PowerPlex® Y23 Developmental Validation

Jonelle Thompson, R&D Scientist

September 2012
PowerPlex® Y23 System
Presentation outline

• Benefits of Y-STR Analysis
• Background information on PowerPlex® Y23
• Developmental requirements of SWGDAM
• PowerPlex® Y23 Developmental Validation Data
• Update on Y-STR Statistical Databases
  • US Y-STR Database
  • YHRD Database
The Benefits of Y-STR Analysis

- Forensic casework on sexual assault evidence
  - Relatively high amount of female DNA
  - Mixtures with DNA from multiple male donors
- Paternity testing
- Familial searching
- Missing persons investigations
- Migration and evolutionary studies
- Historical and genealogical research
Overview of the PowerPlex® Y23 System

- Includes all of the loci from PowerPlex® Y as well as AmpF/STR® Yfiler®
  - Includes six Y-STR loci that are not in any other commercially available kit
- One system capable of extracted and direct amplification applications
- Amplify male genomic DNA in an excess of female genomic DNA
  - No amplification products for female genomic DNA
- Rapid thermal cycling
- Compatible with the Applied Biosystems’ 3130 and 3500 Genetic Analyzers
PowerPlex® Y23 System
Six new loci with high gene diversity

Size (bp)

DYS576 (0.82)  DYS389I  DYS448  DYS389II  DYS19
DYS391  DYS481 (0.85)  DYS549 (0.79)  DYS533 (0.75)  DYS438  DYS437
DYS570 (0.86)  DYS635  DYS390  DYS439  DYS392  DYS643 (0.93)
DYS393  DYS458  DYS385 a/b  DYS456  Y-GATA-H4
### Gene Diversity of STR Loci in Y-STR Systems

<table>
<thead>
<tr>
<th>Locus</th>
<th>Gene Diversity</th>
<th>PowerPlex® Y</th>
<th>AmpFlSTR® Yfiler™</th>
<th>PowerPlex® Y 23</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS643</td>
<td>0.92</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS570</td>
<td>0.85</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS481</td>
<td>0.85</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS385 a/b</td>
<td>0.83</td>
<td>√</td>
<td>√</td>
<td>√</td>
</tr>
<tr>
<td>DYS576</td>
<td>0.82</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS549</td>
<td>0.78</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS458</td>
<td>0.78</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS390</td>
<td>0.75</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS533</td>
<td>0.75</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS635</td>
<td>0.71</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS456</td>
<td>0.70</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS448</td>
<td>0.69</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS438</td>
<td>0.68</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS439</td>
<td>0.67</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS392</td>
<td>0.64</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS19</td>
<td>0.64</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS437</td>
<td>0.62</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS389II</td>
<td>0.62</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>Y GATA H4</td>
<td>0.60</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DYS389I</td>
<td>0.56</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS391</td>
<td>0.53</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
<tr>
<td>DYS393</td>
<td>0.46</td>
<td>√</td>
<td>√</td>
<td></td>
</tr>
</tbody>
</table>
Value of Additional Loci

- NIST concordance study: 12 sets of two individuals matched at all 17 AmpF/STR® Yfiler® loci:
  - With the addition of the new six loci, 8 of 12 sets were distinguished from each other (only 4 sets of two individuals still match)
  - Remaining sets appear to be related individuals based on mitochondrial DNA and autosomal testing
  - NIST manuscript submitted

- UNT concordance study
  - Yfiler had 708 unique profiles
  - Additional 6 loci alone had 557 unique profiles
  - All 23 loci together had 758 unique profiles

### PowerPlex® Y23 System
#### Thermal Cycling

<table>
<thead>
<tr>
<th></th>
<th><strong>PowerPlex® Y23 System</strong></th>
<th></th>
<th><strong>AmpF/STR® Y-Filer®</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>1 cycle</td>
<td>96°C for 2 min</td>
<td>1 cycle</td>
<td>95°C for 11 min</td>
</tr>
<tr>
<td>30 or 26 cycles</td>
<td>94°C for 10 sec</td>
<td>27 or 30 cycles</td>
<td>94°C for 1 min</td>
</tr>
<tr>
<td></td>
<td>61°C for 1 min</td>
<td></td>
<td>61°C for 1 min</td>
</tr>
<tr>
<td></td>
<td>72°C for 30 sec</td>
<td></td>
<td>72°C for 1 min</td>
</tr>
<tr>
<td>1 cycle</td>
<td>60°C for 20 min</td>
<td>1 cycle</td>
<td>60°C for 80 min</td>
</tr>
</tbody>
</table>

- Extracted DNA
- 30 cycles
- 1 h 40 min total time
- Punches and swab extract
- 26 cycles
- 1 h 30 min total time

- Extracted DNA
- 30 cycles
- >3 h total time
- Washed FTA
- 27 cycles
### PowerPlex® Y23 System

**Kit components**

Optimized for up to 17.5μl extracted DNA sample in 25μl reaction volume

<table>
<thead>
<tr>
<th>Component</th>
<th>200 reactions (DC2320)</th>
<th>50 reactions (DC2305)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Pre-amplification</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PowerPlex® Y23 5X Master Mix</td>
<td>4 x 250μl</td>
<td>1 x 250μl</td>
</tr>
<tr>
<td>PowerPlex® Y23 10X Primer Pair Mix</td>
<td>4 x 125μl</td>
<td>1 x 125μl</td>
</tr>
<tr>
<td>2800M Control DNA, 10ng/μl</td>
<td>25μl</td>
<td>25μl</td>
</tr>
<tr>
<td>Water, Amplification Grade</td>
<td>5 x 1,250μl</td>
<td>5 x 1,250μl</td>
</tr>
<tr>
<td><strong>Post-amplification</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PowerPlex® Y23 Allelic Ladder Mix</td>
<td>4 x 25μl</td>
<td>1 x 25μl</td>
</tr>
<tr>
<td>CC5 Internal Lane Standard 500 Y23*</td>
<td>2 x 300μl</td>
<td>1 x 300μl</td>
</tr>
</tbody>
</table>

