EDGE WEBINAR TRANSRIPT

SLIDE 1

Good morning or good afternoon, depending on where you are in the United States. We welcome you to the webinar from the EDGE program, the program for **E**nabling **D**iscovery trough **Ge**nomic Tools. In the room are all the members of the working group, so let's first go around and introduce ourselves. I'm Floh Thiels, the person at the bottom of the list, and I am a program director in the Division of Integrative Organismal Systems and, within that division, a program director of the Neural Systems Cluster.

I'm at the top and I'm Patrick Abbot. I am in IOS in the Behavioral Systems Cluster and a member of the EDGE working group.

And I'm Ford Ballantyne in the Ecosystems Cluster and a program officer for that program.

This is Brad Day and I'm also in IOS and part of this program.

Steve Ellis from the Division of Biological Infrastructure. I work on the Major Research Instrumentation and Infrastructure Innovation for Biological Research programs.

I'm Anthony Garza and am a program officer in the Division of Molecular and Cellular Biosciences and in the Systems and Synthetic Biology Cluster.

This is Diane Jofuku Okamuro. I'm a program director in the Division of Integrative Organismal Systems, and I am associated with the Plant Genome Research Program cluster.

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This slide provides a brief outline of what we are going to cover today. First, we will give a general overview of the program, including the purpose of this program, what it is trying to achieve, examples of what would be good fits with the EDGE solicitation, and, in particular, how it differs from some of the other programs in the Biological Sciences Directorate. We will then go on to talk about the submission requirements that may differ a little bit from other proposals, the particular sections you need to consider and include, and remind you that this, like other bio programs, does not have a deadline for the submission of proposal. Finally, we will go over some of the EDGE-specific review criteria that are in addition to the basic merit review criteria across all of NSF, with which you may be more familiar. This again, is to give you an overview, and we really encourage you to go back and read through the solicitation after the webinar. After this brief outline, you will be able to ask questions through WebEx, and we will go around the room responding to your questions about the solicitation and whatever else.

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The EDGE program falls into a suite of programs in the Biological Sciences Directorate pertinent to a fundamental question in biology, namely, the relation between genome, phenome, and environment. That's a long-standing question, and if this is a question of interest to you, then this program may be an appropriate program for you to consider. The EDGE program has existed for several years. The first competition was in 2016, and we are now in the fourth round of the EDGE program. Its purpose has been and still is to enable the advancement of understanding the relationship between genomes and phenomes, which is

part of the Rules of Llife and Understanding the Rules of Life. Understanding the Rules of Life is one of the 10 Big Ideas put forth by NSF.

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In the current solicitation of the EDGE program, we still have the emphasis as we've had in all of the preceding solicitations, namely, to support the development of tools, approaches, and infrastructure to enable testing of cause-and-effect hypotheses about gene function and phenotype in organisms for which such methods are presently unavailable. In addition to tool development, support goes to rapid dissemination of the tools to the broader community to carry out genome-phenome cause-effect studies. Thus, the idea is to enable investigators who study less commonly used organisms, so-called nontraditional organisms, to address the causal relationship between genome and phenome, and not only correlational studies. This tool development and dissemination track still exists and continues to be a strong emphasis of the program. However, this year we are introducing an additional track, one that expands the program from supporting tool development and dissemination to also support hypothesis testing on the question of the Genome-Phenome-Environment relationship. We are particularly interested in studies that aim to get at the causal relationship between genome and phenome in diverse non-model organisms and that take into account environmental variables, where the environmental context could be developmental, social, or genomic. The emphasis of this track is on complex traits and the gene regulatory mechanisms that underlie them, and the investigation of that relationship in various environmental contexts.

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So, we have these two tracks like we just said, called the functional genomic tools track and the complex multi-genic traits track. As Floh said, the FGT track is the continuation of the previous EDGE program or solicitation you may have been familiar with, building on that previous work with EDGE successes. With EDGE, the kinds of things that you might think about if you're going to submit to the functional genomics track will be development of mutant libraries and/or improving or developing high-quality genomes, and working on the phenotypic level in terms of thinking about genotyping and phenotyping methods; innovative approaches to manipulating genes and multiple genes simultaneously; innovative approaches to test gene function in targeted, single cells; innovative approaches for establishing function of single genes or networks of genes. That's the FGT track you may be familiar with.

