Proof of Concept:
Use of Rapid DNA Systems in Disaster Victim Identification

Timothy Kupferschmid, MFS, MBA
Chief of Laboratories
Presentation Outline

• DVI Process Background

• Regional Mass Fatality Management (MFM) Exercise with Rapid DNA technology

• Results, Conclusions and Recommendations
### DVI process in MFM operations

Victim identification is accomplished by comparing postmortem data to ante mortem data.

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#### DV INFORMATION PROCESS

<table>
<thead>
<tr>
<th>Postmortem</th>
<th>Ante Mortem</th>
</tr>
</thead>
<tbody>
<tr>
<td>DISASTER MORGUE</td>
<td>FAMILY ASSISTANCE CENTER (FAC)</td>
</tr>
<tr>
<td>Process human remains efficiently separate from day to day operations in an infrastructure capable of supporting additional personnel &amp; equipment</td>
<td>Facilitate exchange of timely &amp; accurate information with family and friends of injured/MP/deceased; investigative authorities; ME/Coroner</td>
</tr>
</tbody>
</table>
DVI process in MFM operations

Victim identification is accomplished by comparing postmortem data to ante mortem data

DV INFORMATION PROCESS

Postmortem

DISASTER
MORGUE

DNA UNIT – collect multiple samples from decedents/human remains (blood, muscle, bone, oral swab, etc.)

Ante Mortem

FAMILY
ASSISTANCE
CENTER (FAC)

Relatives can provide reference samples (for future kinship analysis)
Provide decedents’ personal effects (razor, toothbrush, etc.)

Rapid DNA in DVI
DVI process in MFM operations

Traditional DNA Testing can take up to 10 hours of bench work; Overall ID process can take several days

Rapid DNA typing systems can automate above processes:
- reduce sample processing time to < 2 hrs
- mobile and rugged
- simple to use with all consumables in disposable format

Rapid DNA in DVI
**SCENARIO**

10 KILOTON IMPROVISED NUCLEAR DEVICE (IND) DETONATED IN TIMES SQUARE, NEW YORK CITY

- Attack occurs at 0928 local time on May 27, 2014
- Initial estimates: ~ 680,000 persons within 0.6 mi radius
- Currently, the FM Branch is being established 6 days following the detonation
Radiation Plume Radius
MFM EXERCISE – DNA MORGUE (DAY 1 & 2)

IntegenX
RapidHit®200

GE/NetBio
DNAscan™

Rapid DNA in DVI

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Regional MFM Response System Training

June 4, 2014 Clean Morgue (Tent)
  • Tent Temperature Range = 73° F – 87° F

June 5, 2014 Contaminated Morgue (Tent)
  • Tent Temperature Range = 59° F – 79° F

June 6, 2014 Family Assistance Center (Building)
  • Room Temperature = 76° F
MFM Exercise Days 1 - 3

DNA MORGUE
- Simulated Recovered Remains

FAC
- Simulated Family Member Reference Samples

DNAScan™
Rapid DNA Analysis™ System

RapidHit®200

- 4 PM Degraded Muscle Tissue
- 4 PM Fresh Muscle Tissue
- 2 PM Bloodstain FTA Cards
- 5 Buccal Swabs and 10 Buccal Swabs

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MFM Exercise days 1 - 3

DNAScan™
Rapid DNA Analysis™ System

RapidHit®200

SAMPLE PROCESSING

Muscle → cut into chunks
Blood → ~ 3 mm x 3mm
Buccal → swabs provided

Muscle → cut into chunks
Blood → ~ 3 mm x 3mm
Buccal → sterile cotton
MFM Exercise days 1 - 3

DNAScan™ Rapid DNA Analysis™ System

SAMPLE PROCESSING

SAMPLE LOADING

RapidHit®200
## MFM Exercise days 1 - 3

<table>
<thead>
<tr>
<th>Protocol Used</th>
<th>Buccal Protocol</th>
<th>Non Buccal → Other Protocol</th>
</tr>
</thead>
<tbody>
<tr>
<td>Extraction, PCR, CE Automated</td>
<td>Promega® PowerPlex® 16 HS kit</td>
<td></td>
</tr>
<tr>
<td>Data Analyzed Automatically</td>
<td>Integrated software with fixed analysis parameters</td>
<td>SoftGenetics® GeneMarker® HID STR Human Identity Software</td>
</tr>
</tbody>
</table>
MFM Exercise days 1 - 3

DNAScan™
Rapid DNA
Analysis™ System

RapidHit®200

• Small-scale implementation of the Rapid DNA systems was assessed
• Output data were evaluated
  • Profile completeness, alleles called, and peak height balance.
RESULTS

INTEGENX RAPIDHIT DNA
## RESULTS – RapidHIT® (IntegenX)

