Single sample management system for biobanks

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ABSTRACT

Biobanks are a repository or storing biological samples from both human and non-human sources. In the past, biobanks sample storage standards focused more on the heterogeneity of the sample and this defines the design and use of the biobanks. This research objective is to analyze the requirements for a single sample management system in biobanks units and levels. A systematic and meta-analysis review focusing on sample variability and heterogeneity. The laboratory information management system that is fully integrated with the entire process, or in some centers mention it as BIMS, or other methods that have integrated and standardized collecting system that has almost the same principle system in sample management in biobank.

KEY WORDS: Cataloging biobank, Sample variability, Sample heterogeneity

INTRODUCTION

Banks unusually follow stringent protocol in sample collection, processing, and achieving. To harness the heterogeneity and sample variability, there are specific rules for sample storage to maintain the sample integrity. The sample diversity in most biobanks requires heterogeneous samples to be stored in specific biobanks and labeled, but even in the heterogeneous sample, there is further variability depending on how the sample was collected and processed as well as the working condition of the sample collection and processing areas. The biological bank’s storage infrastructures may include the liquid nitrogen tanks, freezers, and fridges, but the sample handling team are responsible for meeting the sampling and storage goals, objectives, and protocols. They also have to document the storage capacity and levels. The biobanks have different storage management systems for various samples based on heterogeneity as heterogeneous samples are storage together.

Rationale and Novelty of the Idea

The current sample management systems are resource intensive as it requires different sample storage systems for the varied heterogeneous samples. It is, therefore, important to develop a single sample management systems (SMS) taking into consideration the inherent variability and heterogeneity of the sample [Table 1].

RESEARCH OBJECTIVE

The objectives of the study are as follows:
1. The feasibility of SMS that can incorporate the samples diversity of the biobanks
2. To determine the requirements for a SMS for biobanks
3. The factors that determine the types of storage units and storage levels for heterogamous and variable samples
4. What are the specification and hierarchical levels to be taken into consideration in the development of a single samples management system for biobanks?
5. How will the data in the varied and disparate databases are migrated to the new comprehensive database
6. How will data integrity be achieved to ensure that data are safe and confidential before, during, and after database migration?

RESEARCH METHODS

Eligibility Criteria

The eligibility criteria of the included were determined by the inclusion and exclusion criteria below. The most important criteria were the study characteristics

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### Table 1: Sample Collection in Biobank Research, Faculty of Medicine Universitas, Indonesia

<table>
<thead>
<tr>
<th>Samples collected in Biobank</th>
<th>Diagnosis:</th>
</tr>
</thead>
<tbody>
<tr>
<td>2014/001/Prostat/A</td>
<td>Poorly differentiated acinar type of prostate adenocarcinoma, Gleason score:</td>
</tr>
<tr>
<td>2014/001/Prostat/B</td>
<td>5+5=10</td>
</tr>
<tr>
<td>2014/002/Buli/A</td>
<td>Adenocarcinoma buli, high grade (Pt1)</td>
</tr>
<tr>
<td>2014/002/Buli/B</td>
<td></td>
</tr>
<tr>
<td>2014/003/Mammae/A</td>
<td>Solid papillary carcinoma Grade 2</td>
</tr>
<tr>
<td>2014/003/Mammae/B</td>
<td></td>
</tr>
<tr>
<td>2016/006/Prostat/A</td>
<td>Poorly differentiated acinar type of prostate adenocarcinoma, Gleason score:</td>
</tr>
<tr>
<td></td>
<td>5+4 = 9</td>
</tr>
<tr>
<td>2016/008/Uretra/A</td>
<td>Jaringan Ureter Sehat</td>
</tr>
<tr>
<td>2016/017/Mammae/A</td>
<td>Invasive carcinoma no special type of left breast invasive carcinoma, grade 2</td>
</tr>
<tr>
<td>2016/017/Mammae/B</td>
<td></td>
</tr>
<tr>
<td>2016/027/Ovarium/A</td>
<td>Mucinous cystadenocarcinoma of ovary</td>
</tr>
<tr>
<td>2016/027/Ovarium/B</td>
<td></td>
</tr>
<tr>
<td>2016/027/Ovarium/C</td>
<td></td>
</tr>
<tr>
<td>2016/027/Ovarium/D</td>
<td></td>
</tr>
</tbody>
</table>