What is new that you may be less familiar with is the complex multi-genic traits track, CMT track we call it. Here we are allowing for hypothesis-driven research for advancing one of these holy grails of biology, which is understanding for the map between genomes and phenomes. We recognize in this track that most traits of interest to biologists are unfortunately not behaving like single traits with no reaction norms, but rather are encoded by complex genetic architectures that vary across different contexts, social, environmental, developmental. So, this track is one where you might be thinking about taking a systems-level approach to looking at, for example, gene regulatory networks underlying complex traits. We might see things that come in that are innovative on the analytical end of things regarding genes and complex traits. We are interested in causation and, as we think about complex traits, we might be seeing things that elucidate the causal connections between levels of biological organization that underlie complex multi-genic traits. One final example, this is not exhaustive of course, is the elucidation of genome and epigenome interactions with the environment. The larger goal would of course be to be able to predict complex phenotypes across the context in which they occur. This is not an exhaustive list, these are just examples to feed you with ideas about the kinds of things that the solicitation will be supporting.

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Now that you have heard a little bit about what EDGE is, let's talk a little bit about what EDGE does not support. EDGE is really about enabling functional genomics in **diverse organisms** that are not supported by other programs. For example, the Plant Genome Research Program in IOS supports the functional genomics of complex traits in economically important crop plants, such as corn, soybean, wheat, and cotton. Proposals in genome-enabled plant systems with significant functional genomic resources would not be appropriate for the EDGE CMT track. However, I should also say that you can use the model organisms in the CMT track, but you have to include an extension to non-model organisms to demonstrate how generalizable the study is. In addition, we have programs that focus on tool development - if a proposal is solely focused on sequencing, setting up bioinformatics platforms, or enhancing software programs for predicting phenotypes through in-silico analysis, it would not be appropriate for EDGE. I would really encourage you to think about contacting the EDGE Working Group and/or send in a one-page summary of what you would like to do, so we can help you target your proposal, your idea to the right program. I have talked a little bit about the other types of programs that support EDGE-like activities -- so I'm going to hand it off to Steve to talk more about tool development.

Diane's last point about sending us a one-pager is really a good idea and several individuals have availed themselves of that opportunity to get guidance on program fit. A few people have written to us with questions about whether this idea for a new kind of instrument is appropriate for EDGE, say a new microscope or a new sequencer or something like that. In most of those cases so far, we have directed them to other programs that support the development of instrumentation relevant for biological research more generally, that is, tools that are not focused on understanding functions of genomes, understanding the complex traits that underpin the relationship between genomes and phenomes. So, if your new microscope or your new ecological sensor has a broader utility across basic biological research, we would help to direct those PIs and those inquiries to other programs for instance IIBR. If you have an informatic tool that already works or is not user-friendly and is to be scaled up in the cloud or something like that, then that might be a proposal ideal and more relevant for the ICB program. So, again, if you have a question whether your proposal fits with EDGE, it's okay to send the EDGE Working Group (to the BIOEDGE@nsf.gov email alias) a one-page or a half-page summary. Two or three pages is not better, so please keep your summaries concise and send it to the Working Group. One of us will respond as fast as we can to give you the appropriate guidance about programs and proposal submissions.

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Submission requirements. There is no submission deadline, we will accept proposals anytime. We want to emphasize that the PI should carefully read the instructions for the proposal preparation in the solicitation and in the relevant sections of the proposal and award policies and procedures guide NSF 19-1 or NSF 20-1. The title must begin with functional genomic tools track, FGT, or complex multi-genic traits track, CMT. The project description for both tracks has to have a section on intellectual merit, on experimental approach, on broader impacts, and then there is an additional subsection for people in the FGT track has to address research community impact. Please note that we list here only sections that are non-standard aspects of the proposal. As Anthony said, please be sure that you read the solicitation and also the appropriate sections in the PAPPG. I want to elaborate briefly on what we hope to see in the project description, which entails the intellectual merit, the experimental approach, and the broader impacts. With respect to the intellectual merit, consider describing not only the goals, and the strategies and approaches to achieve them. Highly competitive proposals also include positive and negative controls, relevant metrics that will help determine whether the

