Casework experiences with DNA profiling

B.H. Parkin, M. Greenhalgh, S. Jones, C. Buffery and J.R. Russell

Metropolitan Police Forensic Science Laboratory, 109 Lambeth Road, London, SE1 7LP

INTRODUCTION

This laboratory has been using DNA profiling in case work for 10 months and during this time has examined 400 cases. Of these, the majority have been sexual assaults, murders and violent assaults. DNA profiles have been obtained in approximately 70% of these cases.

METHOD

A modified southern blotting hybridisation method is used, where DNA is transferred to Hybond-N nylon membrane (Amersham) by vacuum blotting and hybridisation is carried out by the method of Church and Gilbert (1984) in a rotary hybridisation oven. Single locus probes λMS1, λMS31 and λMS43A are used sequentially although not in a specific order.

Allele sizes are calculated by reference to DNA size markers labelled with ^{35}S (Amersham). By use of population frequency tables (Cellmark Diagnostics) the probability of finding a second unrelated individual with the same DNA profile can be computed.

RESULTS

A high success rate of obtaining DNA profiles has been achieved with sexual assault cases.

In an examination of a rape victim, at least two vaginal swabs are routinely taken by a police surgeon. Combining the material extracted from these provides sufficient seminal DNA for profiles to be obtained, even when the swabs are taken up to 20 or 30 hours after the offence. It is our experience that this DNA is usually of good quality and profiles can be obtained from relatively small amounts. Semen stains on clothing are good sources of DNA, and, if large enough, will

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give profiles even when microscopic examination suggests that the sperm concentration is very low.

Bloodstains are more problematic than semen stains. The number of nucleated cells is relatively small, and more material is necessary. Bloodstains also tend to be found on a wider spectrum of clothing and objects, which can cause problems with extraction and subsequent purification. Some textile dyes remain associated with DNA throughout purification, discolouring the DNA. In some cases this prevents restriction occurring.

Head hairs (about 10 anagen hairs) are sometimes used instead of body fluid controls. In case work, hairs found on weapons used in violent assaults can be successfully profiled, but those found on hats or masks (telogen hairs) give little or no success.

Cells derived by centrifugation from salvia can also be used for control purposes and often sufficient cellular material is found on cigarette ends for profiling. No success has yet been achieved from saliva on envelope flaps or stamps. DNA profiles have been obtained from nasal mucous found on handkerchiefs.

The small amounts of flesh from knives used for stabbing and flesh found on vehicles after hit-and-run accidents is particularly suitable for DNA profiling.

By use of single locus probes, mixtures of body fluids from more than one individual can be detected. If a sample from each relevant person is available as a control, we can say that a mixture of their DNA would be expected to produce a composite pattern such as that obtained. However the situation becomes more complex when one or more of the contributors does not provide a sample. This can occur in cases of multiple rape. Mixed profiles are sometimes seen when removal of victims' vaginal or buccal cells by preferential extraction is incomplete (Gill et al 1985).

DNA AUTORADIOGRAPH SCANNER

Due to the large number of measurements and calculations involved in reading results manually, a DNA autoradiograph scanner is being developed in this laboratory. This comprises a video camera and monitor coupled to an IBM AT computer via an Imaging Technology digital frame store. The mounted camera overhangs a light box on which the autoradiograph is placed. A printer is connected so that results, calculations and screen dumps can be printed out. Scanner software enables lanes to be scanned and allele sizes calculated with reference to calibration lanes on the autoradiograph. An error window, initially $\pm$ 1mm, is also calculated.

The probability of occurrence of the combination of alleles produced by the three single locus probes used is also calculated in the three ethnic populations so far studied. When complete, the scanner will transfer the casework results to the laboratory main frame computer for addition to a case data index to enable searching outstanding cases against DNA profiles from nominated subjects and also to update ethnic frequency tables.

Using this DNA scanner data bases for λMS1, λMS31 and λMS43A have been derived from populations comprising 311 white caucasians, 154 Afro-Caribbeans and 60 Asians.

REFERENCES

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