Victoria State Coroner's Inquest into the Death of Jaidyn Leskie
Supplemental report prepared by Dan E. Krane
February 3, 2004

This supplemental report has been prepared at the request of Ms. Rowena Orr and Mr. James Kennan.

Since my original report dated December 4, 2003, I have reviewed the following additional materials supplied to me by Ms. Orr and Mr. Kennan including the underlying electronic data collected by the Victoria Forensic Science Centre (VFSC) during their testing of the evidence in case 6603/967 (involving the death of Jaidyn Leskie); and a database of over 18,000 complete genotypes generated during the course of casework in Australia. I have also reviewed reports from: Dr. William Thompson dated December 10, 2003 and January 29, 2004; a declaration from Carmen Eckhoff regarding DNA testing results performed by the Northern Territory Police, Fire and Emergency Services (NTPFES) Forensic Science Centre; and a report by Dr. Bruce Weir dated January 15, 2004.

As in my original report, and like several other experts who have reviewed the relevant case materials, I agree that the DNA profiles associated with the condom (samples "1 i" and "1 ii" from case 2831/978) and from the bib and track-pants (samples "70 iii a" and "70 vi a" from case 6603/967) match each other across all tested STR loci for which results are available. The alleles observed in the tested loci for these samples also correspond to alleles observed in the reference standard from the complainant, "Ms. P.," in the rape investigation associated with case 2831/978.

In my original report I stated that there are only three possible explanations for a match between a reference and an evidentiary sample:

1) the biological material associated with the evidentiary sample in fact originated from the person who provided the reference sample;

2) the true source of an evidentiary sample is not the person who provided the reference sample but the two individuals do coincidentally match at all loci that have been tested;

3) an error has occurred (either accidental or deliberate) in the handling/collection, testing or interpretation of the evidentiary and/or reference sample.

I originally concluded that accidental contamination with DNA from what is described as the inside of the condom sample (VPFSC case 2831/978) is the most likely cause of the DNA profiling results produced from the bib and track pants (VPFSC case 6603/967). My subsequent review of the underlying electronic data associated with the testing performed by the VFSC during their investigation of the death of Jaidyn Leskie in particular leaves me even more convinced that the STR-DNA profile match observed between the condom of the rape investigation and the bib in the Jaidyn Leskie abduction investigation is the result of contamination.

Additional peaks on electropherograms

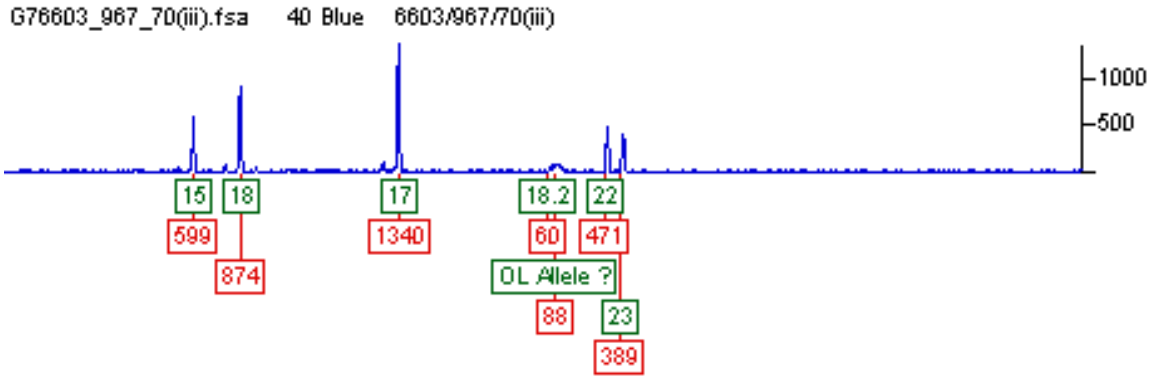
In my original report I commented that I had not had an opportunity to review the electronic data that underlies the DNA profiling performed by the testing laboratory during the course of their investigation of the death of Jaidyn Leskie. I suggested that "a review of that material might allow me to detect, among other things, indications of low levels of signal associated with alleles that Mr. Sheffer does not list in Table 1 of his 30 July, 2003 report. A review of the control samples (a positive, negative and reagent blank) as well as the evidence samples for low level signals that would correspond to Ms. P's alleles in particular" would be appropriate. Now that I have had an opportunity to review the electronic data from the Leskie investigation I, like Professor Thompson, do indeed find low levels of signal that are consistent with Ms. P's DNA profile and lend substantially more credence to the already compelling proposition that she is the source of the DNA associated with the Leskie bib and track pants.