* Optimized for PowerPlex® Y23 only
PowerPlex® Y23 Developmental Validation Data
SWGDAM Guidelines for Developmental Validation

• 2.1 – Inheritance, mapping, detection, polymorphism
• 2.2 – Species Specificity
• 2.3 – Sensitivity studies
• 2.4 – Stability
• 2.5 – Reproducibility
• 2.6 – Case-type samples/non-probative samples
• 2.7 – Population studies
• 2.8 – Mixture studies
• 2.9 – Precision and accuracy
• 2.10 – Specificity and robustness, balance and stochastic, known artifacts, positive and negative controls
PowerPlex® Y23 System
Developmental Validation Collaborators

• Four US laboratories have been identified to participate in the developmental validation
  • Illinois State Police - sponsor for NDIS approval
  • Sorenson Forensics
  • Texas Department of Safety – Casework DNA Section and CODIS Section
  • Promega
2.1

- Inheritance:
  - DYS576 and DYS570 have mutation rates of >1%, considered rapidly mutating
  - NIST studies for father son data in progress

- Mapping
  - Article describes the six new loci included in PowerPlex® Y23
2.2 Species specificity

- Promega tested on both the 3130 and 3500
  - Three higher primates: Chimpanzee, Gorilla, Orangutan
  - Nine domestic animals: pig, horse, deer, cat, rabbit, chicken, dog, cow, mouse
  - Seven microorganisms: *E.coli*, *E.faecalis*, *S.servisiae*, *F.nucleatum*, *M.luteus*, *S.salivarius*, *S.mitis*
  - Results showed no artifacts with 10ng of domestic animal or microorganism DNA
  - Partial profiles obtained from 500pg DNA from higher primates, however profile pattern was not consistent with human male profile

- ISP tested
  - 4 primates: Gibbon, Macaque, DeBrazza’s Monkey, Lemur
  - 4 mammals: Cat, Dog, Fox, Mouse
  - 2 microorganisms: *C.perfringens* and *B.subtilis*
  - One allele was seen in the Macaque sample
  - No other artifacts were seen from the domestic animals or microorganisms
2.2 Species Specificity
500pg Chimpanzee DNA
Developmental Validation
2.3 Sensitivity studies

- Extracted DNA
  - 2 male DNA samples were tested by 3 laboratories
  - All samples were tested in triplicate
  - 1ng, 500pg, 250pg, 125pg, 62.5pg, 31.25pg

- Direct Blood on FTA
  - Blood samples from 5 males were tested by 1 laboratory
  - All samples tested in triplicate
  - 1, 2, or 3 – 1.2mm punches

- Direct Buccal on FTA
  - Buccal samples from 5 males were tested by 1 laboratory
  - All samples tested in triplicate
  - 1, 2, or 3 – 1.2mm punches
Sensitivity of Extracted DNA

Percent of Loci Called vs. Template Amount (pg)

- 1ng, 500pg, 250pg, 125pg, 62.5pg, 31.25pg

Male 1 and Male 2 results shown.
2.3 Sensitivity Studies
Extracted DNA – full profiles consistently down to 62.5pg
2.3 Sensitivity Studies
Extracted DNA on 3500 Genetic Analyzer

![Bar chart showing sensitivity studies for extracted DNA on 3500 Genetic Analyzer]

- Percent Loci Called
- DNA Template:
  - 1 ng
  - 500 pg
  - 250 pg
  - 125 pg
  - 62.5 pg
  - 31.25 pg

Legend:
- Male 1
- Male 2
2.3 Sensitivity Studies
Extracted DNA on 3500 Genetic Analyzer

- 500pg
- 250pg
- 125pg
- 62.5pg
- 31.25pg
2.3 Sensitivity Studies
Direct amplification of blood on FTA
2.3 Sensitivity Studies
Direct amplification of blood on FTA

1 – 1.2mm punch

2 – 1.2mm punches

3 – 1.2mm punches
2.3 Sensitivity Studies
Direct amplification of buccal on FTA

Percent of Loci Called vs Number of 1.2mm punches

<table>
<thead>
<tr>
<th>Number of 1.2mm punches</th>
<th>Percent of Loci Called</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 punch</td>
<td>100%</td>
</tr>
<tr>
<td>2 punch</td>
<td>100%</td>
</tr>
<tr>
<td>3 punch</td>
<td>90%</td>
</tr>
</tbody>
</table>
2.3 Sensitivity Studies
Direct amplification of buccal on FTA

1 – 1.2mm punch

2 – 1.2mm punches

3 – 1.2mm punches
Developmental Validation
2.4 Stability studies – inhibitors

• Three inhibitors
  • Hematin: 500, 750, and 1000µM
  • Humic acid: 100, 200, and 300ng/µl
  • Tannic acid: 100, 200, and 300ng/µl

• 500ng extracted DNA from 2 males were tested in triplicate amplifications for each sample type