*(Contd..)*
Table 1: (Continued)

<table>
<thead>
<tr>
<th>Samples collected in Biobank</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>2016/029/Ovarium/A</td>
<td>Diagnosis:</td>
<td>Kistadenoma musinosum ovarii</td>
</tr>
<tr>
<td>2016/029/Ovarium/B</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2016/044/Cervix/A</td>
<td>Diagnosis:</td>
<td>Moderate to poorly differentiated adenosquamous carcinoma cervix – buruk</td>
</tr>
<tr>
<td>2016/106/Endometrium/A</td>
<td>Diagnosis:</td>
<td>Well differentiated endometrioid adenocarcinoma of endometrium</td>
</tr>
</tbody>
</table>

**Figure 1:** PRISMA framework for the article search protocol
of various researchers by different researchers. The study must have been recent (between 2010 and 2018). The study must have been a scientific study involving randomized controlled trials and quasi-experimental designs. The minimum number of participants in each study must have been 30 for representativeness of the sample. The study must be a published peer-reviewed journal. The exclusion criteria include unpublished journals, <30 samples. The purely qualitative studies will also be excluded from the reason lack of factual evidence.

**Information Source**

The information sources include a medical database such as PubMed (MEDLINE), CINAHL Plus, EMBASE, Cochrane Library, and EBSCO.

**Search Strategy**

The topics “The requirement of a SMS is to harness the inherent variability and heterogeneity in the types of storage units and in the storage levels” were too long, so the researcher truncated the title based on the keywords for the search. The researcher conducted searches across public health databases concerned with medical sciences and epidemiology. The researcher used the keywords; SMS, sample management systems, samples variability and heterogeneity, biobanks, and sample processing. The researcher conducted search medical databases such as PubMed (MEDLINE), CINAHL Plus, EMBASE, Cochrane Library, and Enesco.

**RESULTS**

The result generated by different databases varied as the National Center for Biotechnology Information returned 43 results’ EBSCO returned 1653 results, Cochrane provided five trials. Google Scholar returned 1400 results in 0.15 s. Of the 3101 records identified across the databases, and 10 records identified from Google searches, the researcher remained with only 2000 records after eliminating the duplicates. The researcher screened the records and remained with only 1200 records after excluding 800 records because they did not meet the inclusion criteria. Of the 1200 articles, only 20 articles could be accessed as full text as others we either proprietary or abstract only. Five more articles were eliminated because they did not meet the inclusion criteria based on the keywords searches leaving the researcher with only 15 articles. Only three articles were included in three qualitative syntheses while 12 articles were included in the quantitative systematic analysis [Figure 1].

**Data Collection**

Data were extracted from the sources using pilot forms. The pilot forms were essentially a table within varied columns such as the name of the author(s), date of publication, research objectives, sample size, research finding, and usability rating.

**DISCUSSION**

We reviewing some studies based on the research objective, type of the study and the research findings. Some of the study using qualitative, quantitative and mixed study. Peakman and Elliott, 2010, using qualitative review study and they found some important research findings. They Centralize and standardize as much as possible and limit the impact of variability. Implement quality programs from the start of the study and designing and testing the sample collection protocol in a way that produces high-quality data and samples for research use. A full data audit trail should be generated on the sample collection process to allow the collaborative use of samples and data across different biobanks. Then the programs are implemented to minimize the effect of introduced variability on the integrity of the samples.[1]

Kim, Shin and Park, 2016, aim to develop a Hybrid block-selection method on HDFS based on storage type, using quantitative study. They found The effectiveness of storage I/O on a distributed file system of Hadoop(HDFS) hybrid block-selection method on the HDFS. Improving the performance of storage I/O is very important. The hybrid block system should consider the storage types and capacity to manage the read request from the client through the distributed processing system.[3]