Like Professor Thompson in his supplemental report (dated January 29, 2004), I have prepared a figure that displays the electropherograms generated as part of the testing of the stain found on Jaidyn Leskie's bib that also includes tables indicating the conclusions drawn from those electropherograms by the testing laboratory (Figure 1). Unlike Professor Thompson, I have chosen to present those electropherograms in the same way that the testing laboratory appears to have reviewed them. The electronic data provided to me indicates that the testing laboratory used Macintosh-based versions of GeneScan and Genotyper with a "no smoothing" option invoked whereas Professor Thompson's figures are based on the output of newer, PC-based versions of the software where smoothing does not influence the height of signals ("peaks" on the electropherograms). I generally prefer to use the most current version of GeneScan and Genotyper in my review of casework (and, in fact have used the same PC-based versions in an automated review of this electronic data as described in a Genophiler report which is attached and incorporated into this supplemental report by reference). However, I thought it might also be helpful to consider the output as it was seen by the testing

laboratory primarily for two reasons: 1) no-smoothing with the Macintosh versions of the software systematically makes peak heights larger; and 2) the peak heights generated in this way should be more directly comparable with the threshold established by the testing laboratory in the course of their validation studies. As Professor Thompson points out, "Most laboratories establish a peak height threshold for reporting alleles and make it a practice to ignore peaks falling below that threshold." I, like him, feel that this practice is appropriate but that low-level signals may also contain useful information in investigations such as this one.

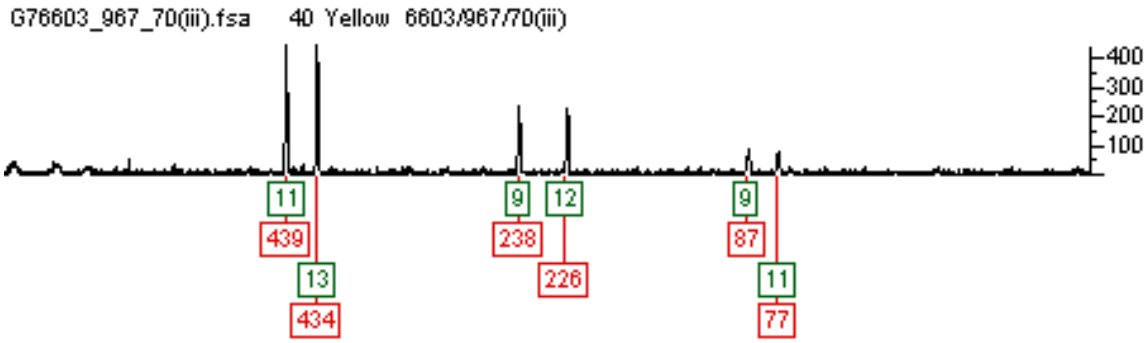
Very briefly, Figure 1 shows that there are several peaks associated with the DNA profile from the bib that are greater than 50 RFUs yet fall below the testing laboratory's apparent threshold of 100 RFUs (determined from the settings they used with their GeneScan software). Specifically, those peaks are objectively (and correctly) labeled by the GeneScan and Genotyper software as corresponding to the following alleles: D18S51 16, 19; and D7S820 9, 11. (The shape of an additional peak at the FGA locus suggests it is the result of a technical artifact and can be disregarded. This unusually shaped peak did not appear on a second electropherogram for this sample.) These correspond precisely to the four alleles possessed by Ms. P at those two loci – a 1 in 649 chance of coincidence when taken by itself.

Figure 1. Actual Electropherogram and Reported Test Results from the Bib (Item 70 iii a). Boxes in green immediately below the peaks label the name of the alleles seen while boxes in red below them indicate their heights in relative fluorescent units (RFUs). Tables below the electropherograms list the results reported by the testing laboratory for locus.



