INTEGRATED BIOBANKING WORKFLOWS WORKING GROUP: Workflow Case Studies and Lessons Learned Series

Workflow Case Study 1 – DNA extraction from automatic-pipetted buffy coat

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Introduction

You may recall from the "ISBER Integrated Biobanking Workflows Working Group" article in the December 2014 newsletter issue that this working group is examining case studies of biobank workflow successes and failures in order to identify common integration bottlenecks. Ultimately this information will be utilized to create an overall technical specification document, or "blueprint", for the complete biobank workflow.

This is the first biobanking workflow case study in the series which will be presented to you. This case study is reviewing the automated process of extracting and quantifying DNA from buffy coat. Briefly centrifuged EDTA blood tubes with sample ID barcode labels are put on a liquid handling workstation to transfer buffy coats from their original tubes into a 96 deep-well plate. DNA extraction is done on a separate instrument, a nucleic acid extractor equipped with pipetting robot. As the 96 deep-well plate cannot contain sample identifiers, labels with sample IDs are sticked on assay sheets which are then scanned in in order to keep traceability during the DNA extraction process. DNA eluates are transferred to 0.5ml cryotubes which are individually labelled with 2D barcodes, labels are then scanned for DNA quantification on a separate instrument. Here we will learn that the technical procedure is unproblematic but that biospecimen-related data may be difficult to manage in an integrated workflow because of the barcode label.

Problem

Adhesive barcode labels: these three words can make a repository staff member shudder. In the industry we have a love-hate relationship with these.

Most of us have dealt with labels that do not stay on the container, labels that are the wrong size for the job, barcodes that do not scan, barcodes that contain the incorrect information, information that gets cut off during printing, ink that wears off, and the list goes on. The issue is that these problems are more than just an annoyance. When correctly identifying samples and obtaining sample data is of the utmost importance, encountering scanning-related problems can have a significant impact on projects, procedures, tasks, collections, time limits, and/or databases.

In this case study, adhesive sample ID labels (with 2D barcodes but without human-readable text of the barcode) are applied to assay sheets and those sample ID labels are manually and individually scanned into the automated nucleic acid extraction system. Because there are multiple labels (up to 96 labels)

which are grouped closely together, accurate scanning becomes difficult. In addition, manual scanning is time consuming.

Workflow Background

Let us discuss what was required within this workflow (the automated extraction of DNA from the buffy coat).

SOPs

- Use and Maintenance: Liquid Handler
- Use and Maintenance: Nucleic Acid Extractor with Automated Liquid Handling Workstation
- Use and Maintenance: Microplate Reader
- Automated DNA Extraction from Non-fixed Materials
- Nucleic acid quantification by spectrophotometry

Equipment

- DNA quantification system by Microplate reader, monochromator-based
- Laboratory information management system (LIMS)
- Liquid handling workstation, automated
- Nucleic acid extractor, automated, with pipetting robot, automated

Consumables

- EDTA 10ml Blood collection tubes
- 96 deep-well plate for DNA extraction
- Cryotubes, 0.5 mL screw-tops
- DNA buffy coat kit for 96-rod robotic head
- Labels

Findings

It was determined that manual scanning of the barcoded labels led to reduced efficiency as it was time-consuming. It was also determined that there is potential for data quality issues due to human error during scanning and due to scanner capabilities. The scanner emitted a sound when a barcode was identified; however, it was not able to identify a duplicate barcode within the dataset of one experiment (in the scenario when a label was erroneously scanned twice). It is also important to note that if a barcode was scanned twice, typically another barcode was not scanned at all which then means missing data in the LIMS.

Solutions

Short-term:

1. Replace labels with those which include both sample ID barcodes and text in order to allow for visual verification during scanning.

2. Only expose the one label to be scanned (by mechanically blocking all other labels on the assay sheet) in order to ensure that labels are not double-scanned.
3. Review the final DNA quantification Excel file to ensure that no duplicate sample IDs exist.

Long-term:

1. Utilize an electronic data transfer system wherein sample IDs are electronically transferred from the liquid handler to the DNA extraction system and to the DNA quantification system by the LIMS.