• Testing performed at 2 laboratories
2.4 Stability Studies – Inhibitors

- Hematin
- Humic Acid
- Tannic Acid

<table>
<thead>
<tr>
<th>Concentration</th>
<th>Hematin</th>
<th>Humic Acid</th>
<th>Tannic Acid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1000μM</td>
<td>100%</td>
<td>0%</td>
<td>0%</td>
</tr>
<tr>
<td>300μg/μl</td>
<td>1000μM</td>
<td>300μg/μl</td>
<td>300μg/μl</td>
</tr>
<tr>
<td>750μM</td>
<td>10000μg</td>
<td>100ng/μl</td>
<td>100ng/μl</td>
</tr>
<tr>
<td>200μg/μl</td>
<td>500μM</td>
<td>200ng/μl</td>
<td>200ng/μl</td>
</tr>
<tr>
<td>100ng/μl</td>
<td>50μM</td>
<td>100ng/μl</td>
<td>100ng/μl</td>
</tr>
</tbody>
</table>
2.4 Stability Studies – Inhibitors

Hematin

- No Inhibitor
- 500uM
- 750uM
- 1000uM
2.4 Stability Studies – Inhibitors
Humic acid

No Inhibitor
100ng/µl
200ng/µl
300ng/µl
2.4 Stability Studies – Inhibitors

Tannic acid

No Inhibitor

100ng/µl

200ng/µl

300ng/µl
Developmental Validation
2.5 Reproducibility

- Extracted DNA
  - NIST 2395
  - Tested by 3 laboratories

- Blood on FTA – 1 – 1.2mm punch
  - 2 males
  - Tested by 3 laboratories

- Buccal on FTA – 2 – 1.2mm punch
  - 2 males
  - Tested by 2 laboratories
### 2.5 Reproducibility

Extracted DNA: NIST 2395

<table>
<thead>
<tr>
<th>Locus</th>
<th>NIST A</th>
<th>NIST B</th>
<th>NIST C</th>
<th>NIST D</th>
<th>NIST E</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS576</td>
<td>18</td>
<td>16</td>
<td>17</td>
<td>18</td>
<td>17</td>
</tr>
<tr>
<td>DYS389 I</td>
<td>13</td>
<td>13</td>
<td>14</td>
<td>12</td>
<td>14</td>
</tr>
<tr>
<td>DYS448</td>
<td>19</td>
<td>21</td>
<td>21</td>
<td>21</td>
<td>20</td>
</tr>
<tr>
<td>DYS389 II</td>
<td>29</td>
<td>28</td>
<td>32</td>
<td>28</td>
<td>31</td>
</tr>
<tr>
<td>DYS19</td>
<td>14</td>
<td>14</td>
<td>16</td>
<td>15</td>
<td>17</td>
</tr>
<tr>
<td>DYS391</td>
<td>11</td>
<td>11</td>
<td>12</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>DYS481</td>
<td>22</td>
<td>23</td>
<td>28</td>
<td>23</td>
<td>28</td>
</tr>
<tr>
<td>DYS549</td>
<td>14</td>
<td>12</td>
<td>11</td>
<td>13</td>
<td>13</td>
</tr>
<tr>
<td>DYS533</td>
<td>12</td>
<td>12</td>
<td>10</td>
<td>9</td>
<td>12</td>
</tr>
<tr>
<td>DYS438</td>
<td>12</td>
<td>9</td>
<td>11</td>
<td>11</td>
<td>10</td>
</tr>
<tr>
<td>DYS437</td>
<td>15</td>
<td>14</td>
<td>14</td>
<td>16</td>
<td>14</td>
</tr>
<tr>
<td>DYS570</td>
<td>17</td>
<td>18</td>
<td>18</td>
<td>17</td>
<td>18</td>
</tr>
<tr>
<td>DYS635</td>
<td>23</td>
<td>21</td>
<td>23</td>
<td>21</td>
<td>21</td>
</tr>
<tr>
<td>DYS390</td>
<td>25</td>
<td>23</td>
<td>21</td>
<td>22</td>
<td>24</td>
</tr>
<tr>
<td>DYS439</td>
<td>12</td>
<td>12</td>
<td>11</td>
<td>11</td>
<td>11</td>
</tr>
<tr>
<td>DYS392</td>
<td>13</td>
<td>11</td>
<td>11</td>
<td>11</td>
<td>12</td>
</tr>
<tr>
<td>DYS643</td>
<td>10</td>
<td>10</td>
<td>15</td>
<td>11</td>
<td>12</td>
</tr>
<tr>
<td>DYS393</td>
<td>13</td>
<td>12</td>
<td>13</td>
<td>14</td>
<td>14</td>
</tr>
<tr>
<td>DYS458</td>
<td>16</td>
<td>15</td>
<td>17</td>
<td>16</td>
<td>16</td>
</tr>
<tr>
<td>DYS385</td>
<td>12,15</td>
<td>14,17</td>
<td>17,20</td>
<td>14,15</td>
<td>13,15</td>
</tr>
<tr>
<td>DYS456</td>
<td>15</td>
<td>15</td>
<td>15</td>
<td>15</td>
<td>15</td>
</tr>
<tr>
<td>YGATAH4</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>11</td>
</tr>
</tbody>
</table>

Note, samples were run on both the 3130 and 3500. All samples were concordant with certificate from NIST for all loci available, and were consistent across all amplifications and platforms for the ones not available.
### 2.5 Reproducibility
Blood and buccal on FTA

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>Promega</th>
<th>Sorenson Forensics</th>
<th>Texas DPS</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Blood</strong></td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td><strong>Buccal</strong></td>
<td>3</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

**Concordant?**

- YES
- YES

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>Promega</th>
<th>Sorenson Forensics</th>
<th>Texas DPS</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Blood</strong></td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td><strong>Buccal</strong></td>
<td>3</td>
<td>3</td>
<td></td>
</tr>
</tbody>
</table>