project is successful, and aspects such as transformation efficiencies if it is a proposal for the functional genomics track. With respect to the item at the bottom of this slide: a section on the research community impact is an extra requirement for functional genomic track. In that section, articulate clearly what the beneficiary community or communities are, how they will be enabled by your project, and identify clearly the bottleneck that will be overcome with the approaches that you propose. It also is helpful if you articulate clearly the scientific questions that can be answered with the approaches you propose and how the proposed tools overcome the impediments currently faced by the community.

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For the EDGE solicitation, there are some features that are distinct and a little bit different from other programs in BIO, and we wanted to highlight the submission requirements that are particular to this program. This is in part because if you don't abide by the requirements of the solicitation your proposal may be returned without review, and no one wants that to be the outcome. We mentioned at the top that it's critical for you all to read and carefully understand the solicitation and send us questions if you have them. The solicitation number is on each slide. We want to highlight that the supplementary document section for this proposal needs to include a few specific documents. First of which is the project management plan that really details how the activity will be coordinated. This document is especially important for EDGE proposals, because we know many of the proposals will be collaborative in nature and involve interactions among different organizations that may be spread out geographically or that may pose other complicating factors. Therefore, we want you to include a three-page plan in your submission as a supplementary document. Note that I say supplementary, not a single copy document. The difference is that single-copy documents are not visible to reviewers but supplementary documents are, and we will ask reviewers to comment on the project management plan. This plan is important if you have more than one institution involved in the project. Another part, the data management plan, is required for all proposals submitted to NSF. Another critical supplementary document, one that can be up to three pages in length, serves to describe how the lessons learned from your project activity will be disseminated. If you are developing a new method to do functional genomics in a nontraditional system, then how will you teach people about it? In the solicitation, there's a whole series of helpful questions for you to think about as you write your narrative for the dissemination and education plan of the supplementary documents. So, please be sure to look at those and make sure you consider the interests of those questions.

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This is Brad, and I will spend a few moments with the review criteria. They give you an idea what happens once your proposal has been submitted to NSF, what advice and insight and expert opinions we are looking for from our panelists and ad hoc reviewers. I also think it's useful as you start to prepare your proposal to go through and begin to evaluate the intellectual merit and the broader impact of the proposal. To highlight a couple of the key points: First and foremost, the proposals should focus on fundamental research that generates knowledge, and for NSF, this is almost always achieved through hypothesis driven research. For the EDGE program, it is really up to you as a submitter to convey to the panelists and the expert ad hoc reviewers that you have presented a compelling case that the research is asking fundamental, exciting questions of a mechanistic nature in an emerging system or a non-model system (i.e., an underrepresented orphan system). In this regard, my advice is for PIs to look at the proposal and make sure you're presenting compelling arguments for why it's important to use your proposed system to address a question about the basic functional mechanisms, or physiological interactions, with the environment etc. In parallel, you should include in the poroposal a short narrative as to why it is important to invest in the systems both in terms of

time and money – specifically emphasizing how this research will advance or accelerate understanding of broader cellular organismal function. I would also recommend that an effort should be made to extend this narrative to include environmental interactions. Above all, it is critical to communicate how this research will contribute to a much broader concept in understanding, simply beyond the scope of the individual organisms (i.e., non-model system). As a final component, and one that I have appreciated in my time as a reviewer for the NSF: the qualifications of the team. Is this team positioned and do they each bring the expertise necessary to address fundamental questions being posed in the research program?

