NOTE:

DNA interpretation has been used for this sample report, however all Proficiency Tests would be reported in a similar manner with results and interpretation relevant to the field being tested.

All laboratory data and conclusions in this report are fictitious. The test is based on the DNA Interpretation Challenge Test but no results submitted for the Challenge Test were used in this report.

The sample report starts on the next page

Sample Report
(2017)

Proficiencytesting@forensicfoundations

DNA Interpretation
2017/S-a

This report replaces Report 2017/S. Please destroy all copies of Report 2017/S.

Authorised by Anna Davey, Managing Director, Forensic Foundations, 4/9/2018.

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Contents

Introduction

Design

Forensic Foundations' Proficiency Tests are designed to address the following issues:
- Relevance to forensic science laboratories;
- Limitation of any potential contextual information;
- Knowledge of the 'ground truth' of the samples;
- Importance of consistency between tests; and
- Cost affordability for the laboratories.

An additional feature of the Forensic Foundations' Proficiency Tests is that they test the end-to-end forensic examination process. The AS 5388 Forensic Analysis series of Standards describes the forensic examination process from collection to reporting. The following figure[1] illustrates the inter-relatedness of all steps in this process and was used as the basis of the Standards' development. The figure is also used as the basis of the development of the Forensic Foundations' Proficiency Tests. Thus, all Forensic Foundations' Proficiency Tests commence with item collection and/or receipt and all the subsequent examination / analysis steps, culminating in the reporting, thus reflecting actual forensic casework. NATA states 'PT samples/items should be handled in the same way as routine casework as far as practicable. The facility's routine test procedures must be used.'[2]
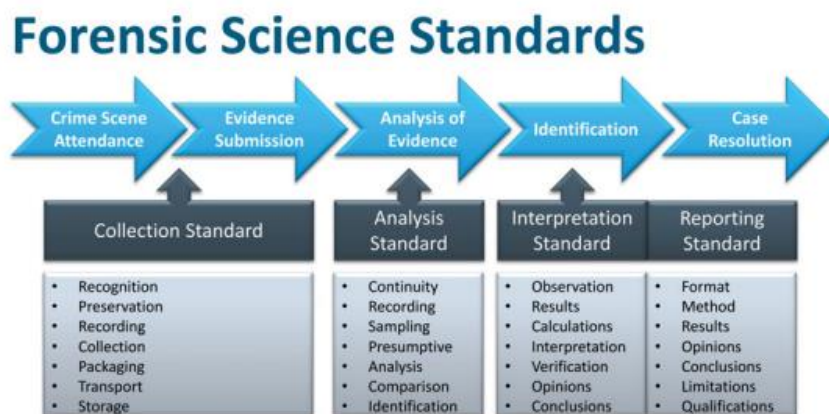
All Forensic Foundations' Proficiency Tests are ISO 17043 compliant. These requirements include a mechanism for participating laboratories to request a review and/or appeal the evaluation of their performance. With respect to this test, and if anonymity is to be maintained, a request or appeal should be forwarded to ANZPAA|NIFS for transmission to Forensic Foundations. Alternatively, the request or appeal can be forwarded directly to Forensic Foundations.

Reports of Proficiency Tests will be made publicly available by Forensic Foundations. Participating laboratories may use the report as outlined in their respective laboratory policies.

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[1] James Robertson, Karl Kent & Linzi Wilson-Wilde (2013) The Development of a Core Forensic Standards Framework for Australia, Forensic Science Policy & Management: An International Journal, 4:3-4, 59-67

[2] NATA (2015) Forensic Science ISO/IEC 17025 Application Document.

DNA Interpretation 1/2017

This Proficiency Test was developed by Forensic Foundations and the results have been fabricated by Forensic Foundations. The manufacture, distribution, assessment and reporting of this test has been provided as an example of how the submitted test results would be recorded and interpreted.

In addition to testing generic issues such as receipt, triage, continuity of items for examination in this test; the aim of this specific Proficiency Test was to compare the proficiency of forensic DNA laboratories to amplify, analyse, interpret, compare and evaluate the profiles of the same set of single-source, mixed and low-level DNA samples, using the laboratories' standard procedures.

In order to remove other sources of uncertainty and variability, the participants were not required to carry out the initial steps of a forensic examination (searching, identification of biological material, extraction and quantification of DNA) and were provided with genomic DNA samples. In order to remove any contextual bias in the interpretation, the participants were told only that the samples were a reference sample or an unknown sample.

Results

Four laboratories 'participated' in this Proficiency Test. All laboratories submitted data with respect to the DNA profiles obtained and the subsequent interpretation.

Although data was not requested with respect to quantification, it was apparent that some laboratories undertook quantification of the samples prior to amplification.

Continuity and description

Laboratory 1 referred information relating to continuity and description to the examination notes (although said notes were not submitted).