**Concordant?**

- YES
- YES
2.6 Case-type samples/non-probative samples

- Case samples tested
  - Sperm and epithelial fractions from:
    - Underwear
    - Bedding
    - Coat
    - Shirt
  - Epithelial fractions from:
    - Underwear
    - Blue jeans
  - Bloodstain:
    - Sheet
2.6 Case-type samples/non-probative samples

This sample is actually an “unstained area” adjacent to an area where semen was identified. Autosomal STR results identified a complete female source profile associated with the person wearing the garment (underwear) and 4 minor alleles plus Amelogenin Y.
2.7 – Population Study -Concordance

• University of North Texas Health Science Center
  • > 950 US population samples tested
    • Concordance in 17 common loci with AmpF/STR® Yfiler® kit
    • Null allele in DYS448 with duplication in DYS576 due to a 42 base deletion.
      • This deletion is also observed with AmpF/STR® Yfiler® and has been published Budowle, et. al., (2008) Null allele sequence structure at the DYS448 locus and implications for profile interpretation, Int J Legal Med 122:421-427.

• National Institute of Standards and Technology
  • > 600 US population samples tested
    • Concordance in 17 common loci with AmpF/STR® Yfiler® kit and 4 new loci (NIST primer sequences)
2.8 Mixture studies

- Male/Male Mixtures
  - 2 male/male mixture sets sent to laboratories, 500pg total DNA
  - 3 laboratories completed studies
  - Samples amplified in triplicate
  - 19:1, 9:1, 3:1, 1:1, 1:3, 1:9, and 1:19

- Male/Female Mixtures
  - Male Varied/Female constant
    - 2 male/female mixture sets sent to each laboratory
    - 3 laboratories completed studies
    - Samples amplified in triplicate
    - Female held constant at 400ng; male at 500pg, 250pg, 125pg, 62.5pg, 31.25pg
  - Male Constant/Female Varied
    - 1 male mixture set used
    - 1 laboratory completed study
    - Samples amplified in triplicate
    - Male held constant at 125pg or 500pg; female at 500ng, 1000ng, 2000ng, or 3000ng
2.8 Mixture Studies
Male/Male Mixtures

- Percentage of Unique Minor Profile Detected
- Mixture Ratio
  - 19:1
  - 9:1
  - 3:1
  - 1:1
  - 1:3
  - 1:9
  - 1:19

- Data for M1M2 and M2M3 mixtures
2.8 Mixture Studies
Male/Male Mixtures, 19 to 1 ratio
2.8 Mixture Studies
Male/Male Mixtures, 1 to 1 ratio
2.8 Mixture Studies
Male/female Mixtures – decreasing male DNA with 400ng female DNA

Percentage of Loci Called

Template Amount (pg)

- 500pg
- 250pg
- 125pg
- 62.5pg
- 31.25pg

Male 1
Male 2
2.8 Mixture Studies
Male Varied/Female Constant Mixtures – 62.5pg of male DNA with 400ng female DNA (6400X)
2.8 Mixture Studies
Male Constant/Female Varied Mixtures – 125pg male DNA with 3000ng of female DNA (24,000X)
2.9 Precision study

- Precision was performed at each laboratory
- Both 3130 and 3500 series of Genetic analyzers were tested
2.9 Precision Studies
AB 3130

Precision of 14 Ladders on 3130 with POP-4®

Precision of 14 Ladders on 3130 with POP-4®

Standard Deviation

Fragment Size (bp)
2.9 Precision Studies
AB 3500xl

Precision of 8 Ladders on 3500xl with POP-4®
2.10.1 Specificity and robustness

• Reaction Volume - 25µl vs 12.5µl
  • Extracted DNA - data not yet available
  • Blood on FTA – 1 – 1.2mm punch
  • Buccal on FTA – 1 or 2 – 1.2mm punch

• Cycle Number
  • Extracted DNA – 28, 30, and 32 cycles
  • Blood on FTA, 1 – 1.2mm punch – 25, 26, and 27 cycles
  • Buccal on FTA, 2 – 1.2mm punch – 26, 27, and 28 cycles
  • Bode Buccal Collector™, 1 – 1.2mm punch, with PunchSolution™ - 25, 26, and 27 cycles
  • Blood on S&S 903, 1 – 1.2mm punch with PunchSolution™ - 25, 26, and 27 cycles
  • Omni swabs with SwabSolution™, 1 entire swab head- 25, 26, and 27 cycles
  • Cotton swabs with SwabSolution™, 1 entire swab head - 25, 26, and 27 cycles
2.10.1 Specificity and robustness

• Annealing Temperature - 59°C, 61°C, 63°C,
  • Extracted DNA – 500pg male DNA
  • Blood on FTA – 1 – 1.2mm punch
  • Buccal on FTA – 2 – 1.2mm punch

• PCR Reaction Components, magnesium and EDTA titration
  • Extracted DNA – 500pg male DNA

• Primer Concentration – 0.75X, 1X, 1.25X
  • Extracted DNA – 500pg male DNA – data not yet available
  • Blood on FTA – 1 – 1.2mm punch
  • Buccal on FTA – 2 -1.2mm punch
2.10.1 Specificity and robustness
Reaction Volume – Blood on FTA
2.10.1 Specificity and robustness

Reaction Volume – Blood on FTA

1-1.2mm punch - 25µl

1-1.2mm punch – 12.5µl
2.10.1 Specificity and robustness
Reaction Volume – Buccal on FTA

- Reaction Volume
  - Buccal
  - 25µl reaction
  - 12.5µl reaction

- Punch sizes
  - 1-1.2mm
  - 2-1.2mm

- Data representation
  - Bar chart
  - Percentage values
2.10.1 Specificity and robustness

