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O/ref. : 21-T02499-02503 and 21-T02540-2544-vic

Report on the forensic genetics analysis of biological specimens

Dear Dr Kuuranne,

We have been asked to determine the DNA concentration of 100 urine samples numbered DN001 to DN100 using the same method which was used for the analysis of the sample 12966171DN (17-T05676a) in 2017.

You also asked our opinion regarding the following statements from the report issued by the Judge, Mr. Walter Pelino, dated 18.02.2021:

p.15 "This involves, therefore, not only the concentration of exogenous testosterone, desired by the hypothetical manipulator, but also of everything else, including DNA, and what the expert has definitely found is just a completely abnormal, unnatural, DNA concentration."

p.16 "In other words, not only does the manipulation hypothesis allow us to explain how and why that abnormal DNA concentration occurred, but this is also, at present, the only convincing explanation."

p.31 "Actually, the experimentation carried out by the expert, Col. PhD Giampietro Lago, has demonstrated that already after 6 months the samples show on average (weighted average) a decay of approximately 70% of the DNA present thereto, a decay that becomes higher, approximately 87%, after 12 months (see supplementary report filed on 3.09.2019, p. 43).

The subsequent supplement to the expert report, filed on 5.09.2020, demonstrated the asymptotic trend of this progressive decay, where the curve that graphically expresses the decrease, very pronounced in the first 6 months, continues over time becoming progressively milder the closer it gets to zero (p. 30)."







Hôpitaux Universitaires Genève p.51 "Moreover, the figure concerning the DNA concentration (14,013 pg/ μ l in urine frozen for a year and a half) was manifestly implausible, given that (as a result of the decay due to freezing, the passage of time and the thermal stress suffered) it would presuppose a concentration at the time of taking the sample of more than 100,000 pg/ μ l, comparable with that of blood or saliva, as repeatedly stated by the expert who was not contested on the point."

p.51-52 "Instead, if we consider that the sample of 27.06.2016, at the time of the analysis (October 2017) had been frozen for a year and four months and we assume, with a conservative estimate, that due to the long time elapsed it had undergone a decay of 80% (the examination showed a median decay after 12 months of 87%), we can estimate the original concentration at 112,104 pg/µl on 4 ml of urine, i.e. 28,026 pg/µl on 1 ml, a concentration significantly higher (approximately +9%) compared to the (already implausible) concentration of 25,780 pg/µl that WADA's Director of Legal Affairs, Sieveking, asserted to be the maximum quantity found at the Lausanne laboratory (see p. 2 of the note of 10.12.2019), without however documenting this assertion in any way."

p.70 "Is it not the case that this phantom study is completely bogus and has been referred to solely in an attempt to make the figure of 14,013 pg/μ l that emerged from the Lausanne analysis of the 27.06.2016 sample appear true, a figure that is completely implausible, especially one year and four months after freezing?"

Our findings and comments are reported thereafter.

This report is valid only for the samples analyzed and within the sensitivity limit of the analytical methods that were used. This report cannot be reproduced, otherwise than entirely, without a written consent from the laboratory. Unless explicitly requested, all samples and DNA extracts will be destroyed within three months after reception.

METHODS

The samples were analyzed using the following methods:

SAMPLING

The requesting authorities forward specimens to the Forensic Genetics Unit (FGU). FGU staff cannot be held responsible for any damage to these samples prior to their reception. The part of the specimen that is submitted for analysis is called a sample. When the transmitted specimen is used in its entirety for analysis, for example in the case of a swab or a piece of clothing, FGU is not responsible for the sampling plan and method. When this is not the case, the FGU is responsible for the sample taken. Where appropriate, these are described in the "Analyzed material" section of this report.

DNA EXTRACTION

The QIAamp Circulating Nucleic Acid Kit (Qiagen) was used to extract and purify the DNA.