In 2008 Elliott and Peakman using mixed study to Analyze the sample handling and storage protocol adopted by UK Biobank. They found A variety of preservatives, anti-coagulants and clot accelerators is used appropriately to the expected end use of the samples. Aliquots of urine, plasma, serum, white cells and red cells stored in ultra-low temperature archives. A standard panel of hematology assays is completed on whole blood from all participants. Samples are stored -80 degrees C automated archive and manual liquid nitrogen archive at -180 degrees C. The SMS is a highly automated for the processing and storage of samples. The systems use a laboratory information management system (LIMS) that is fully integrated with the entire process.[3]

In 2016 Redrup et al using mixed study and aim to make recommendation of sample management for Best Practices and Harmonization from the Global Bioanalysis Consortium Harmonization Team. They found Sampling procedures should be clearly described in the protocol. Sample information must include the volume of the sample collected. Biobank capacity should be indicated including the maximum level. The biobank system should have indicators for variability in the sample to prevent mixture of samples. Chain of custody should be automated through electronic data systems and Laboratory Information Management
Systems (LIMS). Integrated biobanks system should have identified including “room temperature,” “refrigerator,” “freezer,” and “ultra-freezer”\(^{[4]}\)

Downey and Peakman, 2008 design and implement of a high-throughput biological sample processing facility using modern manufacturing principles using mixed method. They found A good facility comprising technology, systems, dedicated process, infrastructure, and an appropriate staff structure. Maintain control of inputs and outputs: avoiding the Forrester effect and standardize process and quality.\(^{[5]}\)

Pereira et al, 2013 using mixed method for Longitudinal Study for Adult Health (ELSA-Brazil) is a multicenter prospective cohort. They found problems such as political issues, budget, difficulties in the importation process and its costs should be considered

planning must take into consideration the implementation and maintenance costs of facilities cryogenic center planning must take into consideration the technical aspects and risks of migration to new systems.\(^{[6]}\)

Vaught J, Henderson MK, 2011 using qualitative study to analyze the biological sample collection, processing, storage, and information management. They found The system must be effective in ensuring that the sample is monitored and controlled by appropriate sample tracking and laboratory informatics systems. A comprehensive QMS, with standard operating procedures and other appropriate controls. Core LIMS functions: Genetic as well as standard clinical analysis, analysis batching and electronic laboratory notebook (ELN) functionality. Other features include Instrument interfaces, Quality control, and diagnostics, Reagent inventory, Invoicing and Document management and laboratory standard of operational repository.\(^{[7]}\)

Olund, Lindqvist and Litton, 2007 develop BIMS: An information management system for biobanking in the 21st century using qualitative study. They found Mapping system to map the human genome and BIMS, a system designed to integrate data from heterogeneous source.\(^{[8]}\)

Owen and Woods, 2008 using mixed study and found The design of the refrigeration system and storage compartment and LN(2) as a refrigerant, enables efficient use of coolant and maintains a uniform temperature over the entire compartment. The systems must have drawers that allow for robotic access whilst maintaining storage conditions.\(^{[9]}\)

**CONCLUSION**

The feasibility of SMS that can incorporate the samples diversity of the biobanks, to ensure that data are safe and confidential before, during, and after database migration can be achieved using the laboratory information management system (LIMS) that is fully integrated with the entire process, or in some centers mention it as BIMS, or other methods that have integrated and standardized collecting system that has almost the same principle system in sample management in biobank that has almost the same system in sample management in biobank. The LIMS system enables the biobanks to determine the requirements for a SMS for biobanks. The LIMS system enables the biobanks to identify the factors that determine the types of storage units and storage levels for heterogamous and variable samples. The LIMS system enables the biobanks to identify the specification and hierarchical levels to be taken into consideration the development of a single samples management system for biobanks.

**REFERENCES**


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