For broader impacts I'm sure you're all familiar with the broader impacts and how important they are to NSF. In general, broader impacts are there to help deliver a potential benefit to society. With the EDGE program, one other criterium that may be important for you to consider – with respect to the scientific broader impacts – is why is it important to invest in investigating the proposed biological question with the proposed system; how will that broaden our general knowledge. To use an example, we know so much about corn, soybean, and wheat. If you're proposing the development of a new plant system, you should ask yourself: How will a particular study in an emerging system broaden the understanding of how plants have evolved, and moreover, how a particular trait enables a plant to adapt? In this vein, this might also be extended to ask questions about the importance of the target complex trait, generational memory related to the trait, etc. For societal broader impacts, which are an equally important component of a successful NSF proposal, what is meant is how this research will reach, educate, and inform society. Also, I think, it is always a good idea to include metrics. When you're describing the broader impact state how you are you going to determine that the broader impacts you propose reached all of the corners of the society.

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This is Ford again. There are some specific criteria associated with the EDGE solicitation, for both the functional genomic track and the complex multi-genic traits track. We are interested in knowing what the impact on the larger community of researchers will be. In particular, we want to know how catalytic the proposed tools will be, how products will help move research forward, and who the beneficiary communities will be. Floh mentioned this earlier, but I'll reiterate that we are also interested in the feasibility of the proposed projects. Proposals have to have a high likelihood of success and must convince reviewers that the potential to achieve stated goals is high. As Steve mentioned, the management plan required for a proposal from multiple institutions will be critically important as a part of the review process. So, it is very important to have a well thought out and clearly articulated management plan for the proposal for either track if it involves multiple organizations. And finally, if you are submitting a functional genomics track proposal, we will be evaluating the quality of your dissemination and education plan, which is the other supplementary document Steve alluded to. For this track, you need to have a well thought-out and well-articulated plan for how you will disseminate the research knowledge you generated, and how it will have an impact on relevant researcher communities.

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This brings us to the end the formal part of our webinar. If you have questions, this is your opportunity to get immediate answers from the entire EDGE working group. Please send your questions via WebEx Q&A. Go to the bottom right side of your screen, you should see the Q&A box. Just type your question. We will read the questions out loud and answer them. The WebEx webinar will posted on the EDGE Program page in the coming weeks. And as Steve and Diane mentioned, as you are preparing the proposal and questions arise, please take advantage of the fact that you can email your questions and/or a one-page description to the EDGE working group. The alias is shown at the bottom of the screen.

QUESTIONS and ANSWERS

One of the questions that we received was whether or not a project that involves multiple institutions has to submit a management plan and the answer to that question is “yes”. We also want to say that proposals involving multiple institutions have to be submitted as a single proposal from a lead institution with subawardees. If you submit it as a collaborative proposal from multiple institutions, it will be returned without review. So, make sure you read that part in the solicitation and also the relevant instructions in the PAPPG for a collaborative proposal from a single institution.

One of the other questions we received is the question of how do you know whether or not you have a non-model organism. The short answer is if you have to ask, you probably don't have a model organism. This is something that we actually struggle with. In general terms, if you're thinking of classical stories about genetics and phenotypes, such as those of fruit flies and white mice; these are really enabled systems for which there is a lot of data available. The purpose of this program is to increase the power and insight gained from comparative biology and include a more diverse cadre of organisms in the research endeavor. If you have a question about this point, please contact us. Some systems that have been used extensively in particular research areas—for instance, songbirds might be established as a model in a given research area. But this system is not enabled to the same extent as other new and emerging experimental systems. Therefore, let us know about your questions before you submit a proposal, so that they are addressed in advance of the proposal submission. We do not comment on priorities, but we can comment on fit and will say if you're better off submitting to another program, for example the PGP program or one of the core programs.

I will extend what Steve said and add that often times what also defines a model from a non-model are also questions that are framed by a biological question. For example, let’s look at plant stomata, their patterning, and how stomata evolved – both in terms of their function, as well as their interactions with the environment. This question could in fact be framed in a context that is completely appropriate for EDGE. If, for example, you look at the evolution of stomata across land plants, and you frame your research to include how stomata evolved – from what is a non-model plant – to a more established system, such as Arabidopsis. What are the factors that evolved to regulate stomata patterning? What are the processes that evolved, in parallel to stomata development, that can be defined using a comparative analysis between a model and a non-model system? Thus, the research is framed by the larger biological question that spans both model and non-model organisms, and in investigating this, we learn not only about the non-model, but gain insight into the broader function of a highly conserved – and specialized – cell type in plants. Thus, the over-arching question one should consider when framing their research for edge is: Why is it important to study this particular plant to understand this given biological process? It's not so much about going in the back of the cave and looking under a rock for something that no one is working on. You still need to connect to a fundamental biological question that will generate knowledge that broadly applicable to all biology's.