DNA QUANTIFICATION

The concentrations of male and total DNA (i.e. male and female) present in the samples are determined prior to amplification by means of real-time quantitative PCR with the Quantifiler Trio kit (Applied Biosystems) on an Applied Biosystems QuantStudio 5 Real-Time PCR System.

Complementary information on the methods can be obtained upon request. In accordance with the Ordinance of the Federal Department of Justice and Police on the DNA analysis laboratories (RO 363.11), the results were confirmed with at least two independent analyses.

MATERIAL AND RESULTS

LAD nb : DN001 to DN100

Material received : about 6 ml urine for each sample Reception date : 11.05.21 Lab nb : 21-T02499a - 21-T02503j and 21-T02540a - 21-T02544j

ANALYZED MATERIAL 4 ml of each urine sample

DNA CONCENTRATION [ng/uL] from 50 uL extract Range : 0.001 - 20.183 ; Mean : 1.845 ; SD: 3.670 See Fig. 1 and the appendix







DNA concentration (ng/uL)

660NQ 260NQ

DOC : 274FO27 ; Version 005

COMMENTS AND INTERPRETATION

The individual DNA concentrations measured from 4mL of each of the 100 urine samples provided (named DN001 to DN100) ranged from 0.001 to 20.183 ng/ul (Fig. 1). The corresponding mean DNA concentration is 1.845±3.670 ng/uL. With DNA extracts of 50 uL, these DNA concentrations correspond to a range of 0.013 to 252.288 ng of DNA per mL of urine and a mean DNA concentration of 23.062±45.880 ng of DNA per mL of urine. This corresponds to the typical amounts of DNA expected to be extracted from urine samples (from 1 to 20 ng/mL according to [1]).

Among the 100 urine samples analyzed, 6 of them had DNA concentrations exceeding 10 ng/uL among which 2 even exceeded 17 ng/uL. This definitely proves that the DNA concentration of 14.013 ng/uL (or 14'013 pg/uL) observed for the urine sample 17-T05676a analyzed in Lausanne with the same method is neither "manifestly implausible" nor "abnormal" or "unnatural" as stated by the Judge, Mr. Walter Pelino, in his report.

During storage, the DNA present within a biological sample may suffer degradation. When we focus on a sample of interest, it is better to consider the characteristics of this particular sample rather than an average value obtained from samples that may not have been exposed to the same environmental conditions.

DNA profiles obtained from good quality DNA samples (*i.e.* not significantly degraded) show peaks with about similar heights between the shortest (on the left side) and the longest loci (on the right side) within the different color channels (Fig. 2). DNA degradation will statistically affect the largest DNA fragments first. At the level of the DNA profile, this will result in the so-called "ski-slope effect", the height of the largest loci being smaller than the one of the shortest loci. Extreme degradation results in partial DNA profiles with alleles missing for the largest loci.



Figure 2 (from Ref [1]): A comparison of DNA profiles from the same person but of different qualities. (a) Intact, good-quality DNA yields a full DNA profile and (b) Degraded, poor-quality DNA yields a partial DNA profile with alleles missing at the larger-sized loci.

Hence, when considering a DNA profile, it is possible to determine whether the corresponding DNA is severely, slightly or not degraded.





Figure 3: DNA profiles (replicates) obtained for the urine sample 17-T05676a. These are full profiles with peaks present at every locus. Furthermore, the height of the peaks corresponding to the largest loci is similar to the one of the shortest loci. These characteristics are diagnostics of good-quality DNA.

As illustrated in Fig. 3, the DNA recovered from the urine sample 17-T05676a can be qualified as a good-quality DNA. Using the method described in [2], we estimated that the integrity index, which is a measure of non-degraded DNA, is equal to 0.86 for this urine sample. This implies that the degradation is about 14%. This represents a slight degradation and certainly not a decay of 80% (or even more) as stated by the Judge, Mr. Walter Pelino, in his report.

