UNITED STATES OF AMERICA,		
Plaintiff,)	
VS.)	
) AFFIDAVIT OF	TINA DELGADO
JEFFREY R. MacDONALD,)	
Applicant/Defendant.)	
)	

NOW COMES the Affiant, Tina Delgado, who, being duly sworn, attests to the following:

- 1. I am employed as the Biometrics Analysis Section DNA Technical Leader of the Federal Bureau of Investigation (FBI) Laboratory. As a technical leader I am accountable for the technical operations of the units in which I oversee.
- 2. I have been employed with the FBI Laboratory since 2000. Prior to my current position, I was assigned to the FBI Laboratory in the Nuclear DNA Unit. My positions have included Biologist, Forensic Examiner, and Supervisory Forensic Examiner. As a biologist I performed laboratory analyses on casework samples as directed by a forensic examiner. As a Forensic Examiner I was involved in the analysis and interpretation of data relating to DNA. Following my analysis in a particular case I prepared laboratory reports containing my conclusions.
- 3. The Nuclear DNA Unit is involved in the analysis of biological evidence submitted in criminal cases from law enforcement agencies throughout the United States. Evidence is subjected to DNA typing which allows for the comparison of DNA from known and unknown sources.
- 4. The FBI Laboratory began investigating the use of DNA for identification and comparison purposes in 1986. Currently, the FBI laboratory utilizes a procedure known as the polymerase chain reaction (PCR), a technique which copies or amplifies specific, small defined portions of DNA. These small defined portions of DNA are called Short Tandem Repeats (STRs). STRs are short sequences of DNA that are repeated numerous times in a head-to-tail manner and their lengths vary between individuals. Multiple STR locations are analyzed simultaneously to generate a DNA profile.
- 5. Conventional STR analysis has been shown through validation to produce reliable and reproducible results. The Nuclear DNA Unit has a quality assurance program which insures that all techniques are validated prior to their use. National

- standards exist which ensures that employed techniques are producing results suitable for entry into the National DNA Index System (NDIS).
- 6. Additional DNA typing methodologies exist which differ from conventional STR analysis in the locations tested or the amount and/or quality of the DNA targeted. These methodologies include Low Copy Number (LCN), miniSTR, and Y-STR analysis. Currently, the applications for these methodologies are quite specific and should only be used in an appropriate fashion.
- 7. "Touch DNA" refers to DNA from skin cells which are deposited when an individual touches or comes into contact with an object. The Nuclear DNA Unit of the FBI Laboratory has demonstrated that samples containing low levels of DNA may not only recover cells from a person of interest, but also from other individuals who have been in contact with the item at some point in time.
- 8. LCN analysis utilizes the same techniques as conventional STR analysis with modifications to increase test sensitivity including the increase of amplification cycles in PCR and post amplification purification of the DNA samples. LCN analysis is an enhancement strategy used for items of evidence potentially containing "touch DNA." LCN analysis generally increases the risk of DNA typing inaccuracies and is not permitted in NDIS. Studies have shown that LCN analysis can profoundly alter the performance characteristics of the PCR and result in demonstrable losses of fidelity and reproducibility.
- 9. LCN typing results fall within a "stochastic zone," in which random fluctuation in the quantity of detected DNA types is known to occur and can lead to erroneous DNA typing if not properly addressed. DNA types can randomly "drop out" and "drop in," resulting in an incomplete and/or erroneous profile which can compromise the reliability of the typing system. Additionally several artifacts of the analysis method may become more prominent and have a heightened chance of being misinterpreted as part of the true DNA profile. These artifacts include "drop in," "drop out," peak imbalance, and increased stutter. Because of these factors, LCN typing results are generally not reproducible and by its nature less robust than traditional STR analysis.
- 10. One of the fundamental limitations of the LCN approach on items of evidence containing "touch DNA" is that results typically exhibit a combination of the various individuals who have handled an item, not exclusively those individuals involved in a criminal act. There is also a greater opportunity for adventitious transfer of DNA in the field (which may preclude testing of "old," unsolved cases) as well as during the manufacture of reagents and consumables that are used in testing. As a result, the potential exists for these materials to contain low-level biological contaminants that may be detected together with, or instead of, sample DNA. It may be impossible to determine if a LCN DNA profile is derived from primary or secondary transfer, casual contact, or from "background" DNA.

Because of these limitations, any results not matching a reference sample cannot be assumed to be exclusionary in the context of a case.

- 11. Currently there are no national guidelines or technical standards governing LCN analysis. In addition DNA test kits, reagents, and supplies are not quality control (QC) checked by the manufacturer under the more sensitized LCN conditions. LCN analysis necessitates enhanced QC procedures from suppliers of reagents and consumables and it entails complex interpretation procedures which must be supported by adequate validation, training, and peer review. Because of these issues with LCN analysis, the FBI Laboratory does not conduct this type of testing.
- 12. MiniSTR analysis is a methodology that may be used on degraded DNA samples to help recover information lost during conventional STR analysis. Degraded DNA can occur due to sample age, humidity, bacteria, chemicals, and/or environmental insults that affect the quality of the DNA. Degraded DNA often does not amplify during the PCR process, resulting in no results. MiniSTR analysis amplifies the same locations, however utilizes smaller PCR products which enhances the recovery of the information from the sample.
- 13. MiniSTR analysis should only be used when samples have been subject to degradation or the quality is poor. The DNA profiles obtained from properly preserved samples from miniSTR and conventional STR analysis will be the same. Therefore, there is no additional benefit in using miniSTR analysis over conventional methodologies.
- 14. Y-STR analysis is a methodology that amplifies DNA from the male Y chromosome. The Y chromosome is passed down from generation to generation from fathers to sons with little or no change. Therefore all individuals within a male lineage will have the same Y-STR profile, thus limiting its discriminatory power. Y-STR analysis does provide valuable information when the overwhelming amounts of female DNA prevent the detection of male DNA in lower concentration, typically in cases of sexual assault.
- 15. MiniSTR and Y-STR test kits, reagents, and supplies are available which have been subject to QC checks. Also, interpretation procedures supported by adequate validation, training, and peer review do exist. However, the applications of these methodologies are quite specific and don't replace conventional STR typing.
- 16. Multiple peer-reviewed publications exist in the field of forensic DNA analysis, specifically covering LCN, miniSTR, and Y-STR analyses. Some of which include the following:

REFERENCES

Aditya, S. *et al* (2011). Generating STR profile from "touch DNA". *JOURNAL OF FORENSIC AND LEGAL MEDICINE, 18*(7), 295-295-298. Budowle, B., Eisenberg, A. J., & van Daal, A. (2009). Validity of low copy number typing and applications to forensic science. *Croatian Medical Journal, 50*(3), 207-217.

Budowle, B., Eisenberg, A. J., & van Daal, A. (2010). Concerns about low copy number typing. *Forensic Science International-Genetics*

Camacho, S. *et al* (2008). Mini-SGM multiplex in degraded samples. *Supplement Series, 1*(1), 100-101.

Coble, M. & Butler, J.M. (2005). Characterization of new miniSTR loci to aid analysis of degraded DNA. *Journal of Forensic Sciences*, 50(1)

Gill, P. (2001). Application of low copy number DNA profiling. *Croatian Medical Journal*, 42(3), 229-229-232.

Gill, P. et al (2006). DNA commission of the international society of forensic genetics: Recommendations on the interpretation of mixtures. Forensic Science International, 160(2-3), 90-90-101.

Graham, E. A. M. (2008). DNA reviews: Low level DNA profiling. *Forensic Science Medicine and Pathology*, 4(2), 129-129-131.

Gross, A. M. *et al* (2008). Internal validation of the AmpF/STR yfiler (TM) amplification kit for use in forensic casework. *Journal of Forensic Sciences*, 53(1), 125-134.

Hanson, E. K., & Ballantyne, J. (2004). A highly discriminating 21 locus Y-STR "megaplex" system designed to augment the minimal haplotype loci for forensic casework. *Journal of Forensic Sciences*, 49(1), 40-51.

Hughes-Stamm, S., Ashton, K. J., & van Daal, A. (2011). Assessment of DNA degradation and the genotyping success of highly degraded samples. *International Journal of Legal Medicine*, 125(3), 341-341-348.

Huo, S., & Lv, Y. (2009). Recent development in analysis method of low copy number DNA. *Chinese Journal of Forensic Medicine*, 24(4), 254-256, 257

Irwin, J. A. *et al* (2007). Application of low copy number STR typing to the identification of aged, degraded skeletal remains. *Journal of Forensic Sciences*, 52(6), 1322-1327.

Kloosterman, A. D., & Kersbergen, P. (2003). Efficacy and limits of genotyping low copy number (LCN) DNA samples by multiplex PCR of STR loci. *Journal De La Societe De Biologie*, 197(4), 351-359.

Koyama, H. *et al* (2002). Utility of Y-STR haplotype and mtDNA sequence in personal identification of human remains. *American Journal of Forensic Medicine and pathology*, 23(2), 181-181-185.

Ma, Y., Kuang, J., & Hou, Y. (2010). Low template DNA profiling and its application in forensic science. Fa Yi Xue Za Zhi, 26(2), 132-6.

Mayntz-Press, K., & Ballantyne, J. (2007). Performance characteristics of commercial Y-STR multiplex systems. *Journal of Forensic Sciences*, *52*(5), 1025-1025-1034.

Petricevic, S. *et al* (2010). Validation and development of interpretation guidelines for low copy number (LCN) DNA profiling in New Zealand using the AmpFlSTR (R) SGM plus (TM) multiplex. *Forensic Science International-Genetics*, 4(5), 305-305-310.

Parson, W., Niederstatter, H., Brandstatter, A., & Berger, B. (2003). Improved specificity of Y-STR typing in DNA mixture samples. *International Journal of Legal Medicine*, 117(2), 109-109-114.

Sinha, S. K. *et al* (2004). Utility of the Y-STR typing systems Y-PLEX(TM) 6 and Y-PLEX(TM) 5 in forensic casework and 11 Y-STR haplotype database for three major population groups in the united states. *Journal of Forensic Sciences*, 49(4), 691-700.

Smith, P. J., & Ballantyne, J. (2007). Simplified low-copy-number DNA analysis by post-PCR purification. *Journal of Forensic Sciences*, *52*(4), 820-829.

Whitaker, J. P., Cotton, E. A., & Gill, P. (2001). A comparison of the characteristics of profiles produced with the AMPFISTR (R) SGM plus (TM) multiplex system for both standard and low copy number (LCN) STR DNA analysis. *Forensic Science International*, 123(2-3), 215-215-223.

Wu, W., Zheng, X., & Hao, H. (2008). The application of MiniFilerTM kit in LCN-STR genotyping. *Chinese Journal of Forensic Medicine*, 23(1), 23-25.

Zhao, H. et al (2009). The establishment of a 8-locus miniSTR fluorescent-multiplex PCR and its application in the analysis of degraded DNA. Chinese Journal of Forensic Medicine, 24(2), 83-86.

Tina Marie Delgado

Subscribed and sworn before me this 10th day of November, 2011.



Notary Public
State of Virginia
County of Stafford