Laboratory 2 & 4 gave a full description of the packaging and item description:
> The samples (both reference & unknown) were received in a sealed 'Security & Transit' bag which had no signature, date or external labelling. Each individual extract was received in an appropriately labelled tube inside two snap sealed bags.
> The reference and unknown samples were separated into two bags within the external packaging.
> No apparent damage or leakage was noted.
> Sample 750. 1x white & yellow labelled tube containing clear liquid
> Sample 751. 1x white & orange labelled tube containing clear liquid
> Sample 752. 1x white & blue labelled tube containing clear liquid
> Sample 753. 1x white & purple labelled tube containing clear liquid
> Sample U1. 1x white & yellow labelled tube containing clear liquid
> Sample U2. 1x red & white labelled tube containing clear liquid
> Sample U3. 1x white & green labelled tube containing clear liquid

The description provided by Laboratory 2 & 4 concurs with the packaging, labelling and samples distributed.

Laboratory 3, in addition to the full description given by laboratories 2 & 4 noted that the samples had been delivered at the ambient temperature, not on ice.

Quantification

Laboratory 3 reported that 'DNA appeared to be markedly degraded' or 'DNA appeared to be degraded'

Laboratory 2 used both Quantifier Human real time PCR and Thermo-Fisher NanoDrop 2000 UV-Vis Spectrophotometer to determine concentrations and obtained levels similar to the manufacturer.

DNA Profile and Interpretation

All participants used the PowerPlex21 amplification and typing kit. 2 participants used a results table different from the one provided with the Test. These tables did not contain the full locus designations. Although not usually a problem, this practice could lead to ambiguity if the typing kit is not stated (e.g. D2 could refer to D2S441 or D2S1338, both of which are present in the GlobalFiler kit).

Laboratory 2 used both the PowerPlex21 and Globalfilter kits.

All participants used the terms "NR" or "-" to indicate the presence of an allele, the identity of which could not be confirmed. This terminology was used where single alleles were detected in profiles that they knew or assumed originated from single sources, to indicate possible allele drop-out at one or more loci. (This practice was not followed where single alleles were detected in profiles that indicated the presence of a mixture.)

Sample 750	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	-		14,18		14,NR		14,18	
vWA	18, NR		17,18		17,NR		17,18	
D16S539	12,13		12,13		12,13		12,13	
CSF1PO	13, NR		13,13		-		13,-	
TPOX	-		11,11		-		11,11	
Yindel			2					
AMEL	X,Y		X,Y		X,Y		X,Y	
D8S1179	11,15		11,15		11,15		11,15	
D21S11	27,NR		27,28		-		27,28	
D18S51	15,17		15,17		15,17		15,17	
DYS391			11					
D2S441			10,14					
D19S433	-		13,15		13,15		13,15	Peak imbalance
TH01	6,6		6,6		6,6		6,6	
FGA	24, NR		19,24		19,24		19,24	
D22S1045			11,17					
D5S818	-		11,12		11,12		11,12	
D13S317	-		11,13		13,NR-		13,-	
D7S820	-		8,11		-		8,11	
SE33			17,29.2					
D10S1248			13,15					
D1S1656	-		13,15		13,15		13,15	
D12S391	21,NR		17,21		17,21		17,21	
D2S1338	-		24,25		24, NR		24,25	
D6S1043	-		11,18		-		11,18	
Penta E	-		13,15		13,NR		13,15	
Penta D	-		9,12		-		9,12	

Sample 751	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	15,NR		15,16		15,16		15,16	
vWA	15,NR		15,17		15,NR		15,17	
D16S539	9,13		9,13		9,13		9,13	
CSF1PO	-		11,13		-		11,13	
TPOX	-		11,11		11,NR		11,11	
Yindel			2					
AMEL	X,Y		X,Y		X,Y		X,Y	
D8S1179	13,14		13,14		13,14		13,14	
D21S11	28.3,NR		28.3,32.2		28,NR		28,32.2	
D18S51	-		15,19		15,NR		15,19	
DYS391			11					
D2S441			14,14					
D19S433	13,15		13,15		13,15		13,15	
TH01	7,9.3		7,9.3		7,9.3		7,9.3	
FGA	23,NR		23,23		23,NR		23,23	
D22S1045			16,18					
D5S818	11,NR		11,12		11,NR		11,12	
D13S317	-		8,11		8,11		8,11	
D7S820	-		8,11		11,NR		8,11	
SE33			15.2,25.2					
D10S1248			14,15					
D1S1656	-		12,15		12,NR		12,15	
D12S391	19,22		19,22		19,22		19,22	
D2S1338	-		24,25		24,NR		24,25	
D6S1043	-		11,18		18,NR		11,18	
Penta E	-		12,18		12,NR		12,18	
Penta D	-		9,13		-		9,13	

