B21 The Singapore National DNA Database Laboratory

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After attending this presentation, attendees will understand how the Singapore National DNA Database maintains its integrity of the DNA profiles uploaded into the Singapore National DNA Database by duplicating the processing of each FTA sample, the system of positional checks of each FTA punch in every PCR plate, and the approval of identical reviewed DNA results from both independently processed PCR plates.

This presentation will impact the forensic community and/or humanity by demonstrating the setup of the DNA database laboratory in ensuring the integrity of the DNA profiles uploaded into the Singapore National CODIS database.

In the design of the Singapore National DNA Database Laboratory, several review processes have been built to ensure the integrity of the evidence and the DNA profiles that are uploaded into the CODIS database. The systems are supported by both the design of the Laboratory Information Management Systems (LIMs) as well as checks performed by the laboratory staff.

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The Singapore National DNA Database Laboratory was launched on 14 February 2003. On its launch day, close to 14,000 blood-stained FTA™ cards were submitted from all the prisons in Singapore which took the laboratory approximately 8 months to complete processing. On a daily basis, approximately 60 samples are submitted to the laboratory.

All FTA™ samples submitted to the laboratory come with a unique barcode. Upon receipt, the sample is logged into LIMs, which will generate a unique laboratory number which is assigned to each submission. Each FTA™ card will be processed in duplicate. A 1.2 mm punch disc will be excised from the FTA™ card into a 96-well PCR plate. This process is repeated to obtain a second 96-well PCR plate of FTA™ punch discs. Before any punch disc is excised from the FTA™ card, the laboratory number of the FTA™ card is captured by the barcode reader attached to the DBS Wallac Puncher, generating a text file documenting the barcode it has captured at the end of completion of the punch process. Similarly another text file will be generated when the second PCR plate is completed. These two text files are uploaded into the LIM system, where it would be compared to check the identical punch sample is in the same PCR well in both PCR plates, ensuring sample integrity. The FTA™ discs in each PCR plate will then be processed using a Beckman Coulter® Biomek® 2000 robotic workstation, followed by PCR. Transfer of PCR products for genotyping is also performed by a second robotic workstation. DNA profiles generated from the two PCR plates having the same FTA™ samples will be read by an analyst. A separate analyst will also read one out of the pair of PCR plates. The two analysts will interpret the DNA results independently and generate a LIMS table. The DNA results in the LIMS table will be compared against one another, using an in-house Excel spreadsheet to check for any interpretation differences. The DNA results from both sets of PCR plates will then be uploaded into the LIM system, where the DNA profiles from both PCR plates will be compared. Only when results from both PCR plates are identical would the LIM system grant approval of the results for direct upload into the CODIS database.

In conclusion, the integrity of the DNA profiles uploaded into the Singapore National DNA Database is maintained by:

a) Duplicate processing of each FTA sample
b) System of positional check of each FTA punch in every PCR plate well
c) Approval of identical reviewed DNA results from both independently processed PCR plates

DNA Database, FTA, CODIS

 ** Presenting Author*