B145 Utility of InnoTyper™ 21 in Analysis of Degraded Human DNA Recovered From Maggot Crop Contents

Sharon E. Zeller, BS, 3940 Oakleys Lane, Richmond, VA 23223; Kyle S. Williams, Virginia Commonwealth University, 104 W Franklin Street, Apt 1703, Richmond, VA 23220; Sudhir K. Sinha, PhD, InnoGenomics Technologies, LLC, 1441 Canal Street, Ste 307, New Orleans, LA 70112; Gina M. Murphy, MS, GMP Forensic Consultants, PO Box 113006, Metairie, LA 70011-3006; Hiromi Brown, PhD, InnoGenomics, 1441 Canal Street, New Orleans, LA 70112; Daniel J. Wescott, PhD, Texas State University, Dept of Anthropology, 601 University Drive, San Marcos, TX 78666-4684; Tracey Dawson Cruz, PhD, Virginia Commonwealth University, 1015 Floyd Avenue, PO Box 843079, Richmond, VA 23284; and Baneshwar Singh, PhD*, Virginia Commonwealth University, Dept of Forensic Science, 1015 Floyd Avenue, Rm 2015, Richmond, VA 23284*

After attending this presentation, attendees will better understand the utility of a new human DNA typing method in nuclear DNA analyses of highly degraded samples (e.g., human DNA recovered from maggot crop contents).

This presentation will impact the forensic science community by providing a new, efficient, and alternate method for analysis of degraded human DNA recovered from maggot crop contents.

Blow flies and flesh flies are well-known for their utility in Postmortem Interval (PMI) estimation, but in some situations they can also provide information on relocation of a corpse, actual source of the maggot, identification of burned remains, and identification of a perpetrator in sexual assault cases.[1-3] This information can be obtained by recovery and analysis of human DNA from maggot crop contents, but recovered human DNA from maggot crop contents tends to be very degraded in a majority of cases. Hence, it generates either incomplete or a total lack of Short Tandem Repeat (STR) profiles.[4] This is primarily because traditional STR kits require longer target DNA fragments for the generation of complete STR profiles. To obtain more information from human nuclear DNA recovered from maggot crop contents, this study utilized InnoTyper™ 21, a novel DNA typing method. InnoTyper™ is a marker system that utilizes a 20 Retrotransposon Insertion Polymorphisms (RIPs) multiplex. Among the advantages of using RIPs are the following: (1) they do not yield stutter artifacts due to slippage during the PCR amplification; (2) there are no known genetic mutations since they are identical by descent only; (3) they are present in very high copy number; and, (4) they have a well-defined genetic lineage that makes them useful for relationship determinations. An innovative primer design allows for the amplicon size for the Alu markers to be reduced to a size (60bp-125bp) that is smaller then currently used STR markers, such that the substantially degraded DNA samples recovered from maggot crops can be analyzed.

To obtain a nuclear profile, DNA was extracted from crop contents of 20 third-instar larvae from two blow fly species (*Calliphora vicina* and *Lucilia sericata*), a positive control (i.e., frozen human liver tissue), a degraded control (30g of the human liver tissue placed under the same conditions as the test samples without exposure to maggots), and a negative control sample using QIAGEN® QIAamp® DNA Investigator kit. Extracted DNA was quantified using *Applied Biosystems® Quantifiler® HP and amplified for 20 RIP loci* and the gender-identifying marker, Amelogenin, using the amplification conditions and run parameters as recommended by the manufacturer. Capillary electrophoresis data were analyzed in GeneMapper® software V4.0.

On average, more than 48% of all alleles (202 out of 420 expected) were successfully recovered by this kit in maggot crops of both fly species. Human DNA recovered from some of the maggot samples actually yielded more complete profiles (90%-100% of all alleles were recovered) than the profiles obtained from the degraded control samples.

In conclusion, InnoTyper™ 21 has huge potential for its utility in the analysis of human DNA recovered from maggot crop contents.

*Presenting Author

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