	D3S1358	vWA	FGA
Reported Result	15, 18	17, 17	22, 23

Amelogenin	D8S1178	D21S11	D18S51
X, X	12, 14	32.2, 33.2	NEG



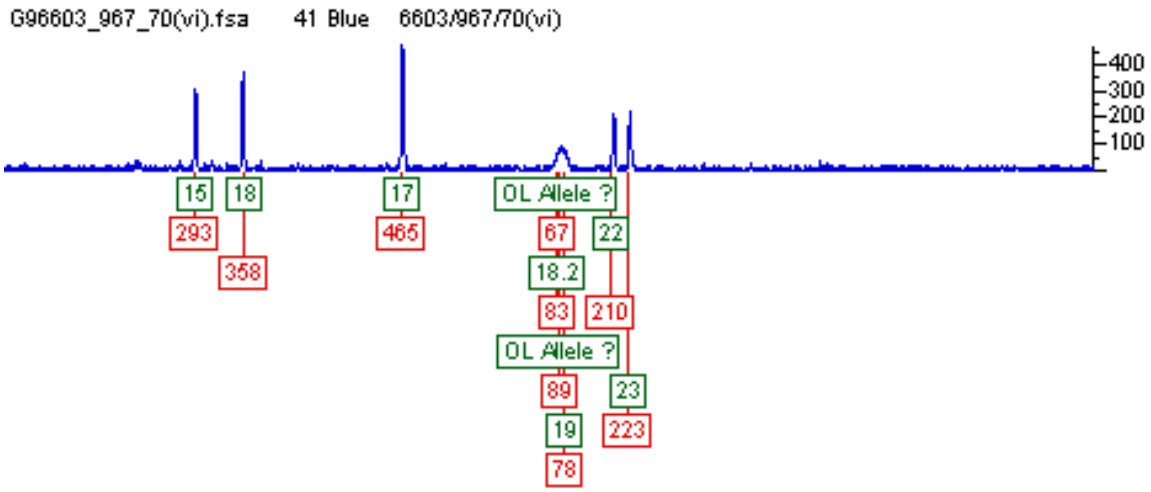
D5S818	D13S317	D7S820
11, 13	9, 12	NEG

It should be noted that there are no indications of Jaidyn Leskie's or anyone else's alleles on this electropherogram (or in any of the associated control samples that were also provided for my review). Further, the electropherogram is consistent with what is seen with a degraded or inhibited sample in that the height of peaks become progressively smaller when considered from left to right. It is common for typing information to be lost from the D18S51, D7S820 and FGA loci first in degraded/inhibited samples.

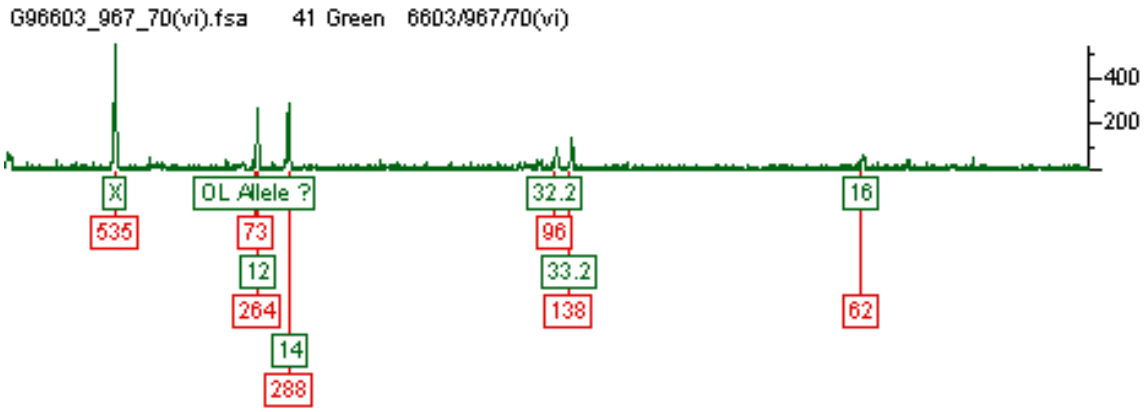
Review of the electropherograms associated with the track pants from the Leskie investigation yields similar results (Figure 2). Specifically, two peaks with heights between 50 and 100 RFUs are objectively (and correctly) labeled by the GeneScan and Genotyper software. Those peaks correspond to the following alleles: D18S51 16; and D7S820 9. (The shape of an additional peak at the FGA locus suggests it is the result of a technical artifact and can be disregarded. It is in the same position and of the same shape as the additional peak parenthetically mentioned in my discussion of the bib electropherogram.) As described earlier, these alleles correspond to two of the four that Ms. P possesses at these loci. There are in fact some indications that peaks that could have arisen from Ms. P's additional two alleles for these loci though these smaller peaks