### Instrument Output (Auto-Analysis)

<table>
<thead>
<tr>
<th>Sample</th>
<th>Ref. Profile Alleles</th>
<th># Correct Alleles Called</th>
<th>% Alleles Called</th>
</tr>
</thead>
<tbody>
<tr>
<td>PM Degraded Muscle Tissue</td>
<td>D1  29</td>
<td>11</td>
<td>38%</td>
</tr>
<tr>
<td></td>
<td>D3  26</td>
<td>6</td>
<td>23%</td>
</tr>
<tr>
<td></td>
<td>D4  29</td>
<td>22</td>
<td>76%</td>
</tr>
<tr>
<td></td>
<td>D5  29</td>
<td>7</td>
<td>24%</td>
</tr>
</tbody>
</table>

**Average % Alleles Called:** 40.7%
### RESULTS – RapidHIT® (IntegenX)

#### Instrument Output (Auto-Analysis)

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</thead>
<tbody>
<tr>
<td><strong>PM Fresh Muscle Tissue</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F1</td>
<td>28</td>
<td>19</td>
<td>68%</td>
</tr>
<tr>
<td>F2</td>
<td>27</td>
<td>0</td>
<td>0%</td>
</tr>
<tr>
<td>F4</td>
<td>26</td>
<td>21</td>
<td>81%</td>
</tr>
<tr>
<td>F5</td>
<td>28</td>
<td>0</td>
<td>0%</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td><strong>37.3%</strong></td>
</tr>
</tbody>
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<th>% Alleles Called</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bloodstained</td>
<td>363 29</td>
<td>29</td>
<td>100%</td>
</tr>
<tr>
<td>FTA</td>
<td>359 29</td>
<td>0</td>
<td>0%</td>
</tr>
</tbody>
</table>

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### RESULTS – RapidHIT® (IntegenX)

<table>
<thead>
<tr>
<th>Sample</th>
<th>F4B</th>
<th>F2B</th>
<th>F5B</th>
<th>359</th>
</tr>
</thead>
<tbody>
<tr>
<td>Range</td>
<td>&lt;180 bp</td>
<td>&lt; 200 bp</td>
<td>&lt; 120 bp</td>
<td>&lt;160 bp</td>
</tr>
</tbody>
</table>

**Automatic primer peak trimming**

LOSS OF RAW DATA = LOSS OF ALLELES

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RESULTS – RapidHIT® (IntegenX)

- IntegenX performed manual data analysis and recovered lost data due to automatic primer peak trimming
- Due to too much input sample

IntegenX was able to recover raw data using their software

- Overall 95% (18/19 loci) of alleles lost during auto analysis was recovered by Manual Recovery
## RESULTS – RapidHIT® (IntegenX)

### Re-Analysis & Manual Review

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<td>22</td>
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</tr>
<tr>
<td>D5</td>
<td>29</td>
<td>7</td>
<td>24%</td>
</tr>
<tr>
<td>~12 ~20</td>
<td>40%</td>
<td>~71%</td>
<td></td>
</tr>
</tbody>
</table>
RESULTS

GE/NETBIO
DNASCAN RAPID DNA ANALYSIS SYSTEM
## RESULTS – DNAscan™ Rapid DNA system

### Instrument Output vs. Manual Review

<table>
<thead>
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</thead>
<tbody>
<tr>
<td>PM Degraded Muscle Tissue</td>
<td>D1 29</td>
<td>“NR” 14</td>
<td>0% 48%</td>
</tr>
<tr>
<td></td>
<td>D3 26</td>
<td>“NR” 5</td>
<td>0% 19%</td>
</tr>
<tr>
<td></td>
<td>D4 29</td>
<td>“NR” 0</td>
<td>0% 0%</td>
</tr>
<tr>
<td></td>
<td>D5 29</td>
<td>“NR” 7</td>
<td>0% 24%</td>
</tr>
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## RESULTS – DNAscan™ Rapid DNA system

Instrument Output vs. Manual Review

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<td>39%</td>
</tr>
<tr>
<td>F2</td>
<td>27</td>
<td>25</td>
<td>93%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>26</td>
<td>96%</td>
</tr>
<tr>
<td>F4</td>
<td>26</td>
<td>24</td>
<td>92%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>24</td>
<td>92%</td>
</tr>
<tr>
<td>F5</td>
<td>28</td>
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Rapid DNA in DVI

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CONCLUSIONS

• The MFM exercise demonstrated that Rapid DNA systems can be used in DVI
• Both instruments were easy to use with little to no training required
• Both generated full and partial profiles, but not until after manual intervention
  – All 25 samples tested on the RapidHIT® produced useable data
  – All but 2 for GE/NetBio’s DNA Scan™ produced useable data
CONCLUSIONS

• Samples resulting in partial profiles were expected, as they were degraded tissue samples ~12-17 years old; or bloodstained cards from 2000

• Allele detection and labeling are dependent upon sample quality, input amount (cutting size), processing protocol and software analysis parameters
GENERAL RECOMMENDATIONS

• Provide user capability to recover pre-processed data (raw data)
• Establish input amount and sample preparation
• Establish instrument protocols based on sample type
• Establish software analysis parameters using various sample types
• Investigate potential inhibitors
• Develop standard operating procedure for rapid DNA systems in DVI
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