Reaction Volume – Buccal on FTA, 1 – 1.2mm punch

- 25µl
- 12.5µl
2.10.1 Specificity and robustness

Cycle Number – Extracted DNA

- Cycle Numbers: 28 cycles, 30 cycles, 32 cycles
- Template Amounts: 1 ng, 500 pg, 250 pg, 125 pg, 62.5 pg, 31.25 pg
- % of Loci Called for each template amount and cycle number.
2.10.1 Specificity and robustness

Cycle Number – 62.5pg, 28 cycles
2.10.1 Specificity and robustness
Cycle Number – 62.5pg, 30 cycles
2.10.1 Specificity and robustness
Cycle Number – 62.5pg, 32 cycles
### 2.10.1 Specificity and robustness

**Cycle Number – Direct Amplifications**

<table>
<thead>
<tr>
<th>Sample Type</th>
<th>0%</th>
<th>10%</th>
<th>20%</th>
<th>30%</th>
<th>40%</th>
<th>50%</th>
<th>60%</th>
<th>70%</th>
<th>80%</th>
<th>90%</th>
<th>100%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bode Buccal</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Omni Swabs</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blood on S&amp;S903</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Buccal on FTA</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blood on FTA</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- **Blue** = 1 fewer cycle than recommended
- **Red** = Recommended Cycle Number
- **Green** = 1 more cycle than recommended
2.10.1 Specificity and robustness
Annealing Temperature – Extracted DNA, 100pg data

![Graph showing specificity and robustness at different annealing temperatures: 59°C, 61°C, and 63°C. The graph depicts the average percent of loci called at each temperature, with 61°C having the highest percentage and 63°C showing slightly lower but still high percent.]
2.10.1 Specificity and robustness
Annealing Temperature – Extracted DNA

- 59°C
- 61°C
- 63°C
2.10.1 Specificity and robustness
Annealing Temperature – Blood on FTA

- Blood, 59°C
- Blood, 61°C
- Blood, 63°C
2.10.1 Specificity and robustness

Annealing Temperature – Blood on FTA

59°C

61°C

63°C
2.10.1 Specificity and robustness
Annealing Temperature – Buccal on FTA

![Bar chart showing percent of loci called for different annealing temperatures: Buccal, 59°C, Buccal, 61°C, and Buccal, 63°C. All values are above 90%.](image)
2.10.1 Specificity and robustness
Annealing Temperature – Buccal on FTA

59°C

61°C

63°C
2.10.1 Specificity and robustness

PCR reaction components – Extracted DNA

- Extracted DNA
- MgCl2
  - 1.25X MgCl2
  - 1X MgCl2
- EDTA
  - 0.1mM EDTA
  - 0.25mM EDTA
  - 0.5mM EDTA
  - 1mM EDTA

Percent Loci Called vs Magnesium Chloride and EDTA Concentration
2.10.1 Specificity and robustness
PCR reaction components – Extracted DNA

- 1.25X MgCl₂
- 1X MgCl₂
- 0.1mM EDTA
- 0.25mM EDTA
- 0.5mM EDTA
- 1mM EDTA
2.10.1 Specificity and robustness
Primer Concentration – Blood on FTA

Percent Loci Called

<table>
<thead>
<tr>
<th>Concentration</th>
<th>0%</th>
<th>10%</th>
<th>20%</th>
<th>30%</th>
<th>40%</th>
<th>50%</th>
<th>60%</th>
<th>70%</th>
<th>80%</th>
<th>90%</th>
<th>100%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood, 0.75X Primer</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blood, 1X Primer</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blood, 1.25X Primer</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
2.10.1 Specificity and robustness
Primer Concentration – Blood on FTA

0.75X

1X

1.25X
2.10.1 Specificity and robustness
Primer Concentration – Buccal on FTA

Percent Loci Called

- Buccal, 0.75X Primer
- Buccal, 1X Primer
- Buccal, 1.25X Primer
2.10.1 Specificity and robustness
Primer Concentration – Buccal on FTA

- 0.75X
- 1X
- 1.25X
2.10.2 Balance and stochastic
500pg Male DNA

- DYS576
- DYS389 I
- DYS448
- DYS389 II
- DYS19

- DYS391
- DYS481
- DYS549
- DYS533
- DYS438
- DYS437

- DYS570
- DYS635
- DYS390
- DYS439
- DYS392
- DYS643

- DYS393
- DYS458
- DYS385
- DYS456
- YGATAH4

Promega
2.10.2 Balance and stochastic
62.5pg Male DNA
2.10.3 Known Artifacts

Artifacts Listed in the Technical Manual

Table 4. DNA-Dependent Artifacts.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Artifact Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS19</td>
<td>n−2; n+2</td>
</tr>
<tr>
<td>DYS448</td>
<td>n−9 to n−15</td>
</tr>
</tbody>
</table>

1Two bases below and above the true allele peak, respectively.

2These variably sized peaks on the Applied Biosystems® 3130 and 3500 Genetic Analyzers may represent double-stranded DNA derived from the DYS448 amplicon. (Double-stranded DNA is known to migrate faster than single-stranded DNA on capillary electrophoresis [CE] instruments.)

3The low-level, DNA-dependent artifact is noticeable only with high input template amounts and allele peak heights.

Table 5. DNA-Independent Artifacts.