I want to build on what Brad just said. For the genomic tools track, the idea is to focus on organisms that are not genomically enabled organisms, that is, organisms for which these tools are not available, and cause-effect tests cannot yet be conducted in these communities because the tools are not available. And it's important to emphasize what Brad said: You have to articulate one or several fundamental questions in biology to justify the development of those tools for use in the target organisms. With respect to the multi-genic traits track, it is permitted to test the relationship between G and P in an environmental context in a model

organism, if that's where you want to do the proof-of-principle. However, you have to propose experiments that extend into so-called non-model organisms. Ultimately, we would like to get the community into a place where they can apply the tools to address meaningful biological questions, and they can address the questions in the organisms most suited for that question. The community should not be held back by the lack of appropriate tools and approaches to address fundamental questions.

We have a couple of questions asking whether it's okay to submit single PI-proposals to the EDGE program and or whether the EDGE program is designed to prioritize multi-institution proposals. Single PI-proposals are acceptable as long as you're asking a compelling question that is relevant to the EDGE program and you present a feasible plan. That's how we evaluate all proposals no matter where they come from. So, we don't have an explicit requirement or intent to fund only multi-institution collaborative proposals. But those are okay. It’s all about the plan you develop and present.

Another question is whether inclusion of tool development is required for proposals. It is required for the first track, that is, if you're focusing on the functional genomics tools track. So, “yes”, we expect those proposals to include tool development and dissemination. Don't forget the dissemination piece. With respect to the complex multi-genic traits, for that track, the T stands for traits and not tools. It is not necessary to develop new tools. A competitive proposal probably includes the development of appropriate analytic approaches or theory that can drive the experimental work, but it is not required that the proposal include tool development. If you wish, the idea of the EDGE program is first, in phase 1, to support tool development, and in phase 2, to allow addressing big questions using those tools. It doesn't mean you have to use tools that were developed under the EDGE program, but the idea is that you deploy cutting-edge tools to go after the GxPxE relationship.

I would like to elaborate a little bit as well for the CMT track, the complex multi-gene traits track. It's quite possible that in order to address the question of interest, you need to develop some tools in addition to the tools that are already available. That would be okay as well.

We had a question come in: For the CMT type, do we have to have all candidate genes in hand or may candidate [genes] be identified as part of the proposal. How does the program define complex trait? A trait that is regulated by more than one or just one gene, or a trait that is regulated in a complex way? The EDGE program is open to a range of ideas, as suggested by what we say in the solicitation. We want to advance our understanding of complex traits, and if there are, as examples, environmental, developmental, or epigenetic regulators of trait expression, penetration, or impact, then that seems like it could be relevant. And if you had all the answers before the proposal was ready, then you would not have anything to submit. So, you don't have to all the candidate genes in hand. But, generally speaking, if you say “I'm going to look for stuff and then I will investigate what I found,” that tends to be a problem with interdependent aims, and reviewers start to question the feasibility of the endeavor. So, think about how you craft the submission. If your activities are first dependent on discovering something that is critically important, then what happens if you don't? What if it is a bunch of factors with small effects?

The CMT track was written intentionally to stimulate those kinds of questions about what is that map between genes and traits, how to we characterize that map, where it may involve a complex gene architecture, a complex regulatory network, or complex traits. Come to us with that one-pager and have that conversation to see to see if the EDGE program is a good fit for your question.

One of you asked whether preliminary data is required. Preliminary data is always a very effective way of addressing reviewers' concerns, and reviewers are asked to judge feasibility. So, preliminary data helps reviewers to evaluate the feasibility, and that applies in general to all proposals, not just to EDGE proposals.