fall below 50 RFUs in height and are difficult to distinguish from baseline noise associated with the test. The absence of Ms. P's two alleles in this degraded/inhibited sample may be due to a phenomenon commonly known as "allelic dropout" that particularly afflicts low level samples. Given that allelic dropout is due largely to stochastic processes, reamplification of the evidence sample might give rise to electropherograms that contain D18S51 19 and D7S820 11 peaks above 50 or even 100 RFUs at the same time that other small peaks such as the D18S51 16 and D7S820 9 peaks in Figure 2 fall below these levels. In fact, reamplification of the DNA associated with the track pants by the Northern Territory Police, Fire and Emergency Services Forensic Laboratory shows that very thing for the D7S820 locus (the presence of a D7S820 11 peak and the absence of a D7S820 9 peak).

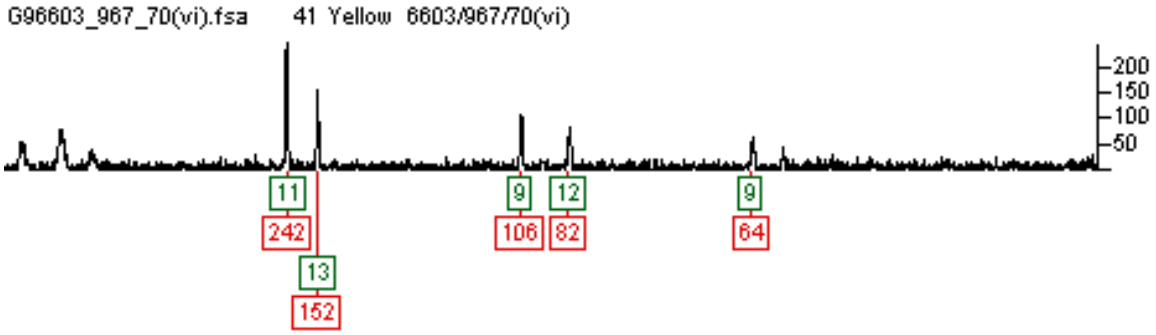
Figure 2. Actual Electropherogram and Reported Test Results on Track Pants (Item 70 vi a). Boxes in green immediately below the peaks label the name of the alleles seen while boxes in red below them indicate their heights in relative fluorescent units (RFUs). Tables below the electropherograms list the results reported by the testing laboratory for locus.



	D3S1358	vWA	FGA
Reported Result	15, 18	17, 17	22, 23



Amelogenin	D8S1178	D21S11	D18S51
X, X	12, 14	NR	NEG



D5S818	D13S317	D7S820
11, 13	NR	NEG

Re-testing by the Northern Territory Police, Fire and Emergency Services Forensic Science Centre

I agree with Professor Thompson that the findings of the NTPFES Forensic Laboratory as described in the declaration of Carmen Eckhoff are consistent with those supported by VFSC's electronic data. This consistency lends substantial credence to the proposition that reference and evidence samples were genotyped correctly.

Perhaps even more importantly though, the DNA testing performed by the NTPFES Forensic Laboratory scrutinizes the reference sample of Ms. P and the bib and track pants stains at three additional polymorphic loci (THO1, TPOX and CSF). General correspondence between the genotypes of Ms. P and the bib and track pants at these three additional loci in addition to the seven to nine that can be typed using the electropherograms in Figures 1 and 2 make it profoundly unlikely that someone other

than Ms. P (including her relatives) is the source of the DNA found on Jaidyn Leskie's bib and track pants.