<table>
<thead>
<tr>
<th>Dye Label</th>
<th>Instrument</th>
<th>Artifact Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fluorescein</td>
<td>Applied Biosystems® 3130 Genetic Analyzers with POP-4™ polymer</td>
<td>68–71 bases¹</td>
</tr>
<tr>
<td></td>
<td>Applied Biosystems® 3500 Genetic Analyzers with POP-4™ polymer</td>
<td>66–69 bases¹</td>
</tr>
<tr>
<td>JOE</td>
<td>Applied Biosystems® 3130 Genetic Analyzers with POP-4™ polymer</td>
<td>60–62 bases¹</td>
</tr>
<tr>
<td></td>
<td>Applied Biosystems® 3500 Genetic Analyzers with POP-4™ polymer</td>
<td>58–60 bases¹</td>
</tr>
</tbody>
</table>

¹The signal strength of these artifacts increases with storage of the amplification plate at 4°C, sometimes in as short a time period as overnight but more commonly when plates are left at 4°C for a few days. We recommend storing amplification products at −20°C.
2.10.3 Known Artifacts

**Artifacts Listed in the Technical Manual – POP7**

- The PowerPlex®Y23 System is optimized for POP-4™ polymer. We recognize that some laboratories use POP-7™ polymer and therefore have included a protocol in this manual.
- Some DNA-independent artifacts migrate in the panel range with the POP-7™ polymer.
- Global filters used for database analysis will generally filter these artifact peaks. However, these peaks may be labeled with casework samples.
- Internal validation should be performed and interpretation guidelines created that describe the artifacts and their impact on data analysis.

<table>
<thead>
<tr>
<th>Dye Label</th>
<th>Instrument</th>
<th>Artifact Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fluorescein</td>
<td>Applied Biosystems® 3130 Genetic Analyzers with POP-7™ polymer</td>
<td>65–68 bases</td>
</tr>
<tr>
<td>JOE</td>
<td>Applied Biosystems® 3130 Genetic Analyzers with POP-7™ polymer</td>
<td>66–69 bases</td>
</tr>
</tbody>
</table>

1 The signal strength of these artifacts increases with storage of the amplification plate at 4°C, sometimes in as short a time period as overnight but more commonly when plates are left at 4°C for a few days. We recommend storing amplification products at −20°C.
2.10.4 Positive Control
500pg 2800M
2.10.4 Negative Control
Stutter Samples
### PowerPlex® Y23 System

