Set 1 of Frequently Asked Questions for Broad Agency Announcement 12-11

Question 1--What are the relative roles that the contractor vs. the Government will have in organizing the working group? (i.e., should most members of the working group come from people that are receiving funding through the prime contractors, or will this be mostly a mixture of government staff along with a few contractor-invited subject matter experts)?

Answer 1--The composition of the working group will be determined through discussions between the Department of Homeland Security (DHS) Contracting Officer's Representative (COR) and the Prime Contractor. The Prime Contractor will have the responsibility for organizing the meeting. It is anticipated that the group will consist of Contractors funded under the TFA, members of Government agencies that are stakeholders in the project, and possible outside Subject Matter Experts (SMEs).

Question 2--Will the government or the contractor be responsible for identifying and paying for meeting venues for the working group? Also, will the contractor be expected to pay for attendance by SMEs who are not part of the contractor's team?

Answer 2--The working group sessions will be held at a Government facility in the Washington DC metropolitan area so there will be no cost for the venue. The DHS COR will identify the facility at a later date. Any potential outside SMEs that are invited to participate in the working group should be covered by the contractor.

Question 3--During Phase 1, will the contractor be populating databases (government- or contractor-provided) with genome data? Or will this phase be devoted to just identifying what genomic data are available? Will all building and populating of the database be NCBI's responsibilities?

Answer 3--The database for the genomes will be developed and hosted by NCBI. The Contractor will be expected to identify available genomic data and populate the database as they are able to collect the genome data.

Question 4--In TFA3, is this a call for bioinformatic analysis of whole genome sequences that are already sequenced or is it a call to provide and sequence new strains?

Answer 4--This call has multiple tasks. The first task is to determine and collect what has already been sequenced for the bacterial species listed in the BAA and deposit these sequences into a database at NCBI. The second task is to perform a gap analysis to determine and prioritize what strains need to be sequenced for each of the bacterial species. The third task is to sequence new strains.

Question 5--For TFA-3, since Phase 2 doesn't have a defined scope, duration, or funds available, should the white paper have costing for Phase 2? Or would it be acceptable to

describe the general approach to meet the objectives of phase 2 and state that costs remain to be determined. Alternatively, should we provide a notional level of effort for Phase 2 and cost accordingly?

Answer 5--Since cost is an evaluation criterion for source selection, prospective vendors should provide a notional level of effort and cost accordingly for Phase 2. Prospective vendors should include a cost analysis for a high quality draft sequence of a microbial genome. DHS does realize that sequencing costs continue to decrease with technology improvements but prospective vendors are requested to provide your best estimate.

Question 6--TFA-3 specifies bacteria, virus, and fungi. Does DHS have a particular fungal threat list in mind to focus on?

Answer 6--The fungal threats are located in the plant pathogen column in Appendix E.

Question 7--Regarding TFA-2: Development of a procedure to support the transfer of viral cDNA generated in a BSL-3/4 laboratory to BSL-2 laboratory for genomic analysis, would it be acceptable to submit a proposal for the development of a system that would simplify sample preparation, library preparation, and next-gen sequencing in containment, rather than transporting cDNA out of containment for sequencing? Such a system would serve to reduce the sample to sequence time without having to deal with the issues of handling positive stranded RNAs outside of containment?

Answer 7--This would be considered a non-responsive proposal.

Question 8: Is some sequencing new samples required for topic 1?

Answer 8--Not necessarily.

Question 9--Is there a need to demonstrate tool utility by conducting experiments for topic 1?

Answer 9--In silico experiments can be used along with publically available data to demonstrate utility.

Question 10--Is benchmarking or comparison of tools to known methods, such as SNP phylogeny panel analyses needed?

Answer 10--As much as possible, benchmarking tools relative to existing methods is encouraged.

Question 11--Is bioinformatics tool intended for the use of NBACC at Fort Detrick?

Answer 11--Multiple U.S. Government customers will have access to the bioinformatics tool. As stated in the Broad Agency Announcement, the software should be made freely available to non-commercial users, preferably using an open-source license.

Question 12--What is context of sample? Air, clinical, soil, water, 10%contamination? Low abundance thresholds?

Answer 12--Forensic samples can be collected from several matrices. But that is a sample collection/sample processing problem. Proposers should assume viable DNA has been collected and sequenced, and focus on developing a method for data analysis that is flexible and applicable to any sample.

Question 13--Are alignment and alignment-free approaches within the scope of topic 1?

Answer 13--Yes.

Question 14--Are experiments expected to show proof of concept of pipeline under topic 2?

Answer 14--Yes.

Question 15--Are host/microbe variation studies and sample sequencing expected under topic 3?

Answer 15--Yes.

Question 16--TFA-1 makes this assumption: "The proposed methods should assume sensitive alignments (e.g. BLAST) between all sequencing reads and the search database are available…" We do not feel that BLAST alignments are necessarily either the only or the best way to approach the stated desired end goal of "development and application of mathematical models for (1) estimating the likelihood of a genome being present in a metagenomic sample, and (2) the most likely composition of a metagenomic sample including a list of genomes and their relative abundance." If we propose a metagenomic solution that is not based on poorly-scaling BLAST alignments, will this be considered non-responsive?

Answer 16--Yes, this would be considered non-responsive.