INTRODUCTION

Since the establishment of DNA profiling as a technique for genetic identification, many changes and adaptations have been implemented to increase the efficiency and success of DNA analysis techniques; from blood to trace to the recent introduction of new more sensitive DNA analysis kits.

This has also contributed to the significant increases in the DNA casework backlogs in forensic laboratories globally, as more and more samples are required to be analysed. One process adopted by some laboratories is the reduction in samples analysed per volume crime case; to one sample.

While this would contribute to a clear improvement to the efficient processing of DNA profiling cases, questions may be raised as to whether this is an appropriate balance between sample throughput and identifying a potential offender. In addition, 2012 – 2013 saw the introduction of new DNA analysis kits into Australian laboratories, reflecting an increase in the number of core DNA markers used on the National Criminal Investigation DNA Database (NCIDD) from nine (plus a sex indicating marker) to eighteen (plus a sex indicating marker) (See Figure 1). The impact of the introduction of any new DNA analysis kit would also change the analysis and processing of casework, thereby affecting the sample throughput and backlog levels.

MATERIALS AND METHODS

To investigate the differential success rates of DNA profiling in respect to the number of samples profiled, case files analysed using the old DNA analysis system (dated prior to 2003) were examined and selected for analysis according to two criteria:

1. Crimes which pertained only to property (volume crimes).
2. Crimes where DNA analysis was completed for two or more samples.

Under these criteria, 103 cases were obtained. For each case, details including reference numbers, incident type, sample number, sample description and the DNA profile result per sample were recorded. The data obtained analysed and in each case the samples were ranked in the order they would have been examined according to known material success rates (blood, semen, saliva, trace).

Where samples of the same kind were present, it was assumed that quantitative analysis could predict which sample would produce the most successful profile and hence the most successful result was assigned to the first sample. The data obtained is presented in Table 1. In addition to this analysis, the 246 casework samples analysed in Powerplex 21 were compared to 267 similar casework samples analysed in PowerPlex 21.

The data was used to prepare a list of the success rates of DNA profile attainment for various different sample types. The data is presented in Table 2. Success was determined as greater than or equal to 6 alleles (minimum upload for NCIDD) and either a single source or whether a major can be extrapolated from a mixture. Unsuccessful profiles were determined as either no result, less than 6 alleles or too complex to interpret.

RESULTS

From Table 1 it is clear that a significantly larger number of profiles were obtained from the first and second samples. In addition to this, the rate of success for the first sample is clearly very high, with no fewer than 85 profiles reported to the database from a total of 103 cases (Table 2), while the success rate for the second sample reported only 33 profiles.

The clear dilemma is that at the very least, another profile should have been reported for every 2.5 cases from the DNA profile of a sample and one in every 1.5 if the figures are analysed critically to produce the highest possible value. From the number of profiles reported, it is clear that the same initial profile was obtained more than 50% of the time by the second sample.

The number of new profiles reported by the second sample, however, is significant at approximately one for every 2.5 reported by the first sample. After the second sample, very few subsequent samples produced a new profile, with the third sample producing only one newly reported profile in every 10-11 produced by the first sample. In addition, it may be seen that the number of unsuccessful profiles increased in the second and third samples.

Table 2 shows the success rates of a variety of different materials as calculated from the number of profiles obtained as a percentage of the total number of DNA profiles performed for that sample type. Blood samples provide the greatest chance of obtaining a profile in blood traces, followed by saliva. The data, followed by salivary trace samples, coupled to the significant increase in the number of probable non-friction trace samples.

DISCUSSION

The results obtained from this analysis clearly demonstrate that the number of reported DNA profiles obtained from a given crime scene sample is far greater for the first sample than from subsequent samples, which seems to support the validity in the current direction of forensic laboratories in reducing the number of samples analysed per volume crime case. However, while one sample may be sufficient in most cases, overlooking the second sample could greatly affect the accuracy of the information being provided to the justice system and may reduce the ability to identify additional suspects. It is possible that the analysis of subsequent samples may simply begin to provide profiles of the victim and others who had been at the crime scene before or after the crime was committed. Profiles generated from third samples provide little additional information.

Of the trace items analysed, clothing items appeared to give greater success rates than non-clothing items. Sample type and quality are vital considerations and were crucial to obtaining a useful DNA profile, with blood followed by saliva yielding the least complex DNA profiles. Trace DNA collected from a known direct contact location yielded less complex DNA profiles than those taken from speculative contact areas. The results suggest more complex DNA profiles are obtained from trace DNA samples due to the increased sensitivity of the new profiling kits. However, it is possible that the necessity for accurate results when providing evidence for the use of courts and with all results considered, it appears that in general the most efficient and most accurate number of samples to be processed using DNA profiling is two. This should ensure the attainment of at least one profile and in cases with multiple individuals, perhaps two. If no profile is obtained from the first two samples, it would be up to the discretion of the forensic institution and the case officer in charge to decide whether it was relevant to resort to another sample. If there was sufficient evidence of other forms on which to convict a suspect, clearly no further profiling would be required.