#### Stutter Values

<table>
<thead>
<tr>
<th>n=105</th>
<th>Average</th>
<th>St.Dev</th>
<th>Average + 3SD</th>
<th>Max</th>
<th>Count</th>
<th>Occurrence</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS576</td>
<td>0.108</td>
<td>0.013</td>
<td>0.147</td>
<td>0.150</td>
<td>94</td>
<td>89.52%</td>
</tr>
<tr>
<td>DYS389I</td>
<td>0.052</td>
<td>0.010</td>
<td>0.081</td>
<td>0.076</td>
<td>85</td>
<td>80.95%</td>
</tr>
<tr>
<td>DYS448</td>
<td>0.026</td>
<td>0.005</td>
<td>0.040</td>
<td>0.037</td>
<td>83</td>
<td>79.05%</td>
</tr>
<tr>
<td>DYS389II</td>
<td>0.114</td>
<td>0.012</td>
<td>0.152</td>
<td>0.153</td>
<td>93</td>
<td>88.57%</td>
</tr>
<tr>
<td>DYS19</td>
<td>0.068</td>
<td>0.013</td>
<td>0.106</td>
<td>0.102</td>
<td>88</td>
<td>83.81%</td>
</tr>
<tr>
<td>DYS391</td>
<td>0.074</td>
<td>0.016</td>
<td>0.123</td>
<td>0.184</td>
<td>93</td>
<td>87.62%</td>
</tr>
<tr>
<td>DYS481</td>
<td>0.207</td>
<td>0.031</td>
<td>0.298</td>
<td>0.280</td>
<td>94</td>
<td>89.52%</td>
</tr>
<tr>
<td>DYS549</td>
<td>0.077</td>
<td>0.012</td>
<td>0.114</td>
<td>0.147</td>
<td>92</td>
<td>87.62%</td>
</tr>
<tr>
<td>DYS533</td>
<td>0.068</td>
<td>0.013</td>
<td>0.107</td>
<td>0.131</td>
<td>92</td>
<td>87.62%</td>
</tr>
<tr>
<td>DYS438</td>
<td>0.031</td>
<td>0.006</td>
<td>0.050</td>
<td>0.062</td>
<td>76</td>
<td>72.38%</td>
</tr>
<tr>
<td>DYS437</td>
<td>0.050</td>
<td>0.012</td>
<td>0.084</td>
<td>0.116</td>
<td>83</td>
<td>79.05%</td>
</tr>
<tr>
<td>DYS570</td>
<td>0.109</td>
<td>0.017</td>
<td>0.159</td>
<td>0.172</td>
<td>94</td>
<td>89.52%</td>
</tr>
<tr>
<td>DYS635</td>
<td>0.068</td>
<td>0.016</td>
<td>0.115</td>
<td>0.112</td>
<td>91</td>
<td>86.67%</td>
</tr>
<tr>
<td>DYS390</td>
<td>0.086</td>
<td>0.016</td>
<td>0.134</td>
<td>0.125</td>
<td>93</td>
<td>88.57%</td>
</tr>
<tr>
<td>DYS439</td>
<td>0.069</td>
<td>0.013</td>
<td>0.107</td>
<td>0.121</td>
<td>93</td>
<td>88.57%</td>
</tr>
<tr>
<td>DYS392</td>
<td>0.102</td>
<td>0.023</td>
<td>0.171</td>
<td>0.188</td>
<td>93</td>
<td>88.57%</td>
</tr>
<tr>
<td>DYS643</td>
<td>0.024</td>
<td>0.005</td>
<td>0.039</td>
<td>0.037</td>
<td>66</td>
<td>62.86%</td>
</tr>
<tr>
<td>DYS393</td>
<td>0.102</td>
<td>0.016</td>
<td>0.151</td>
<td>0.194</td>
<td>95</td>
<td>90.48%</td>
</tr>
<tr>
<td>DYS458</td>
<td>0.097</td>
<td>0.016</td>
<td>0.147</td>
<td>0.185</td>
<td>95</td>
<td>90.48%</td>
</tr>
<tr>
<td>DYS385</td>
<td>0.092</td>
<td>0.019</td>
<td>0.149</td>
<td>0.150</td>
<td>93</td>
<td>88.57%</td>
</tr>
<tr>
<td>DYS456</td>
<td>0.111</td>
<td>0.013</td>
<td>0.150</td>
<td>0.156</td>
<td>94</td>
<td>89.52%</td>
</tr>
<tr>
<td>Y-GATA</td>
<td>0.074</td>
<td>0.013</td>
<td>0.111</td>
<td>0.116</td>
<td>93</td>
<td>88.57%</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>n=105</th>
<th>Average</th>
<th>St.Dev</th>
<th>Average + 3SD</th>
<th>Max</th>
<th>Count</th>
<th>Occurrence</th>
</tr>
</thead>
<tbody>
<tr>
<td>DYS576</td>
<td>0.017</td>
<td>0.010</td>
<td>0.048</td>
<td>0.050</td>
<td>25</td>
<td>23.81%</td>
</tr>
<tr>
<td>DYS389I</td>
<td>0.012</td>
<td>0.003</td>
<td>0.022</td>
<td>0.016</td>
<td>7</td>
<td>6.67%</td>
</tr>
<tr>
<td>DYS448</td>
<td>0.027</td>
<td>0.009</td>
<td>0.055</td>
<td>0.094</td>
<td>80</td>
<td>76.19%</td>
</tr>
<tr>
<td>DYS389II</td>
<td>0.018</td>
<td>0.010</td>
<td>0.048</td>
<td>0.047</td>
<td>25</td>
<td>23.81%</td>
</tr>
<tr>
<td>DYS533</td>
<td>0.014</td>
<td>0.006</td>
<td>0.031</td>
<td>0.023</td>
<td>12</td>
<td>11.43%</td>
</tr>
<tr>
<td>DYS438</td>
<td>0.008</td>
<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
<td>0</td>
<td>0.00%</td>
</tr>
<tr>
<td>DYS437</td>
<td>0.008</td>
<td>0.008</td>
<td>0.036</td>
<td>0.047</td>
<td>30</td>
<td>28.57%</td>
</tr>
<tr>
<td>DYS570</td>
<td>0.012</td>
<td>0.004</td>
<td>0.024</td>
<td>0.017</td>
<td>4</td>
<td>3.81%</td>
</tr>
<tr>
<td>DYS635</td>
<td>0.012</td>
<td>0.003</td>
<td>0.020</td>
<td>0.016</td>
<td>5</td>
<td>4.76%</td>
</tr>
<tr>
<td>DYS390</td>
<td>0.011</td>
<td>0.005</td>
<td>0.027</td>
<td>0.028</td>
<td>19</td>
<td>18.10%</td>
</tr>
<tr>
<td>DYS439</td>
<td>0.051</td>
<td>0.018</td>
<td>0.105</td>
<td>0.115</td>
<td>88</td>
<td>83.81%</td>
</tr>
<tr>
<td>DYS643</td>
<td>0.015</td>
<td>0.004</td>
<td>0.027</td>
<td>0.026</td>
<td>72</td>
<td>68.57%</td>
</tr>
<tr>
<td>DYS393</td>
<td>0.010</td>
<td>0.004</td>
<td>0.022</td>
<td>0.021</td>
<td>12</td>
<td>11.43%</td>
</tr>
<tr>
<td>DYS458</td>
<td>0.015</td>
<td>0.014</td>
<td>0.056</td>
<td>0.031</td>
<td>3</td>
<td>2.86%</td>
</tr>
<tr>
<td>DYS385</td>
<td>0.021</td>
<td>0.006</td>
<td>0.038</td>
<td>0.035</td>
<td>56</td>
<td>53.33%</td>
</tr>
<tr>
<td>Y-GATA</td>
<td>0.012</td>
<td>0.005</td>
<td>0.026</td>
<td>0.019</td>
<td>13</td>
<td>12.38%</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>n=105</th>
<th>Average</th>
<th>St.Dev</th>
<th>Average + 3 STD</th>
<th>Max</th>
<th>Count</th>
<th>Occurrence</th>
</tr>
</thead>
<tbody>
<tr>
<td>N-2</td>
<td>0.081</td>
<td>0.007</td>
<td>0.102</td>
<td>0.099</td>
<td>90</td>
<td>85.71%</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>N=105</th>
<th>Average</th>
<th>St.Dev</th>
<th>Average + 3 STD</th>
<th>Max</th>
<th>Count</th>
<th>Occurrence</th>
</tr>
</thead>
<tbody>
<tr>
<td>N+2</td>
<td>0.025</td>
<td>0.004</td>
<td>0.038</td>
<td>0.036</td>
<td>44</td>
<td>41.90%</td>
</tr>
</tbody>
</table>
### PowerPlex® Y23 System

