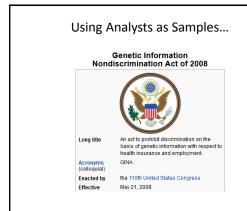
| Excellence in Forensic Leadership Policy and Practice in the 21st Century 12rd Annual Symposium ASCLD AMERICAN SOCIETY OF SIMPLIAN PRAYON DIRECTORS | |
|--|--|
| An Application of the Kipling Method to DNA Validation in the 21 st Century | |
| Thinking Ahead | |
| Mike Coble | |
| | |

Planning for the next validation

- Use the same samples you have tested for your old STR multiplex for the next STR multiplex.
- Positive controls, current employees, and NIST SRM components are popular examples, but have limitations.



Planning for the next validation

- Consider buying a large supply of blood (anonymously collected) from a blood bank.
- Characterize as much as you can (nice summer intern project).
- Why?

FSI-Genetics 5(5):376-80

Analysis and interpretation of mixed profiles generated by 34 cycle SGM $Plus^{\circledR}$ amplification

Jon H. Wetton*, John Lee-Edghill, Emily Archer, Valerie C. Tucker, Andrew J. Hopwood, Jonathan Whitaker, Gillian Tully

Forensic Science Service, 2960 Trident Court, Birmingham Business Park, Solihull B37 7YN,

| Table 2 |
|--|
| The final distribution of major and consensus profiles across the template input and |
| ratio range after completion of the RO requested rework. |

| Ratio | Total input | Major/minor | Major/ consensus | Consensus only | Unduplicated |
|-------|----------------|-----------------|---------------------|----------------|--------------|
| 5:1 | 1 ng | 12 | | 3 | 1 |
| | 500 pg | 10° | | 6 | |
| | 250 pg | 11 ^a | 1 | 6 4 9 | |
| | 100 pg | 34 | 4 | 9 | |
| | 50 pg | 2 | | 14 | |
| | Total | 38 | 5 | 36 | 1 |
| 2:1 | 1 ng | 1 | | 14 | 1 |
| | 500 pg | 1ª | | 14 | 1 |
| | 250 pg | 14 | | 15 | |
| | 100 pg | | 1 | 14 | 1 |
| | 50 pg | | 10 | 15 | |
| | Total | 3 | 2 | 72 | 3 |
| 1:1 | 1 ng | | | 8 | |
| | 500 pg | | | 8 | |
| | 250 pg | | | 8 8 7 | |
| | 100 pg | | | 8 | |
| | 50 pg | | 1ª | 7 | |
| | Total | 0 | 1 | 39 | 0 |

mutation in the Quantifiler primer binding region that underestimated the relative ratios in the study...

One individual had a possible

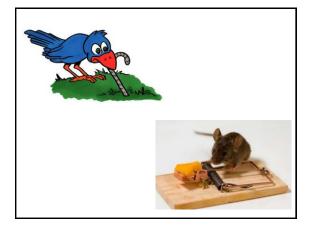
³ One observation in each of these major profile categories was due to a single individual with a possible mutation affecting the accuracy of the Quantifiler⁸ concentration estimate which may have caused the input of this individual to be underestimated by half. This would tend to double its relative representation at each mixture ratio as well as the true amount of femplate available in the PCR. In the other rows the affected mixture was scored as a consensus.

Planning for the next validation

- Don't be an island consider joining with other labs to plan validation studies. Other labs may have ideas that can streamline your validation.
- Share resources, cost, time. Perhaps you may find a "Steven Myers" type who saves your lab hours with a neat Excel spreadsheet.
- Inter-laboratory challenges to monitor progress.

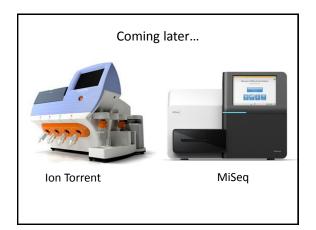
No matter what you are validating now...

- This is NOT your last validation!
- Should you be an early adopter?
- Should you go kicking and screaming?









NGS Thoughts

- Large Multiplexes SNPs, aSTRs, mtDNA, Y-STRs, Y-SNPs, X-STRs... If data is generated, it must be analyzed.
- Need for allele frequency databases
- Data storage!

Final thoughts

- Proper validation is hard work. It takes a great deal of time and effort to conduct the studies, write the new SOPs, train everyone, and monitor the progress.
- It really shouldn't be "easy" as it's your job to find the limits of the system.

The second stanza of The Elephant's Child

- I KEEP six honest serving-men (They taught me all I knew);
 Their names are What and Why and When And How and Where and Who.
- I send them over land and sea,
 I send them east and west;

 But after they have worked for me,
 I give them all a rest.

| Acknowledgme | nts |
|--|-----|
| National Institute of Justice and NIST Law Enforcement Standards Office | |
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