Sample 752	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	15,18		15,18		15,18		15,18	
vWA	17,19		17,19		17,19		17,19	
D16S539	11,13		11,13		11,13		11,13	
CSF1PO	10,12		10,12		10,12		10,12	
TPOX	8,8		8,8		8,8		8,8	
Yindel			2					
AMEL	X,Y		X,Y		X,Y		X,Y	
D8S1179	10,12		10,12		10,12		10,12	
D21S11	28,31.2		28,31.2		28,31.2		28,31.2	
D18S51	13,13		13,13		13,13		13,13	
DYS391			11					
D2S441			10,10					
D19S433	15,15		15,15		15,15		15,15	
TH01	6,9		6,9		6,9		6,9	
FGA	20,22		20,22		20,22		20,22	
D22S1045			11,15					
D5S818	11,12		11,12		11,12		11,12	
D13S317	11,11		11,11		11,11		11,11	
D7S820	9,11		9,11		9,11		9,11	
SE33			15,27.2					
D10S1248			14,16					
D1S1656	11,17.3		11,17.3		11,17.3		11,17.3	
D12S391	18,23		18,23		18,23		18,23	
D2S1338	23,26		23,26		23,26		23,26	
D6S1043	11,12		11,12		11,12		11,12	
Penta E	12,18		12,18		12,18		12,18	
Penta D	11,13		11,13		11,13		11,13	

Sample 753	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	16,17		16,17		16,17		16,17	
vWA	16,16		16,16		16,16		16,16	
D16S539	11,11		11,11		11,11		11,11	
CSF1PO	11,12		11,12		11,NR		11,12	
TPOX	11,NR		8,11		11,NR		8,11	
Yindel								
AMEL	X,X		X,X		X,X		X,X	
D8S1179	10,13		10,13		10,13		10,13	
D21S11	29,29		29,29		29,29		29,29	
D18S51	14,14		14,14		14,14		14,14	
DYS391								
D2S441			11.3,14					
D19S433	14,16		14,16		14,16		14,16	
TH01	9,9.3		9,9.3		9,9.3		9,9.3	
FGA	20,20		20,20		20,20		20,20	
D22S1045			15,16					
D5S818	11,NR		11,13		11,13		11,13	
D13S317	9,NR		9,11		11,NR		9,11	
D7S820	7,11		7,11		7,11		7,11	
SE33			28.2,28.2					
D10S1248			14,15					
D1S1656	12,15		12,15		12,15		12,15	
D12S391	15,15		15,15		15,15		15,15	
D2S1338	17,19		17,19		17,NR		17,19	
D6S1043	11,11		11,11		11,11		11,11	
Penta E	-		10,17		-		10,17	
Penta D	10,13		10,13		-		10,13	

Sample U1	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	14,18		14,18		14,18		14,18	
vWA	17,18		17,18		17,18		17,18	
D16S539	12,13		12,13		12,13		12,13	
CSF1PO	-		13,13		13,NR		13,13	
TPOX	-		11,11		11,NR		11,NR	
Yindel			2					
AMEL	X,Y		X,Y		X,Y		X,Y	
D8S1179	11,15		11,15		11,15		11,15	
D21S11	27,28		27,28		27,28		27,28	
D18S51	15,17		15,17		15,17		15,17	
DYS391			11					
D2S441			10,14					
D19S433	13,15		13,15		13,15		13,15	
TH01	6,6		6,6		6,6		6,6	
FGA	19,24		19,24		19,NR		19,24	
D22S1045			11,17					
D5S818	11,12		11,12		11,NR		11,12	
D13S317	-		11,13		-		11,13	
D7S820	8,11		8,11		-		8,11	
SE33			17,29.2					
D10S1248			13,15					
D1S1656	13,15		13,15		13,15		13,15	
D12S391	17,21		17,21		17,21		17,21	
D2S1338	24,25		24,25		24,25		24,25	
D6S1043	11,18		11,18		11,18		11,18	
Penta E	13,15		13,15		-		13,15	
Penta D	12,NR		9,12		9,NR		9,12	

Sample U2	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	16,17		16,17		16,17		16,17	
vWA	16,16		16,16		16,16		16,16	
D16S539	11,11		11,11		11,11		11,11	
CSF1PO	11,12		11,12		11,12		11,12	Peak imbalance
TPOX	8,11		8,11		8,11		8,11	
Yindel			-					
AMEL	X,X		X,X		X,X		X,X	
D8S1179	10,13		10,13		10,13		10,13	
D21S11	29,NR		29,29		29,29		29,29	
D18S51	14,14		14,14		14,14		14,14	
DYS391			-					
D2S441			11.3,14					
D19S433	14,16		14,16		14,16		14,16	
TH01	9,9.3		9,9.3		9,9.3		9,9.3	
FGA	20,20		20,20		20,20		20,20	
D22S1045			15,16					
D5S818	11,13		11,13		11,13		11,13	
D13S317	9,11		9,11		9,11		9,11	
D7S820	7,11		7,11		7,11		7,11	
SE33			28.2,28.2					
D10S1248			14,15					
D1S1656	12,15		12,15		12,15		12,15	
D12S391	15,15		15,15		15,15		15,15	
D2S1338	17,19		17,19		17,19		17,19	
D6S1043	11,11		11,11		11,11		11,11	
Penta E	10,17		10,17		10,17		10,17	
Penta D	10,13		10,13		10,13		10,13	