Another question that came into chat is: For the intellectual merit, can you elaborate more about including metrics of whether the project is successful, and is it something like an assessment plan for an educational outreach program? What is meant by metrics is basically you want to think about the risks of your project, regardless of whether it's a tool development and dissemination project or a hypothesis-testing project, what are the risks in getting to the outcome. One way to address the question is to include alternative outcomes and basically give the reviewers an idea of what you will do if you don't observe the expected outcomes. Likewise, with tool development and dissemination, there are risks. You may not be successful in developing the tool. What are your alternate paths to get to the point of enabling the community as you hoped to enable it?

I think that's the thing to think about when crafting your dissemination plan. We don't want great tools to be developed by individual labs and stay in those labs. We require them to be available to the community to advance the way that the whole community pursues its research. We did have a question about asking us to talk more about the dissemination plan and if we can give examples. Think about how techniques are broadly distributed. There are wet lab workshops and summer training camps, or there are labs that encourage visitors or online forums. There is a journal that talks about experiments as an example, and that journal has online video tutorials and details about how to execute a particular technique. So, there are any number of ways that you can do it. There is no right answer. It is whatever you can convince yourself and then the reviewers and program that is going to be a feasible compelling and effective way to disseminate your findings and broaden the use of your successful approaches.

I would like to add that the dissemination plan is needed only if you submit a proposal to the functional genomics tools track, and when thinking about that plan, it is not a bad idea to consult with the beneficiaries of your tools. So, if you want to develop something and you want to have a robust user community, it's a good idea to contact that user community and do market research. Get some input from the users, not just about the specifics of the tool that satisfy their needs, but also about what means of dissemination are easily accessible to them, so that they can use the tools in their laboratory.

Another question we received asks if can we talk about the relationship between the EDGE CMT track and the standard solicitation, e.g., to MCB. It depends on the project and if the project is focusing on systems tools and if the project is developing the tools for a system that's not a model and does not have a tool available and also if you're interested in a G to P relationship with respect to multi-genetic traits. If that is the focus of the research project, then it might be appropriate for EDGE. I guess I would have to hear the specific project to tell you if it was appropriate for any particular division.

That goes back to the prior advice to work on your one-pager and send it to the EDGE working group for guidance on program fit, and again that email address for sending those summaries to is a BIOEDGE@NSF.gov.

Another question we have received is whether or not EDGE proposals are reviewed by other programs or whether the reviewing community is only selected by the EDGE program. That depends if you feel strongly that your proposal should be reviewed by another program. It is useful if you signal that to the program officer by contacting the EDGE working group. In principle, they are no standing plans for having co-review of the proposals. However, if we deem it appropriate or if you think it will be appropriate, we will certainly consider that possibility.

I do want to emphasize that this is a working group with representatives from all four divisions in BIO. So, when we get a one-pager or when we get the proposal, we can better assess whether it should be reviewed by the EDGE program or if there is a better fit for it in another program. We are the working group, but we are not the only program directors, and we talk with fellow program directors about proposals we are managing, especially when we see there might be relevance to or overlap with other programs. NSF can encompass a lot of different review mechanisms. Just as an example, other program directors help suggest ad hoc reviewers to get the right perspective. And they may or may not contribute funds from the other program. We will take care of that. Your job as PI is to submit the most compelling proposal you can.

I guess embedded in what just transpired is that the working group involves members from all of the divisions in the BIO Directorate, and we welcome if you see this as an opportunity to integrate across the research areas typically supported by the various divisions. It's obvious how EDGE involves the Division of Biological Infrastructure, but this may be an opportunity for you, if you're someone who typically applies to MCB programs, to think more or push yourself to go more in the systems-level direction, and those who work typically in the evolutionary domain or the ecological domain to take advantage of some of the new gene manipulation tools that have come online. So, really this is the edge of the platform for integration.

Another question just came in asking whether reviewers will be skeptical if proposals use agricultural animal models, as an example. We tell the reviewers to be skeptical of everything that comes in. We want them to assess the extent to which the proposal makes a compelling argument in the experimental system that was selected. It's up to the PI to make that compelling case about why this is the right experimental system to investigate, why the question is important for basic biology and for understanding genome to phenome in context. The program is species-agnostic, except we don't study human health. Beyond that, it is up to the PI to make a case for why they have the right system.