#### Stutter Filters for GeneMapper ID-X

<table>
<thead>
<tr>
<th>Marker Name</th>
<th>DYS576</th>
<th>0.147</th>
<th>3.25</th>
<th>4.75</th>
<th>Minus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Marker Name</td>
<td>DYS389 I</td>
<td>0.081</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS448</td>
<td>0.04</td>
<td>5.25</td>
<td>6.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS389 II</td>
<td>0.152</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS19</td>
<td>0.107</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS481</td>
<td>0.298</td>
<td>2.25</td>
<td>3.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS481</td>
<td>0.055</td>
<td>2.25</td>
<td>3.75</td>
<td>Plus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS549</td>
<td>0.114</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS533</td>
<td>0.107</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS438</td>
<td>0.05</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS437</td>
<td>0.084</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS570</td>
<td>0.159</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS635</td>
<td>0.115</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS390</td>
<td>0.134</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS439</td>
<td>0.107</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS392</td>
<td>0.171</td>
<td>2.25</td>
<td>3.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS392</td>
<td>0.105</td>
<td>2.25</td>
<td>3.75</td>
<td>Plus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS643</td>
<td>0.039</td>
<td>4.25</td>
<td>5.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS393</td>
<td>0.151</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS458</td>
<td>0.147</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS385</td>
<td>0.149</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>DYS456</td>
<td>0.151</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
<tr>
<td>Marker Name</td>
<td>YGATAH4</td>
<td>0.111</td>
<td>3.25</td>
<td>4.75</td>
<td>Minus</td>
</tr>
</tbody>
</table>
The value of 0.06 will filter the plus stutter for DYS481 (5.5%) but not for DYS392 (10.5%). This is noted in the Technical Manual.
Y-STR Statistical Databases
### Overall Database Summary:

<table>
<thead>
<tr>
<th>Haplotype Type</th>
<th>Frequency</th>
<th>Confidence Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall</td>
<td>0.002176</td>
<td>1 in every 460</td>
</tr>
<tr>
<td>African American</td>
<td>0.000000</td>
<td>1 in every 121</td>
</tr>
<tr>
<td>Caucasian</td>
<td>0.010103</td>
<td>1 in every 99</td>
</tr>
<tr>
<td>Hispanic</td>
<td>0.000000</td>
<td>1 in every 93</td>
</tr>
<tr>
<td>Native American</td>
<td>0.00677</td>
<td>1 in every 148</td>
</tr>
</tbody>
</table>

As of 8/9/12, 1375 samples contained all 23 loci. This number is anticipated to increase with submissions in the upcoming months.
Updated Y-HRD Database Interface

YHRD.Org 3.0

Search

Haplotypes
SNPs
Populations
Contributors
Contributions

Analyse Research Contribute Meet

Download Manual

YHRD Standard | Promega PowerPlex Y | Applied Biosystems AmpFISTR Yfiler | Promega PowerPlex Y23

DYS576 DYS389I DYS448 DYS389II DYS19 DYS391 DYS481 DYS449 DYS533 DYS438 DYS437

DYS570 DYS615 DYS390 DYS439 DYS392 DYS463 DYS393 DYS458 DYS385 DYS456 YGATH4

National database | Metapopulations | SNP

Whole database

Search Reset

Please note: The database size will vary based on the loci you have entered.

- 7 loci haplotype (DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, DYS393): 104174 haplotypes
- Minimal Haplotype (+ DYS385ab): 102377 haplotypes
- SWGDAM haplotype (+ DYS448, DYS456, DYS458, DYS635, YGATAH4): 75290 haplotypes
- Promega PowerPlex Y (+ DYS437): 55747 haplotypes
- Applied Biosystems AmpFISTR Yfiler (+ DYS448, DYS456, DYS458, DYS635, YGATAH4): 44469 haplotypes
- Promega PowerPlex Y23 (+ DYS576, DYS481, DYS549, DYS533, DYS570, DYS643): 951 haplotypes
Summary
Performance Summary

• PowerPlex® Y23 System is a very flexible system that is capable of working for multiple applications including casework (extracted) samples as well as multiple substrates for direct amplification

• Full profiles obtained consistently at 62.5pg of male DNA

• Ability to overcome excessive amounts of female with full profiles of 125 pg in 3000 ng of female DNA

• Rapid cycling of 1 hour 40 minutes for casework samples and 1 hour 30 minutes for direct amplification samples

• Robust against many of the commonly encountered inhibitors; humic acid, hematin, and tannic acid
Supported instruments & software summary

Thermal Cycler:
- GeneAmp® PCR System 9700 (Applied Biosystems)

Capillary Electrophoresis Instrument:
- 3500 & 3500xL Genetic Analyzer (Applied Biosystems)
- 3130 & 3130xl Genetic Analyzer (Applied Biosystems)
- ABI PRISM® 3100 & 3100-Avant Genetic Analyzer (Applied Biosystems)

Data Analysis Software:
- GeneMapper® ID-X Software, version 1.2 (Applied Biosystems)
  - Includes plus stutter filters for DYS481 and DYS392 (trinucleotide repeat loci)
  - Includes N-2 and N+2 filters for DYS19
- GeneMapper® ID Software, version 3.2 (Applied Biosystems)
Acknowledgements

• Developmental Collaborators
  • Illinois State Police
  • Sorenson Forensics
  • Texas DPS
    • DNA section
    • CODIS section

• Population Data Collaborators
  • NIST
  • UNT

• R&D
  • Doug Storts
  • Cindy Sprecher
  • Jonelle Thompson
  • Margaret Ewing
  • Dawn Rabbach
  • Patricia Fulmer

• Oligo Synthesis
  • Ned Reimer
  • Kevin DeGrand

• QA
  • Alyssa TenHarmsel

• Marketing
  • Lotte Downey
  • Ann MacPhetridge
  • Rohaizah James
  • Melissa Schwandt

• Project Manager
  • Brian McNamara

• Manufacturing
  • Kris Pearson
  • Katie Hebble
  • Anna Markhardt
  • Kara Raymond
  • Jennifer Setlak
  • Charlie Stollberg
Questions?