Sample U3	Lab 1		Lab 2		Lab 3		Lab 4	
Locus	Alleles	Comments	Alleles	Comments	Alleles	Comments	Alleles	Comments
D3S1358	15,16,17		15,16,17		15,16,17		15,16,17	
vWA	15,16,17		15,16,17		15,16,17		15,16,17	
D16S539	9,11,13		9,11,13		9,11,13		9,11,13	
CSF1PO	11		11,12,13		11,12,13		11,12,13	
TPOX	8,11		8,11		8,11		11	
Yindel			2					
AMEL	X,Y		X,Y		X,Y		X,Y	
D8S1179	10,13,14		10,13,14		10,13,14		10,13,14	
D21S11	29		28,29,32.2		28,29,32.2		28,29,32.2	
D18S51	14,15,19		14,15,19		14,15,19		14,15,19	
DYS391			11					
D2S441			11.3,14					
D19S433	13,14,15,16		13,14,15,16		13,14,15,16		13,14,15,16	
TH01	7,9,9.3		7,9,9.3		7,9,9.3		7,9,9.3	
FGA	23		20,23		20,23		20,23	
D22S1045			15,16,18					
D5S818	11		11,12,13		11,12		11,12,13	
D13S317	8,9,11		8,9,11		8,9,11		8,9,11	
D7S820	11		7,8,11		7,8,11		7,8,11	
SE33			15,25.2,28.2					
D10S1248			14,15					
D1S1656	12,15		12,15		12,15		12,15	
D12S391	15,19, 22		15,19,22		15,19,22		15,19,22	
D2S1338	17,24		17,19,24,25		17,24,25		17,19,24,25	
D6S1043	11,18		11,18		11,18		11,18	
Penta E	-		10,12,17,18		10,12,17,18		10,12,18	
Penta D	9,10		9,10,13		9,10,13		9,10,13	

NR = 2nd allele could not be confirmed - = No reportable allele
Grey indicates loci present in GlobalFiler that were not typed in PP21.

There was a wide variation in the number of alleles for which typing results were reported, as indicated in the table below:
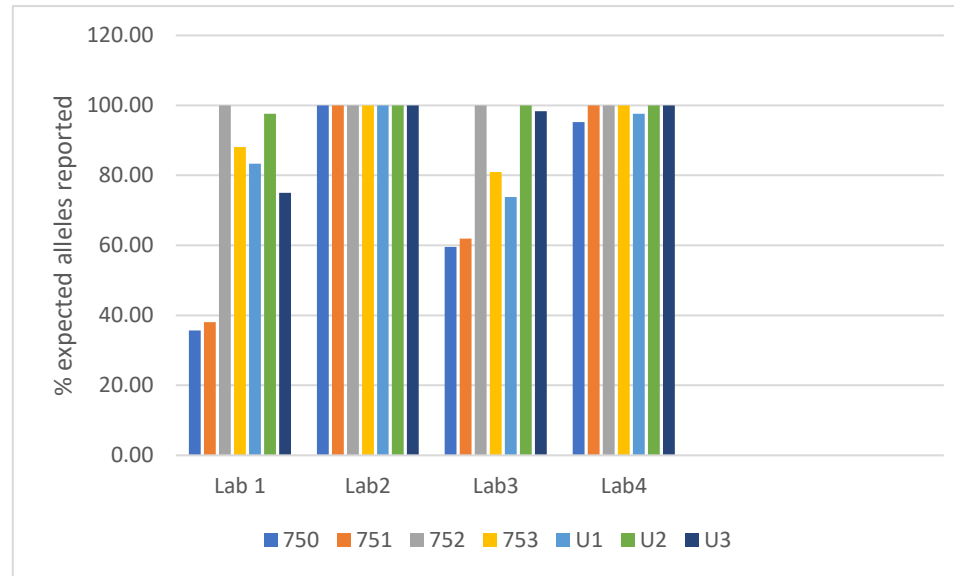
Profile comments

The results for each Test stated the number of contributors for each unknown sample. The results for Lab 4 tempered this by stating that Sample U3 "appeared" to originate from two individuals and indicated that this was an assumption. Lab 2 & 3 stated that sample U3 was a mixture that originated from at least two individuals. Lab 1 stated that sample U3 gave a mixed DNA profile that was "consistent with having come from two individual" (sic), without also stating that it was consistent with DNA from more than 2 individuals.