We had a question come in asking whether the project management document is appropriate for within-university groups, or is that document only required for collaborative proposals, those with several multiple organizations and submitting with subawards. So, if it's all within your university, you just describe the roles of the investigators and coordination in the usual way.

Another question was about using or performing field trials with phenotypes. Again, it will come down to the manipulation or the complex multi-genic traits and their expression in different contexts, including ecological contexts, and whether you are asking an interesting question about that. There are other resources available, for instance, programs funded by BIO within the NSF, such as the NEON program. The NEON program webpage provides a resource for different ecological data sets that could prove to be useful.

With respect to the project management question, the reason we are asking for a project management plan in the case of multiple institutions is that we would like to have in writing

from you how you envision efficient communication between the different institutions, something that comes more easily when you're on the same campus but can be a challenge when the proposal is from institutions across the country. The principal purpose of the project management plan is to clarify how you're going to accomplish that. It also tells us more about the work, in particular outcomes from the project, which can get a little bit more difficult if you're in different institutions.

Just to build on what Diane just said, a multi-investigator proposal, whether from the same or different institutions, needs to articulate clearly who contributes what piece of the project. That is always a good idea, because we tend to link that information with the corresponding biosketches to evaluate whether or not the expertise and qualification of the investigative team is appropriate.

On a related note, in the solicitation, it explicitly emphasizes that generic letters of support are not appropriate or allowed with these submissions. There is a standard format described in the PAPPG for how collaborators can indicate their willingness to perform those roles and responsibilities described in the project description. So, use that form. Do not include letters from famous people who say what a grand investigator you are and how this would be nice, but they don't actually commit any resources or promise to do anything that you would describe in the project description. Those generic letters of support are not allowed.

We have one more question here. What is a trait for the CMT track? Is it anything that is measurable and is it required for it to be complex? I would say that's really up to you to make the case for it. As the person writing the proposal, you have to make a compelling case that this is a well-defined trait and something about it can be measured that is ecologically or behaviorally or socially relevant. You have to think about the context and in which that trait emerges. It is up to you to decide what's the right level of complexity and how to study the underlying genomic basis for how that trait emerges and, potentially, even evolves. We are trying to understand the relationship between the genome and phenome. So, you have to make the case, and presumably, what you're proposing in the organism or organisms you are proposing to study can shed light on that essential relationship in a way that's compelling and novel and edgy. So, it is really up to you, and if you have any questions about it, I will reiterate what Steve said, which is: reach out to us here with that one-pager and have that conversation. We are here to help in that regard.

We received another question, one that we occasionally have received before because it is relevant to earlier versions of the EDGE program: whether letters of support are permitted from the community that will be the beneficiaries of the tool. Letters of collaboration from individuals who collaborate on the project are permitted, and their activities should be articulated in the proposal. If you want to demonstrate that you reached out to the community, that there is in fact interest by a beneficiary community, then including, for instance, a description of the community in the proposal is a good idea. And if you have a letter of collaboration from the corresponding professional societies--something we have seen in proposals--, or from other groups that benefit from the proposal, that's all appropriate. Letters of support you will have to remove because they are not permitted.

There may be better ways to demonstrate interest by the community if you have evidentiary support for your argument that what you propose will be helpful. For instance, white papers or challenge documents published by societies and in peer-reviewed journals that highlight the need for a system. Such evidentiary support is what you want to develop, It can be very compelling, much more so than one individual that the reviewers or program people may not

know. Also, the people that would benefit from your work, if they're actively involved in your project, for example, by going to help lead a training course at their home institution and their roles are described in the proposal, then they are functionally collaborating on the dissemination effort and have the right to write a letter of collaboration.

Thank you all for joining the webinar and sending interesting questions. Hopefully, we addressed all your questions and if more questions arise, please email us, and we look forward to receiving your proposals. That concludes today's conference. and thank you for your participation.