Q&As from QIAGEN's Webinar on Biobanking and Biorepositories
March 16, 2010

1. **Attendee # 1: "I am interested in hearing more about how there is no manual transcription for accessioning"**

   Answer: Samples are electronically pre registered into the RUCDR LIMS system. This information contains all study identifying information as well as meta data that is connected to the sample for QC purposes. When samples arrive they are photographed and scanned; the information is checked against the tube and then validated for processing. There is no manual entry of data once the samples arrives at the repository. There is a mechanism to edit data that may have been entered wrong but this is only done with the proper authority and audit trail in place.

2. **Attendee #1: "I would like to hear about the sample preregistration, etc"**

   Answer: The sample pre registration captures information including and not limited to: study ID, alternate ID, gender, age, family status, date collected, etc... The system automatically assigns services based on unique ID's on every blood tube in the kit provided by the RUCDR which is linked to every service approved for each project. The pre-registration is done through a web interface in the LIMS which is accessed directly by the investigator or collection center acquiring the sample.

3. **Attendee #2: "Are there data for miRNA storage and assay?"**

   Answer: We have a deep database of QC data on miRNA enrichment from total RNA derived from PaxGene tubes. We use QPCR to qualify and quantify miRNA from our isolation/enrichment. Please contact me with a specific request for data on these metrics.

4. **Attendee # 3: "DNA Distribution: Do you thaw a so called master tube, aliquot into a second container, and send those picked collections in plate form or tube?"**

   Answer: Depending on the sample (i.e. DNA, RNA, plasma, etc...), we store many different numbers of aliquots. With that said, for DNA we use stock tubes to create distribution sets that are sent to investigators. We do not have "working stocks" in most cases as DNA is stable and can withstand many freeze thaw cycles needed to fulfill distribution requests.

5. **Attendee # 3: "Is this data published?"**

   Answer: if you can let me know which data from the presentation you are more interested in I am happy to provide the references.

6. **Attendee # 4: "With respect to sample acquisition for biobanking, in order to minimize mix-up errors, does it make sense to have a biological code associated with the sample at time of collection?"**

   Answer: Yes, this concept would be beneficial. With that said the solution would have to have the scalability and cost commensurate with the task. I would imagine for larger banks you would need a system that could code millions of aliquots at a cost of pennies per sample to fit into an established repository. Data management for this concept would also be critical.

7. **Attendee # 4: "Freeze thaw data - how was quality of RNA assessed as 50% intact after 10 freeze/thaws?"**

   Answer: The quality has been assesed by generating QPCR and microarray profiles compared to baseline. Sample quality was measured by correlation to profiles at baseline.

8. **Attendee # 5: "Is Nuegen amplified RNA suitable for Nextgen RNA-seq?"**

   Answer: Yes, NuGEN has a commercial RNA amplification product for RNA-seq.

9. **Attendee # 6: "Do you handle DNA from saliva, i.e. Oragene DNA kits? Do you treat that differently from blood DNA?"**

   Answer: Yes, we do extractions from saliva, specifically Oragene kits. We do treat them differently in both extraction and QC protocols. Most investigaters would like to know how much human DNA is present per sample and not how much DNA is extracted per sample as is the case with WB DNA. The QC metrics we use for quality are also different for saliva DNA.

10. **Attendee # 7: "Do you have a publication available on your 96 SNP panel for QC?"**

    Answer: No, the work is in press and soon to be available commercially for purchase.

11. **Attendee # 8: "What kind of data are you collecting to go with the samples you are collecting?"**

    Answer: There is a vast amount of clinical and study data collected with every sample. The amount and type of information is study dependant. With that said, NONE of the clinical or study data resides in the RUCDR proper. All of the sample data is stored in a separate database in a separate infrastructure in another state! No one in the repository can access that data or link it to a sample. All samples do have some meta data associated with them (i.e. Gender, age, date collected, family status) that allows the RUCDR to QC samples effectively.

12. **Attendee # 9: “Is the Institute able to provide advice to new banks to be created in emerging countries?”**

    Answer: Yes, we would be happy to help in any way we can and have helped other programs in the past. You can contact me at brooks@eohsi.rutgers.edu to discuss how we might be able to help you with your project.

13. **Attendee # 10: “How do you see Biobanking changing in the next 5-10 years?”**

    Answer: Biobanking will be evolving over the coming years in response to new technologies being used for analyses as well as the growth of molecular and personalized medicine. I think that large and small medical centers alike will be investing and building local biobanks for both research and clinical centers.

14. **Attendee # 11: “What technology trends do you see impacting Biobanking moving forward?”**

    Answer: Most definitely the development of new analytical tools that will impact biobanking efforst moving forward. There will be better utilization of every sample collected. Additionally, new chemistries that maximize the utility and isolation of individual components from each sample will lead to big changes. Overall, technologies geared towards the creation and more efficient use of renewable biological resources will shape the field.

15. **Attendee # 11: How much sharing of samples and information occurs at the global level? Are there specific factors that impact sharing?”**

    Answer: Unfortunately there are more issues that impact sharing than facilitate sharing at this point but this Is rapidly changing. As new studies and biobanks are being created the focus on sharing of samples is rapidly evolving. Consents are being written for broader storage and usage of samples that will ultimately lead to more efficient usage and sharing of samples across programs.

16. **Attendee # 11: “What guidance can you offer to a group that is interested in setting up a biobank?”**

    Answer: Spend some time with established bionbank programs to gain the practical operational experience needed to be successful. Additionally, define the scope of what your repository will do and more importantly will not do. Lastly, when starting a biorepository be sure to start small. Do few things extremely well and then grow your capabilities and services in time. High quality data and sample processing is of paramount importance.

17. **Attendee # 11: “How do scientists find sample of interest if these samples sit in different biobanks?”**

    Answer: Unfortunately there is no single source to find most biobank samples. With that said most NIH institutes (and foundations) have established biobanks that can be searched

and accessed at a variety of levles. Pick your disease area of interest and search federal and private programs to check on the existence of data and samples in those areas.