Sample	Lab 1	Lab 2	Lab 3	Lab 4
750	NA	Full profile using Powerplex 21 and Globalfiler	DNA appeared degraded Partial profile	NA
751	NA	Full profile using Powerplex 21 and Globalfiler	Partial profile. DNA appeared degraded	NA
752	NA	Full profile using Powerplex 21 and Globalfiler	Single source, full powerplex 21 profile	NA
753	NA	Full profile using Powerplex 21 and Globalfiler	Partial profiler. DNA appeared degraded with allele imbalance at 3 loci, accepted as true alleles.	NA
U1	No. of contributors: 1	Single source profile	No. of contributors: 1	Single source profile, refer STRmix deconvolution
	Not excluded: 750 Excluded: 751, 752, 753	==DNA profile obtained matched profile of sample 750== ==It is estimated to be >100 billion==	Not excluded: 750 Excluded: 751, 752, 753	Not excluded: 750 Excluded: 751, 752, 753 ==LR>100 billion favouring contribution==

Sample	Lab 1	Lab 2	Lab 3	Lab 4
		==time more likely if it originates from 750 than if it originates from another unknown individual chosen at random from the Australian population==		
U2	No. of contributors: 1	No. of contributors: 1	No. of contributors: 1	Single source profile, refer STRmix deconvolution
	Not excluded: 753 Excluded: 750, 751, 752	DNA profile obtained matched profile of sample 753 ==It is estimated to be >100 billion time more likely if it originates from 753 than if it originates from another unknown individual chosen at random from the Australian population==	Not excluded: 753 Excluded: 750, 751, 752	Sample matched reference 753 ==LR>100 billion favouring contribution==

Sample	Lab 1	Lab 2	Lab 3	Lab 4
U3	No. of contributors: 2	No. of contributors: 2	No. of contributors: 2	Mixed DNA profile from 2 contributors, approximately equal proportions
	Not excluded: 751, 753 Excluded: 750, 752.	DNA profile obtained indicated it was a mixture of DNA from at least two individuals. 750 and 752 are both excluded as potential contributors. 751 and 753 are not excluded as possible contributors to this mixture. ==The mixed DNA profile was estimated to be >100 billion times more likely if unknown (U3) contained a mixture of DNA from donors 751 and 753, than if it originated from two other unknown==	Not excluded: 751, 753 Excluded: 750, 752	Excluded as potential contributor: 750 and 752 ==751: LR >100 billion favouring contribution== ==753: LR 460 million favouring contribution==

Sample	Lab 1	Lab 2	Lab 3	Lab 4
		individuals chosen at random from the Australian population		

All participants correctly reported that the respective donors of samples U1 and U2 were not excluded as the sources of these samples, and correctly excluded the donors who were not the sources of samples U1 and U2. Two participants reported likelihood ratios for these matches, truncated to greater than 100 billion.

With respect to sample U3, all participants correctly excluded reference donors 750 and 752 as contributors.

Reference donor 751 was not excluded by any participants, and 2 participants reported a Likelihood Ratio, which ranged from 60 million to greater than 100 billion.

Reference donor 753 was not excluded by any participants, and 2 participants reported a Likelihood Ratio, which ranged from 60 million to greater than 100 billion.

One participant also calculated a Likelihood Ratio greater than 100 billion by comparing (H1) contributions from both 750 and 753 with (H2) 2 unknown contributors from the Australian population.

One participant did not state the propositions used to calculate any of the Likelihood Ratios and did not indicate which population the values referred to.

Two participants did not report any Likelihood Ratios.

The reported Likelihood Ratios and the contributors assumed in the propositions used for Labs 2 & 4 are summarised in the Table below:
(H1 = contributor, H2 = unknown contributor(s), LR = likelihood ratio of H1 compared to H2)

Sample U1	Lab 2	Lab 4
H1	750	750
H2	Another unknown individual chosen at	Not given

LR   >100 billion   >100 billion

Sample U2
H1   753   753
H2   Unknown   Not given
LR   >100 billion   >100 billion

Sample U3
H1   751
H2   Not given
LR   >100 billion

H1   753
H2   Not given
LR   460 million

H1   751 + 753
H2   2 Unknowns
LR   >100 billion

Conclusion

The aim of this test was to examine the end-to-end forensic examination and analysis process with special reference to the proficiency of forensic DNA laboratories to amplify, analyse, interpret, compare and evaluate the profiles of the same set of single-source, mixed and low-level DNA samples, using the laboratories' standard procedures. To minimise extraneous elements to the interpretation, genomic DNA samples with limited contextual information were provided to the participating laboratories.

The four participating laboratories all submitted results which have been incorporated in this report.

There appeared to be a discrepancy between the DNA concentrations provided by the manufacturer and those produced by at least one laboratory. Two sources of this discrepancy can be postulated:
1. The methods of quantification used measured different aspects of the DNA present (total verses amplifiable human); and
2. DNA samples degraded during transport from the supplier to Forensic Foundations, from Forensic Foundations to the participating laboratories.

Both of these issues will be addressed in subsequent Proficiency Test programs.

There was a wide variation in the number of alleles for which typing results were reported. It is not clear from the results submitted whether the laboratories which reported a larger number of alleles had reamplified samples which had previously generated a partial profile.

All participating laboratories obtained results which were concordant with the expected results.

