Curriculum Vitae

Professor's Name:
Richard Li

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John Jay College of Criminal Justice
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ACADEMIC APPOINTMENTS:
Associate Professor
2008 – to date
Department of Science
John Jay College of Criminal Justice
The City University of New York

Doctoral Faculty
2012 - to date
Program in Forensic Science
Specialization of the Doctoral Program in Criminal Justice
John Jay College of Criminal Justice
The City University of New York

Doctoral Faculty
2011 - to date
Ph.D. Program in Biochemistry
Graduate Center
The City University of New York

EDUCATION:
University of Wisconsin, Madison; Ph.D. in Molecular Biology

TEACHING EXPERIENCE IN FORENSIC SCIENCES

- ***FOS 108 Concepts of Forensic Science***

A discussion of the fundamental principles of the physical and biological sciences with emphasis on the application of these principles in the resolution of legal questions. The role of forensic science in criminal and civil investigations where questions regarding the interpretation of physical evidence are crucial will also be examined.

- ***BIO 413 Molecular Biology II***

BIO 413 consists of lectures and laboratory experiments in molecular biology with special emphasis placed on forensic DNA analysis. Lecture topics include an overview of forensic biology, statistics and population genetics including: sample collection; bioethics; DNA extraction, quantitation, and typing; databases; lab validation including quality assurance and quality control, and emerging technologies. Laboratory experiments introduce advanced experimental techniques such as autosomal STR and "linkage markers" (Y-STR and mtDNA) analysis, DNA quantitation, and PCR-STR analysis of simulated "crime scene samples."

- ***FOS 733 Advanced Molecular Biology***

This course provides an in-depth treatment of selected topics in forensic DNA analysis. Lecture topics include: forensic biology; population genetics; sample collection and storage; DNA extraction, quantitation, and typing; databases and emerging technology. The laboratory uses state-of-the-art technology to introduce students to the instrumentation and methods used in forensic DNA analysis: DNA extraction and quantitation, PCR-STR typing of autosomal and Y chromosomal loci, and mitochondrial DNA typing. QA/QC topics will be addressed in the laboratory environment.

RECENT PUBLICATIONS IN FORENSIC SCIENCES

- Li, R., & Klempner, S. (2012). The effect of an enzymatic bone processing method on short tandem repeat profiling of challenged bone specimens. *Leg Med, http://dx.doi.org/10.1016/j.legalmed.2012.12.002*.

  Forensic analysis of DNA from bone can be important in investigating a variety of cases involving violent crimes and mass fatality cases. To remove the potential presence of co-mingled remains and to eliminate contaminants that interfere with forensic DNA analysis, the outer surface of the bone fragment must be cleaned. This study evaluated two methods for processing bone specimens prior to DNA isolation. Mechanical sanding and enzymatic trypsin methods were compared in this study. The effects of these methods on the yield of DNA isolated and the quality of DNA analysis were studied. It was revealed that comparable values of DNA yields between the two methods were observed. Additionally, to evaluate the capabilities of the cleaning effect of the bone processing methods, the presence of polymerase chain reaction inhibitors in the DNA extracts was monitored using the internal positive control. Similar C(t) values of the internal positive control were observed as the DNA extracts of the trypsin method compared with that of the sanding method. The characterization of the effects of the trypsin treatment on the quality of DNA profiling was also carried out. To evaluate the integrity of the nuclear DNA isolated, the percentage of allele calls and the peak-height values of alleles of the short tandem repeat profiles were compared between the two methods. A paired-sample t-test revealed no significant difference between the two methods. Our data suggested that the trypsin method can be used as an alternative cleaning method to mechanical cleaning methods. This method can be used to process multiple samples simultaneously. This can be very important for achieving high-throughput DNA isolation through potential automation, which can be extremely valuable for situations such as the forensic DNA analysis of skeletal remains from mass fatality incidents.

- Li, R., *Forensic serology*, in *Forensic Chemistry Handbook*, L. Kobilinsky, Editor. 2012, John Wiley and Sons: Hoboken, NJ. p. 269-290.

  Forensic serology is an important component of modern forensic science. The primary activity of forensic serologists is the identification of bodily fluids. Bodily fluid stains are commonly associated with violent criminal cases. Proving the presence of bodily fluids can confirm alleged violent acts for an investigation.

- Li, R., & Liriano, L. (2011). A bone sample cleaning method using trypsin for the isolation of DNA. *Leg Med, 13*(6), 304-308.

  Cleaning the surface of bone samples is a necessary step to remove contaminants prior to isolating DNA for forensic DNA analysis. In this study, a simple

trypsin method for cleaning bone samples prior to DNA isolation was developed. Cleaning the surface of human bone samples was achieved by the application of trypsin solution. Light microscopy and scanning electron microscopy results indicated that trypsin treatment was effective in removing the outer surface of bone samples. The yield of DNA isolated from trypsin-treated bone samples was sufficient for subsequent short tandem repeat (STR) analysis. STR analysis revealed no adverse effect on the DNA profile after the trypsin treatment. The data suggest that this trypsin method can potentially be an alternative cleaning method to mechanical cleaning methods.

- Li, R., Chapman, S., Thompson, M., & Schwartz, M. (2009). Developing a simple method to process bone samples prior to DNA isolation. *Legal Medicine, 11*(2), 76-79.

  Bone tissue is often used for recovering DNA samples for the purpose of human identification. However, the initial cleaning and sampling of the bone specimen is a labor-intensive and time-consuming step, which must be completed prior to isolating DNA. Thus, it is difficult to adapt the current method for automation. To address this issue, we have developed a simple processing method using a trypsin treatment prior to DNA isolation. The use of the trypsin-based procedure potentially reduces the amount of labor required by a physical method such as sanding. By incubating samples with the trypsin solution, the soft tissue and outer surface of the bone fragment samples are removed. The processed bone fragment or a portion of the fragment can then be used for DNA isolation.

- Wise, J., Danielson, T., Mozayani, A., & Li, R. (2008). Analysis of amphetamine, methamphetamine, methylenedioxyamphetamine and methylenedioxymethamphetamine in whole blood using in-matrix ethyl chloroformate derivatization and automated headspace solid-phase microextraction followed by GC-MS. *Forensic Toxicology, 26*(2), 66-70.

  The in-matrix alkyl chloroformate derivatization method for amphetamine, methamphetamine, methylenedioxyamphetamine (MDA), and methylenedioxymethamphetamine (MDMA) was adapted for use with the whole blood matrix. This derivatization method was followed by automated headspace (HS)-solid-phase microextraction (SPME) and gas chromatography-mass spectrometry (GC-MS) analysis. The sensitivity of this method, expressed as limit of detection, was approximately 10 ng/ml for these analytes tested in the blood matrix, which was sufficient to detect toxic concentrations of amphetamines in blood. The limit of quantitation for target analytes ranged from 0.05 to 0.2 µg/ml. The intraday precision and accuracy studies generally showed satisfactory results for all target compounds except MDA, in which a larger variation was observed. The in-matrix ethyl chloroformate derivatization of amphetamine, methamphetamine, MDA, and MDMA for HS-SPME was tested in other matrices such as stomach fluid, bile, thoracic cavity fluid, vitreous humor, brain, liver, spleen, and skeletal muscle. As a result, stomach fluid,

thoracic cavity fluid, and vitreous humor showed SPME efficiencies higher than that of whole blood; however, this method was not suitable for solid tissue matrices under the present conditions.