Dried Blood Spot DNA Extraction Guidelines to Ensure Robust Performance in NBS Molecular Assays

Suzanne K. Cordovado, Ph.D.

Molecular Quality Improvement Program Newborn Screening and Molecular Biology Branch

Division of Laboratory Sciences National Center for Environmental Health



Validating DNA Extracted from DBS

- How much DNA do you need and what extraction is appropriate?
- Are there inhibitors present in your extract?
- Is your DNA fragmented and does it matter?
- Testing DNA for contamination and sample identity
- Next Generation sequencing... Will DBS work?



DBS DNA Extraction Methods Used in Newborn Screening

Qiagen Lysis Method - Ex: Solutions 1 & 2

Multiple wash steps, followed by boil

Boil Prep Method

No wash, followed by prolonged boil

Methanol Boil Prep Method

Fixation of proteins, followed by prolonged boil



Measuring DNA Concentration quantitative PCR



Concentration represents amplifiable DNA
 Unknown concentrations are calculated relative to a standard curve

DNA Yield from 3 mm Adult DBS Punch

| | Lysis (Qiagen) | Boil | Methanol Boil | |
|--------------------|----------------|----------------|----------------|--|
| Sample* | DNA yield (ng) | DNA yield (ng) | DNA yield (ng) | |
| Adult CF PT (low) | 44.50 | 6.05 | 4.05 | |
| Adult CF PT (med) | 122.50 | 32.51 | 8.75 | |
| Adult CF PT (high) | 289.50 | 54.59 | 19.60 | |

* Extracted from NSQAP's Cystic Fibrosis PT specimens with known high, medium and low concentrations

DNA extracted using the Boil and Methanol Boil Methods is significantly lower than the Qiagen Lysis Method

qPCR to Detect Inhibitors Quantifiler Duo Assay

Detect PCR inhibitors using an internal positive control (IPC)

- IPC is an artificial template simultaneously amplified with human DNA
- IPC C^T values ≥ 31 indicate an extract may be inhibited

qPCR to Detect PCR Inhibition Internal Positive Control (IPC)



1st cluster amplifies as expected (IPC Ct<31)
 2nd cluster amplifies later indicating inhibition (IPC Ct>31)

How DNA Becomes Fragmented
Exposure to prolonged high temperatures
Mechanical shearing – pipetting, mixing, etc.
DNAse enzyme activity

Genomic DNA Fragmentation



Most NBS assays are small target sizes (< 1kb)
 Fragmented DNA often results in better amplification
 Can amplify 6 kb fragment from Lysis Prep

DNA Contamination and Identity

- "DNA fingerprinting" uses repeats or microsatellites (2 - 6 bp) found in the genome
- Microsatellite length is variable and inherited
- If marker has >2 alleles, may indicate contamination
- Also useful for identity testing between discrepant samples



DBS DNA Work and Next Gen Sequencing Ion Torrent

Uses semi-conductor technology in high-density array

- Massive parallel DNA sequencing
- Target(s) amplified using highly multiplexed primer pool

 DNA input recommended - 10 ng per pool
 Barcoding allows multiple samples per chip



Ion Torrent Next Generation Sequence Data from DBS

□ Goal 1: ≥ 90x coverage for all amplicon targets

Goal 2: 100% concordance with identified mutations/ variations

| | | Ion Torrent Next Generation Sequencing Results | | | | |
|-------------------------------|-----------|--|------------------|---------------|--------------------------|--|
| | | Target coverage ≥ 90x | | % Concordance | | |
| Cystic Fibrosis Sample | | Liq Blood | DBS | Liq Blood | DBS | |
| Mutations | variants* | (Column) | (Qiagen Lysis) | (Column) | (Qiagen Lysis) | |
| 3905insT | 8 | 100% | 100% | 100%# | 100% # | |
| E60X / delF508 | 10 | 100% | 100% | 100% | 100% | |
| 2055 del 9 ins A | 5 | 100% | 97% | 100% | 100% | |
| R75X / R74W / D1270N | 0 | 99% | 84% [‡] | 100% | 100% # | |
| R1158X | 11 | 100% | 92% | 100% | 100% | |
| delF311 | 13 | 100% | 100% | 100%# | 100% [#] | |
| G551D / R117H | 8 | 100% | 92% | 100% | 100% | |
| delF508 / delI507 | 11 | 98% | 100% | 100% # | 100% # | |

* Excludes the TG_X/T_Y repeat in Intron 9 which is still in development by Life Technologies

⁺ Library preparation not optimal

Samples for the 3' UTR 8/9T region (c.*133delT) were manually called

DNA extracted from liquid blood (column) and DBS (lysis) performs well

Conclusions

- Not all DBS DNA extraction methods are created equal
 - Boil prep and Methanol Boil prep methods give significantly lower yields than the Qiagen Lysis method
- qPCR can quantify DNA and identify PCR inhibitors
- DNA extractions with prolonged heat steps result in fragmented DNA
- Short tandem repeats used to identify contamination and resolve discrepant results
- DNA from DBS can be used for Next Gen Sequencing Ion Torrent platform (CFTR)

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For more information please contact Centers for Disease Control and Prevention 1600 Clifton Road NE, Atlanta, GA 30333 Telephone, 1-800-CDC-INFO (232-4636)/TTY: 1-888-232-6348 E-mail: cdcinfo@cdc.gov Web: www.cdc.gov

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