Two participating laboratories did not provide any statistical interpretation of the results. The two laboratories which did provide statistical interpretation did so using Likelihood Ratios. Three of these four laboratories provided the propositions they used to calculate the Likelihood Ratios. Although the values of the Likelihood ratios varied, as would be expected, they were all in the same order of magnitude.

This test and the collation of results, has provided Forensic Foundations with much information which can be used to generate continuous improvement within the Forensic Foundations' Proficiency Testing program. It is anticipated that the test, the results (individual and collated) and this Final Report will provide data which can be used by the forensic laboratories in their respective continuous improvement programs.

Appendix A

Proficiencytesting@forensicfoundations

PROGRAM PLAN

Program	Forensic Science - DNA	
Round	Sample (S)	
Advisory Group		
Program Coordinator	Mrs Anna Davey Director, Forensic Foundations PO Box 2279 North Ringwood, 3134	
Technical Advisor(s)	Dr Henry Roberts c/- Forensic Foundations PO Box 2279 North Ringwood, 3134	
Supplier(s)	Initial sample collection & test production Results interpretation.	DNA profiling
	Forensic Foundations PO Box 2279 North Ringwood, Victoria 3134	DNA Labs Level 1, 14 Giffnock Ave Macquarie Park NSW 2113
Aims/Objectives	The aim of the program is to assess the laboratories' ability to competently interpret DNA profiles	
Purpose	To assist the laboratories by ensuring their methods / procedures are performing adequately.	
Program Design		
Tests	1	
Number of samples	7	
Type of sample	Genomic DNA of known concentrations extracted from buccal cells.	
Levels	The concentration of the samples (ng/ul) will be determined post extraction and diluted as appropriate.	
Range of values/assigned values	The allelic values will be identified within the known allelic size range.	
Traceability/origin of assigned values	1. Identification of biological material recorded upon collection. 2. DNA extracted by DNA Labs – continuity maintained. DNA profile obtained and independently interpreted by two individuals. 3. Dilutions and mixtures verified by obtaining DNA profiles and independently interpreted by two individuals.	
Methods	DNA Profiles will be obtained following extraction, quantification, amplification and electrophoresis.	
Design	Known ratios of DNA sample(s) will be used to generate the unknown data.	

Selection Criteria	Selection of unknowns to be determined once the profiles of the original samples was known.
Potential Major Sources of Error	Failure to identify and/or classify peaks as true alleles /artifacts
Participants	6 / 7 Forensic Biology laboratories in Australia and New Zealand. This test would also be relevant to international participants.
Reporting Criteria, Accuracy	NA
Analysis	Correctly identify all true alleles and interpret mixtures and partial profiles.

Pre-testing	
Homogeneity Testing	Dilutions and mixtures to be created in precalculated ratios, homogeneity was established by thorough mixing and immediate subsampling. One subsample was profiled, one subsample retained for subsequent homogeneity/repeatability checking if required. The remaining samples used for testing purposes
Stability Testing	NA – Genomic DNA remains stable in solution for periods in excess of the duration of the test.
Homogeneity/Stability Acceptance Criteria	See homogeneity testing – historical data demonstrating stability of genomic DNA in solution.
Technical Advisor Review (internal)	
Participant Instructions	Provide copy of Instructions and evidence of Technical Advisor Review
Results Sheet	Provide copy of Results Sheet and evidence of Technical Advisor Review
Report	Include copy of Report and evidence of Technical Advisor Review

Sample Preparation	
Storage requirements	4ºC / 20ºC for extended storage. Room Temperature for shorter periods and during transport
Distribution requirements	Distributed via ANZPAA|NIFS
Sample checks	NA
Sample Identification	Sample 750. White tube, yellow cap labelled 750 Sample 751. White tube, orange cap labelled 751 Sample 752. White tube, blue cap labelled 752 Sample 753. White tube, purple cap labelled 753 Sample U1. White tube, yellow cap labelled U1 Sample U2. White tube, red cap labelled U2 Sample U3. White tube, green cap labelled U3

Program Dates	
Invitation letter	17 January 2017
Sample distribution	First week in April 2017
Results due	30 June 2017
Manufacturing Information to be sent	July 2017
Final report due date	First week of September 2017
Statistical Analysis	
Homogeneity Testing	NA
Stability Testing	NA
Data Entry	Include evidence of data entry checks in file
Normality	NA
Review by Statistician	NA
Reporting	
Report No:	S/2017
Master copy	Reports folder
Availability	Website

Program Coordinator signature: Anna Davey

Date: 1/3/2017

Samples packed by: Anna Davey/ Maggie Pennacchia

Checked by: Dale Parsell

Result data input by: Maggie Pennacchia

Data checked by: Dale Parsell

Statistics and report collated by: Henry Roberts/ Anna Davey

Report checked by: Dale Parsell

Appendix B

Test segment: the header says "1/2017 Test".

Proficiencytesting@forensic foundations
DNA Interpretation
S/2017

Welcome to the first Forensic Foundations Proficiency Test.

We hope that you find this test useful and welcome any feedback on the design of further tests.

