B143 Use of Rapid DNA Systems in Disaster Victim Identification

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After attending this presentation, attendees will understand how Rapid DNA systems can be implemented for use in disaster victim identification.

This presentation will impact the forensic science community by informing attendees about how Rapid DNA systems can shorten the time it takes to process, compare, and identify victims of a mass fatality incident.

Disaster Victim Identification (DVI) can be a very meticulous and lengthy process despite the number of casualties. This is especially true if DNA testing is part of the DVI process and is used to assist in the identification of victims. Processing and analyzing DNA samples from decedents or relatives can take several days. Rapid DNA typing systems eliminate this wait by utilizing a tabletop, self-contained, and automated instrument. Within the past few years, several companies have developed and improved such systems. Rapid DNA systems reduce the time needed to process a DNA sample from days to less than two hours. In contrast, traditional methods of DNA profiling from cheek swabs require upwards of ten hours and involve multiple laboratory personnel. The currently available rapid DNA systems allow for DNA extraction, amplification, separation, and genotyping analysis to be completed in less than 90 minutes, without analyst intervention. This represents a significant savings of time and personnel over traditional STR typing methods. Among the rapid DNA instruments that are available, each generates a DNA profile in a similar manner but with varying sample capacity, run times, and cost.

Rapid DNA systems are particularly practical for disaster recovery and identification. Besides being fast, the systems are mobile, rugged, and simple to use, with all consumables provided in a disposable, ready-for-use format. With rapid DNA systems on-site at a Family Assistance Center (FAC), DNA analysis of samples collected from family members can be processed and the resulting DNA profiles analyzed in a family pedigree chart.

Concurrently, if disaster recovery is occurring and a mobile morgue is set up, postmortem samples can be collected on-site and processed immediately. Transport, sample tracking at the laboratory, and the requirements of multiple laboratory personnel are eliminated. The DNA team at the mobile morgue can collect and process samples immediately. The profiles generated from decedents at the mobile morgue and relatives at the FAC can be readily input into a current victim identification program and kinship analysis performed.

The New York City Office of Chief Medical Examiner (NYC OCME) Department of Forensic Biology has evaluated two rapid DNA systems in order to evaluate their application for DVI: the IntegenX RapidHIT® Human Identification System and GE Healthcare Life Sciences (GE) and NetBio DNAScan™ Rapid DNA Analysis™ System. Initial evaluations were conducted at the NYC OCME and the performance of each instrument was further evaluated at a full-scale mass disaster exercise. Specifically, the RapidHIT® and DNAScan™ Rapid DNA systems were evaluated on-site at the FAC and DNA unit of the mobile morgue during the Fifth Annual Regional Mass Fatality Management (MFM) Training, which occurred from June 2 to 6, 2014, at Fort Hamilton Army Base in Brooklyn, NY. During the FAC portion of the exercise, reference samples were collected from volunteers simulating family members and processed on both instruments. During the mobile morgue portion of the exercise, eight postmortem muscle and two postmortem blood samples, simulating recovered remains, were processed and typed in the DNA unit of the mobile morgue on both instruments. Samples were loaded into either the RapidHIT® system sample cartridges or the DNAScan™ BioChipSet™ cassette, both using Promega's® PowerPlex® 16 HS kit optimized for rapid DNA analysis. The DNAScan™ data were automatically analyzed using NetBio's integrated software with fixed analysis parameters. The RapidHIT® data were automatically analyzed with the on-board SoftGenetics® GeneMarker® HID STR Human Identity Software.

The output data for both rapid DNA systems were compared to a reference database of traditionally-typed STR profiles. Output data were also manually confirmed by a DNA analyst and evaluated based on alleles called, profile completeness, and peak height balance. See data in Tables 1 and 2 below.

The MFM exercise has demonstrated that rapid DNA systems can be utilized in DVI. Sample preparation for input into cassettes, respective software analysis parameters, and logistics, as far as instrument transport and chip storage, need to be considered and incorporated into a standard operating procedure for rapid DNA system operations in DVI.

Table 1 — GE/NetBio DNAScan™ DNA Morgue and FAC Results with Promega® PowerPlex® 16 HS Chemistry

			#Alleles		% Alleles		
Sample		**Ref. Profile Alleles**	**Auto**	**Confirmed****	**Auto**	**Confirmed****	**% Alleles Recovered by Analyst Review**
Degraded Muscle Tissue	D1	29	0*	14	0%	48%	48%
	D3	26	0*	5	0%	19%	19%
	D4	29	0*	0	0%	0%	0%
	D5	29	0*	7	0%	24%	24%
Fresh Muscle Tissue	F1	28	0*	11	0%	39%	39%
	F2	27	25	26	93%	96%	4%
	F4	26	24	24	92%	92%	0%
	F5	28	28	28	100%	100%	0%
Bloodstained FTA® Card	363	29	0*	0	0%	0%	0%
	359	29	0*	26	0%	90%	90%
Buccal Swabs	1	29	29	29	100%	100%	0%
	2	26	0*	22	0%	85%	85%
Average % Alleles Recovered							26%

* = DNAScan™ Software flagged alleles as "NR" or not reliable, based on fixed analysis parameters.

** = DNA analyst visually reviewed electropherograms and confirmed peaks labeled as "NR"

Table 2 — IntegenX RapidHIT® Human Identification System DNA Morgue and FAC Results with Promega® PowerPlex® 16 HS Chemistry

			#Alleles		% Alleles		
Sample		**Ref. Profile Alleles**	**Auto**	**Manual****	**Auto**	**Manual****	**% Alleles Recovered by Analyst Review**
Degraded Muscle Tissue	D1	29	11	23	38%	79%	41%
	D3	26	6	15	23%	58%	35%
	D4	29	22	29	76%	100%	24%
	D5	29	7	14	24%	48%	24%
Fresh Muscle Tissue	F1	28	19	29	68%	104%	36%
	F2	27	0*	17	0%	63%	63%
	F4	26	21*	23	81%	88%	8%
	F5	28	0*	20	0%	71%	71%
Bloodstained FTA® Card	363	29	29	29	100%	100%	0%
	359	29	0*	20	0%	69%	69%
Buccal Swabs	1	29	29	29	100%	100%	0%
	2	26	26	26	100%	100%	0%
Average % Alleles Recovered							31%

* a very high signal peak (saturated) resulted in the primer trim step cutting into read region during auto analysis

** Manual = Raw data re-analyzed in SoftGenetics® GeneMarker® HID STR Human Identity Software version 2.6.0 by a DNA analyst.

Mass Disaster, Rapid DNA, Disaster Victim Identification