

## Questions and Answers (Q&A): BioForensics BAA Call 14

Question #	Reference	Contractor's Questions	Government Responses
1	BAA 14-003/Call 0014 page 3, Section 4.1.1.2 <b>TTA2</b>	Is it a requirement that a sample must be extracted with a single method to yield DNA and RNA from the full range eukaryotes, prokaryotes and viruses? Or, is it possible to subject a sample to more than one extraction method, each optimized for particular target types?	The preference would be to have one method that would extract all DNA and RNA. If multiple methods are proposed the rationale for this approach should be described in the proposal.
2	BAA 14-003/Call 0014 page 3, Section 4.1.1.2 <b>TTA2</b>	What are examples of background sample types of highest interest? How many different matrices are expected to be evaluated? Is there an upper limit to the mass or volume for a sample being processed?	DHS is interested in complex sample types such as soil. It is anticipated that the sample volume could be up to 10 grams
3	BAA 14-003/Call 0014 page 3, Section 4.1.1.2 <b>TTA2</b>	How deep of coverage is desired to detect targets present at trace levels?	The goal of the DHS project is to be able to detect trace level of DNA in complex sample types
4	BAA 14-003/Call 0014 page 3, Section 4.1.1.2 <b>TTA2</b>	Is the purpose of the sequencing to prepare a profile of the components of a sample, or to detect specific biological agents, or both?	It is both
5	BAA 14-003/Call 0014 page 3, Section 4.1.1.2 <b>TTA2</b>	Since TTA 3 is a separate topic, is it acceptable in TTA2 to use currently available tools to allow determination of the quantitative detection limits for targets of interest?	It is up to the proposer to determine the optimal methods needed to support the goals of TTA2, and TTA3.
6	BAA 14-003/Call 0014 page 3, Section 4.1.1.2 <b>TTA2</b>	Since proposers may not have all possible NGS platforms, will DHS provide access to platforms not in the proposer's lab? Or should the proposer include the costs for vendors to provide sequencing services?	No, it is anticipated that the proposer will gain access to sequencing platforms needed to support the project.
7	BAA 14-003/Call 0014 page 3, Section 4.1.1.3 <b>TTA3</b>	Is DHS interested in a systematic evaluation of existing metagenomics methods currently available, or in the development of a completely new approach?	DHS is interested in having widely accepted, scientifically sound, process to conduct metagenomics analysis

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8	BAA 14-003/Call 0014 page 3, Section 4.1.1.3 <b>TTA3</b>	Will DHS consider commercial metagenomics tools that may require renewable licensing agreements to be in place for their continued use?	Potentially, but they would have to be well justified.
9	BAA 14-003/Call 0014 page 3, Section 4.1.1.3 <b>TTA3</b>	Will DHS provide the proposer with real-world datasets for development and testing of the metagenomics software?	The data sets will have to be generated by the proposer.
10	BAA 14-003/Call 0014 page 3, Section 4.1.1.3 <b>TTA3</b>	Is DHS interested in tools designed to carry out the comparative analysis of multiple samples (i.e., similarity algorithms) or solely in the profiling of individual samples?	Yes to both
11	BAA 14-003/Call 0014 page 3, Section 4.1.1.3 <b>TTA3</b>	Is DHS interested in a completely self-contained system (e.g., reporting tool, GUI, pre-processing tools, etc.), or in the development of an algorithm amenable to being incorporated into existing DHS workflows?	The output of the project does not need to be self-contained. DHS is interested in having widely accepted, scientifically sound process to conduct metagenomics analysis.
12	BAA 14-003/Call 0014, page 3, section 4.1.1.3	Is the primary purpose of the analysis detection of biological threat agents, or collection of contextual information for identifying the provenance or delivery route of the threat agent?	The purpose of the BAA is to provide full characterization of complex metagenomics samples that will include supporting the identification of biological agents.
13	BAA 14-003/Call 0014, page 3, section 4.1.1.3	Is the desired information resulting from the metagenomic analysis the taxonomic identification of organisms and community structure of the sample, or identification of the gene and/or allele content of the samples, or both?	Yes to all of the elements that can be derived from metagenomics data.
14	BAA 14-003, page 3, Section 4.1.1.1, paragraph 1	Is the goal to simply sequence the isolates, or is there also a need to assemble and do some basic analysis on the isolates as well?	DHS is interested in having widely accepted, scientifically sound process to conduct metagenomics analysis.
15	BAA 14-003/Call 0014 page 3, Section 4.1.1.1 <b>TTA1</b>	Can the near neighbors include species that are outside of the genus <i>Francisella</i> , but are phylogenetically close to <i>Francisella</i> ?	Yes.