Attached you will find the case 'Examination Request and Item Submission' form and the test commences with the receipt of the items followed by your routine processes - item description, examination, DNA profiling and interpretation. The information submitted to the laboratory will direct what testing needs to be undertaken. Please use the attached results sheets. Additional pages may be added if required.

To meet the requirements of the National Privacy Principles, DNA Profiles of the donors must not be permanently uploaded onto a DNA database

The attached results sheets should be returned to ANZPAA|NIFS by Friday 30 June 2017.

The results of the test will be assessed qualitatively. For example:
- Item receipt and description: Do items submitted match items on submission form? Are details correct? Are continuity/evidence seals intact? Is the condition of the samples appropriate?
- DNA profile interpretation: Inclusion/exclusion with relevant reference samples.
- Statistical interpretation: It would be expected that there would be some differences in the figures given as different databases and methods of calculation would be used. These would not be 'marked' as such but it will be of interest to see what figures the different labs would report from the same samples.

Appendix C

Proficiciencytesting@FORENSICFOUNDATIONS	
EXAMINATION REQUEST AND ITEM SUBMISSION	forensic FOUNDATIONS™

OFFENCE:	Sexual Assault
DATE OF OFFENCE	20/01/2017
BRIEF STATEMENT OF FACTS	

These samples have been previously examined by the Eastern Australian Police Laboratory. DNA profiles were obtained from four reference samples and three unknown samples. These results were interpreted and a report produced.
The accused has requested your laboratory to reinterpret the results independently. To reduce any cognitive effects influencing the interpretation the reference samples are labelled 750, 751, 752, 753 and the unknow samples are labelled U1, U2 and U3.

ITEMS SUBMITTED FOR EXAMINATION

Sample 750 – reference sample – genomic DNA 7.8ng/ul
Sample 751 – reference sample – genomic DNA 10.3ng/ul
Sample 752 – reference sample – genomic DNA 8.5ng/ul
Sample 753 – reference sample – genomic DNA 3.3ng/ul
Sample U1 – unknown sample – genomic DNA 7.8ng/ul
Sample U2 – unknown sample – genomic DNA 1.1ng/ul
Sample U3 – unknown sample – genomic DNA 8.0ng/ul

Appendix D

Suite10, 12 Maroondah Hwy, Ringwood, VIC, 3134
PO Box 2279, Ringwood North VIC 3134
Office: 03 9018 8919
Mobile: 0429 966 012
Fax: 03 9870 1308

anna.davey@forensicfoundations.com.au
www.forensicfoundations.com.au

ABN 23 839 112 155   ACN 130 236 618

Proficiencytesting@FORENSIC FOUNDATIONS
DNA INTERPRETATION S/2017

MANUFACTURER'S INFORMATION

Sample Collection

Six 'Coplan' brand swabs were used to collect buccal cells from four donors (three males and one female).

DNA extraction

DNA was extracted individually from each of the swabs using Roche MagNA Pure 96 DNA and Viral SV kit and a Roche MagNA Pure instrument.

DNA samples were eluted in 50ul.

DNA quantification

The nucleic acid concentration and purity ratios were determined using Thermo Fisher NanoDrop 2000 UV-Vis Spectrophotometer.

DNA concentrations ranged from 4.3ng/ul to 36.9ng/ul. [one swab which yielded 1.1ng/ul was discarded.]

Initial DNA amplification

2ng of sample DNA was amplified using Applied Biosystems GlobalFiler Express kit.

DNA electrophoresis

Amplified samples were run on an ABI3500. RFU threshold for calling an allele was 175RFU.

Results

Sample ID	242569751	242569750	242569753	242569752
D3S1358	15,16	14,18	16,17	15,18
vWA	15,17	17,18	16,16	17,19
D16S539	9,13	12,13	11,11	11,13
CSF1PO	11,13	13,13	11,12	10,12
TPOX	11,11	11,11	8,11	8,8,
Yindel	2	2		2
AMEL	X,Y	X,Y	X,X	X,Y
D8S1179	13,14	11,15	10,13	10,12
D21S11	28,32.2	27,28	29,29	28,31.2
D18S51	15,19	15,17	14,14	13,13
DYS391	11	11		11
D2S441	14,14	10,14	11.3,14	10,10
D19S433	13,15	13,15	14,16	15,15
TH01	7,9.3	6,6	9,9.3	6,9
FGA	23,23	19,24	20,20	20,22
D22S1045	16,18	11,17	15,16	11,15
D5S818	11,12	11,12	11,13	11,12
D13S317	8,11	11,13	9,11	11,11
D7S820	8,11	8.11	7,11	9,11
SE33	15,25.2	17,29.2	28.2,28.2	15,27.2
D10S1248	14,15	13,15	14,15	14,16
D1S1656	12,15	13,15	12,15	11,17.3
D12S391	19,22	17,21	15,15	18,23
D2S1338	24,25	24,25	17,19	23,26

Proficiency Test Sample preparation

DNA eluates from each individual were combined:
- 111111750 – 6 swabs.
- 111111751 – 6 swabs
- 111111752 – 5 swabs
- 111111753 – 6 swabs

The combined samples were diluted.

