	Conduct Heliaphen analyses of drought stress in select MAGIC lines at INRA	Langlade	Identification and validation of MAGIC lines that exhibit drought resistance for downstream breeding programs
5	Prepare manuscripts for publication; public presentation of results	Andrade-Sanchez, Bali, Burke, Dechaine, Donovan, Langlade, Rieseberg, White	Publications and public presentations of research results
5	Train undergraduates, graduate students, and postdoctoral researchers	Burke, Dechaine, Donovan	Training opportunities for 2 postdoctoral researchers, 4+ graduate students, and 8+ undergraduates
5	Train Science Research Leadership Interns from CWU at UGA	Burke, Dechaine, Donovan	Training opportunities for 2-3 undergraduate interns who will take research knowledge back to a primarily undergraduate institution
5	Middle school outreach in collaboration with Hilsman Middle School	Burke, Donovan	Educational opportunities for 40+ middle school students
5	Train high school interns via the Young Dawgs internship program	Burke, Donovan	Training opportunities for six high school students

6. GENERAL INFORMATION (required of all proposals recommended for funding):

- Please provide a final title of the project (without abbreviations):

Title: Evolutionary genomics of abiotic stress resistance in wild and cultivated sunflowers

- Identify any changes in PI or co-PI status. With respect to Dr. Bali, please provide a CV and Current & Pending Support document so that he can be added as a coPI as Dr. Wang's replacement.

Response: These documents have been included as e-mail attachments. There are no other changes in PI or co-PI status.

- Please check with your Office of Sponsored Programs to find out if the indirect cost rate at your institution has changed or will change between the time of proposal submission and the projected start date of the award (estimated at June 1, 2015). If any changes in the negotiated rate are expected, another revised budget would be required because new policy dictates that awards are based on current negotiated rate at the time of award, not at the time of proposal submission.

Response: None of the indirect cost rates have changed since submission of the proposal, and will still be current as of June 1, 2015.

- Confirm that this proposal is not under consideration elsewhere.

Response: This proposal is not under consideration for funding elsewhere.

- Provide an **award abstract** that will be entered into a public awards database. The first paragraph should be related to broader impacts and the second should provide some background and a description of the project. More details about the award abstract are provided here:

The heading of the abstract should list the PI, coPIs and any collaborators with institutional affiliations.

The first paragraph should be a nontechnical explanation of the project's broader significance and importance. This paragraph serves as a public justification for NSF funding. The text should be understandable to an educated reader who is not a scientist or engineer. It may provide information about why the proposed research is important, what fundamental issues may be resolved by the research, how society will be impacted, or how the project contributes to ongoing research in the discipline. The impact of the project outcomes should be emphasized.

The second paragraph should be a technical description of the project that states the problem to be studied, the goals and scope of the research, and the methods and approaches to be used. In many cases, this part of the abstract may be a modified version of the project summary submitted with the proposal. The text, however, should be written in the third person and should refer to the "project" or "research" and not use the term "proposal". Please also include a discussion of how the public can access data and biological materials and provide specific websites.

Response: A draft of the award abstract has been included as a separate e-mail attachment.