The Quantifiler Trio kit used for the DNA quantification provides a degradation index (DI). DI is calculated as the ratio of the DNA concentration of a short autosomal DNA target of 80 bases and the DNA concentration of a large DNA target of 214 bases. The DI of the urine sample 17-T05676a provided with this method is 1.0. This means that the concentration of the short DNA fragments is equal to the concentration of the large DNA fragments. According to the manufacturer user guide [3], a DI <1 typically indicates the absence of DNA degradation, whereas a DI between 1 and 10 indicates that the DNA is slightly to moderately degraded. The DNA is significantly degraded when the DI is reaches values >10.

All these considerations indicate that the urine sample 17-T05676a contains good-quality DNA. This sample has been stored frozen for a year and four months but it clearly does not show signs of at least 80% decay as written by the Judge, Mr. Walter Pelino, in his report. Consequently, the calculation made by the expert, taking into account such an exaggerated decay, in order to estimate an "original concentration of 112,104 pg/uL" is totally erroneous and fallacious.

As a summary, we measured the DNA concentrations of 100 individual urine samples and examined the DNA profiles obtained for the urine sample 17-T05676a. Contrary to what the Judge, Mr. Walter Pelino, has written in his report, the scientific elements presented here prove that the DNA concentration of urine measured for the sample 17-T05676a is high but not "manifestly implausible" nor "abnormal" or "unnatural" and also proves the absence of severe degradation of DNA in this urine sample.

Should you need any further information, please feel free to contact us.

With our best regards,

M.Sc. C. GEHRIG Forensic geneticist SSLM

DrSc. V. CASTELLA, PD, MER Forensic geneticist SSLM

Bibliography:

[1] Butler, JM. Advanced topics in forensic DNA typing: methodology. Waltham, MA: Elsevier, 2012, 704 pp

[2] Comte J, Baechler S, Gervaix L, Lock E, Milon M-P, Delemont O and Castella V (2019) Touch DNA collection - Performance of four different swabs. Forensic Science International: Genetics 43: 102113 (open access)

[3] Applied Biosystems (2018) Quantifiler™ HP and Trio DNA Quantification Kits User Guide Rev. H. P/N 4485354.

Appendix 1 : DNA concertation of 100 urine samples

Appendix to the report 21-T02499-02503 and 21-T02540-02544 DNA concentration of 100 urine samples

28.06.2021

N° LAD DNA conc. ng/uL N° LAD DNA conc. ng/uL DN001 0.122 DN051 8.817 DN002 0.119 DN052 0.33 DN003 0.017 DN053 0.113	
DN002 0.119 DN052 0.33	
DN004 0.003 DN054 3.813	
DN004 0.500 DN055 1.987	
DN006 0.103 DN056 0.425	
DN007 0.083 DN057 0.023	
DN007 0.000 0.000 DN058 0.009	
DN009 0.071 DN059 2.243	
DN009 0.071 DN060 0.248	
DN010 0.094 DN061 0.795	
DN014 0.000 7400	
DN010 0.004 0.025	
DN017 0.021 10000 4.070	
DIN010 0.041 DIN020 0.04	
DN019 0.010 2.620	
DN020 0.020 DN074 12.200	
DN022 0.041 DN070 42.004	
DN024 0.000 DN075 1.600	
DN023 0.107 DN072 0.571	
DN020 0.100 DN077 4494	
DN027 0.120 DN070 6 500	
DN020 0.001 0.712	
DN029 0.021 DN000 0.262	
DN030 0.100 0.000	
DN031 0.04F	
DN032 0.000 DN000 0.04	
DN034 0.141 DN005 0.100	
DIVOUD	
DN037 0.102 DN000 0.000	
DIN039 0.001 DIN020 0.410	
DIN040 0.004 DN001 0.02	
DN042 0.007 DN000 0.122	
DN043 0.204 DN004	
DIN043 1.040 1.702	
DN040 10.100 DN007 0.000	
DN047 0.201 DN000 10.471	
DN046 2.021 DN000 0.100	
DN049 20.100 DN1400 0.446	
DN050 1.146 DN100 0.446	

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