Reference samples

Aliquots of 20ul of each diluted sample were labelled:
- 750
- 751
- 752
- 753

These samples comprised the reference samples.

Unknown samples

U1
- 10ul aliquot of 111111750

U2
- Further dilution of 111111753A
- 10ul of this further dilution

U3
- 2:1 mixture of 111111751 & 111111753
- 10ul of this mix

Samples from 750, 751, 752, 753, U1, U2 & U3 were quantified using both Thermo Fisher Qubit and values compared with the expected theoretic values.

Samples were then amplified and separated as described previously.

Results

Sample ID	750	751	752	753	U1	U2	U3
D3S1358	14,18	15,16	15,18	16,17	14,18	16,17	15,16,17
vWA	17,18	15,17	17,19	16,16	17,18	16,16	15,16,17
D16S539	12,13	9,13	11,13	11,11	12,13	11,11	9,11,13
CSF1PO	13,13	11,13	10,12	11,12	13,13	11,12	11,12,13
TPOX	11,11	11,11	8,8,	8,11	11,11	8,11	8,11
Yindel	2	2	2		2		2
AMEL	X,Y	X,Y	X,Y	X,X	X,Y	X,X	X,Y
D8S1179	11,15	13,14	10,12	10,13	11,15	10,13	10,13,14
D21S11	27,28	28,32.2	28,31.2	29,29	27,28	29,29	28,29,32.2
D18S51	15,17	15,19	13,13	14,14	15,17	14,14	14,15,19
DYS391	11	11	11		11		11
D2S441	10,14	14,14	10,10	11.3,14	10,14	11.3,14	11.3,14
D19S433	13,15	13,15	15,15	14,16	13,15	14,16	13,14,15,16
TH01	6,6	7,9.3	6,9	9,9.3	6,6	9,9.3	7,9,9.3
FGA	19,24	23,23	20,22	20,20	19,24	20,20	20,23
D22S1045	11,17	16,18	11,15	15,16	11,17	15,16	15,16,18
D5S818	11,12	11,12	11,12	11,13	11,12	11,13	11,12,13
D13S317	11,13	8,11	11,11	9,11	11,13	9,11	8,9,11
D7S820	8,11	8,11	9,11	7,11	8,11	7,11	7,8,11
SE33	17,29.2	15,25.2	15,27.2	28.2,28.2	17,29.2	28.2,28.2	15,25.2,28.2
D10S1248	13,15	14,15	14,16	14,15	13,15	14,15	14,15
D1S1656	13,15	12,15	11,17.3	12,15	13,15	12,15	12,15
D12S391	17,21	19,22	18,23	15,15	17,21	15,15	15,19,22
D2S1338	24,25	24,25	23,26	17,19	24,25	17,19	17,19,24,25

Amendment Record:

Issue Date	Comments
4/9/18 Issue A	"Authorisation" and "END of REPORT" added to document in the appropriate place

END of REPORT

DNA Interpretation Proficiency Test Feedback

Forensic Foundations prides itself in providing flexible fit-for-purpose forensic programs. The manufacture, distribution and assessment and reporting of this test has provided, and will provide the basis for continuous improvement for both Forensic Foundations and the forensic laboratories. To this end we would appreciate your comments to assist us to improve the tests.

Please tick the appropriate box and make any relevant comments.

	Strongly Agree	Agree	Disagree	Strongly Disagree	N/A
1. The test was too basic for our facility	☐	☐	☐	☐	☐

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2. The samples supplied were suitable	☐	☐	☐	☐	☐

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3. The results required were not outlined sufficiently	☐	☐	☐	☐	☐

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....

4. The final report provided suitable detail	☐	☐	☐	☐	☐

....
....
....
....

5. The tests involved should be more challenging	☐	☐	☐	☐	☐

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....
....
....

Please comment briefly on the following:

6. Are there additional aspects which could be included in the test?

....
....
....

7.   Any additional comments

....
....
....

9.   Facility (optional)

....

10.   Would you like us to contact you to discuss your feedback?

....

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Forensic Foundations' Proficiency Tests are required to be fit-for purpose. To assist us to provide the relevant tests, please use the following form to suggest further tests for development.

Recommendation for Proficiency Test development

Contact	Name	
	Email	
	Phone	
Discipline/ subdiscipline		
Specific issues(s) to be addressed*. Note: The tests can be designed to be multidisciplinary.		
Suggested technical advisor (if known)		
Suggested manufacturer (if known)		

∗ All Proficiency Tests will include the end to end process (receipt & continuity, triage, description, examination, analysis, data generation, interpretation, reporting) but one aspect may be of particular interest/focus.

This form can be emailed to quality@forensicfoundations.com.au or you can discuss your suggestions on either 03 9018 8919 or 0429 966 012.