Analysis of the FSD Genelink DNA Database

In December of 2003 I was provided a spreadsheet that lists DNA profiles on the FSD Genelink DNA Database as of the close of business on January 8, 2003. While the spreadsheet contained genotype information for a total of 18,967 apparently unmixed samples, only 15,021 had complete genotype information at all nine STR loci that were tested.

With those 15,021 genotypes it is possible to perform 112,807,710 pairwise comparisons. When those comparisons were made, 8,576 were found to have identical genotypes across all nine tested loci. It is possible that some of those pairwise matching profiles are the result of the type of "fortuitous match" being considered as a possible explanation for the perfect match between Ms. P and the evidence in the Leskie investigation. For reasons described in my original report (as well as the reports of Drs. Thompson and Weir) it is much more likely that these pairwise matches are the result of multiple genotypings of the DNA from single individuals that happened to be associated with more than one evidence or reference sample (in 1,864 cases the pairs were found to have the same "intCaseID" designation). When the 3,860 ostensibly redundant genotypes are removed from consideration, genotypes from 11,161 different individuals remain.

The average number of shared alleles between these 11,161 genotypes was relatively low and is consistent with the diverse origins of Australians. Specifically, 5.56 alleles (out of 18) or 30.89% (SD=1.77) were shared between pairs on average (compared to: 33.05% between pairs of individuals in the US Federal Bureau of Investigation database; 34.85% between pairs of Chippewa-Cree Indians; and 42.29% between pairs of Navajo Indians). However, the Australian dataset displayed an unusual spike of allele sharing at the high end of its distribution (Table 1).

Table 1. Number of observed pairs of non-redundant genotypes in the FSD Genelink DNA Database sharing large numbers of alleles.

Shared alleles	Observed occurrences
14	401
15	27
16	1
17	16

Given the otherwise normal distribution of the counts of pairwise shared alleles (and that this spike is not observed when the analysis is repeated with a randomized version of the original genotypes), it is worth considering that the 16 observed pairs of genotypes that differ from each other by only a single allele are in fact also genotypes of the same individual but where a single allele was incorrectly typed in one sampling. Four of the 16 pairings do have matching "intCaseID" information (samples with the following pairs of "IntProfileID" designations: 12838:15804, 14979:16127, 15252:15324, and 19155:19162). The remaining 12 pairs (6202:9024, 7030:22754, 8064:8782, 8533:8534, 9472:9485, 9476:9504, 11595:13064, 11774:14506, 12841:15967, 15490:15499, 19850:20759, 20656:20701) have different "intCaseID" information and may represent testing results from different investigations.

I have requested but have not received additional information about the 32 samples enumerated in the preceding paragraph. A review of the circumstances surrounding the genotyping of these samples as well as the underlying electronic data that was generated during their testing might give valuable insights into the rate at which samples are incorrectly typed by the testing laboratory during the course of its routine casework. (It is generally accepted that evidence samples should be interpreted without knowledge of the DNA profiles of possible contributors. There would be less opportunity for "self-correction" to occur during interpretation across different cases. As such, the 12 pairs of almost perfectly matching genotypes that come from different "intCaseID"s may give a better estimate of true mistyping rates as it may occur in routine casework.)

An error rate for mistyping would have very little direct bearing on the possibility of the observed match between the genotypes of Ms. P and the stains associated with Jaidyn Leskie's bib and track pants. The genotypes associated with these samples have been confirmed by re-testing and independent review of the underlying electronic data. However, a sum of the mistyping and contamination error rates would effectively take into account all the accidental (but not the hopefully remote possibility of deliberate) errors associated with the third possible explanation for matching DNA profiles between reference and evidence samples as described at the beginning of both this supplemental report and my original report (at the bottom of page 1 in both reports).

Conclusions

On balance, it is profoundly more likely that the presence of a DNA profile matching Ms. P's on Jaidyn Leskie's bib and track pants is the result of contamination than the result of a coincidental match with someone other than Ms. P (either related to her or not).

I have carefully reviewed all of the materials provided to me and I have not withheld any issues of significance to this inquest.

Sincerely,

Dan E. Krane
Associate Professor of Biological Sciences,
Wright State University,
Dayton, OH USA 45435-0001