

Rapid DNA Identification of Human Remains in Diverse Conditions: What Works, What Doesn't

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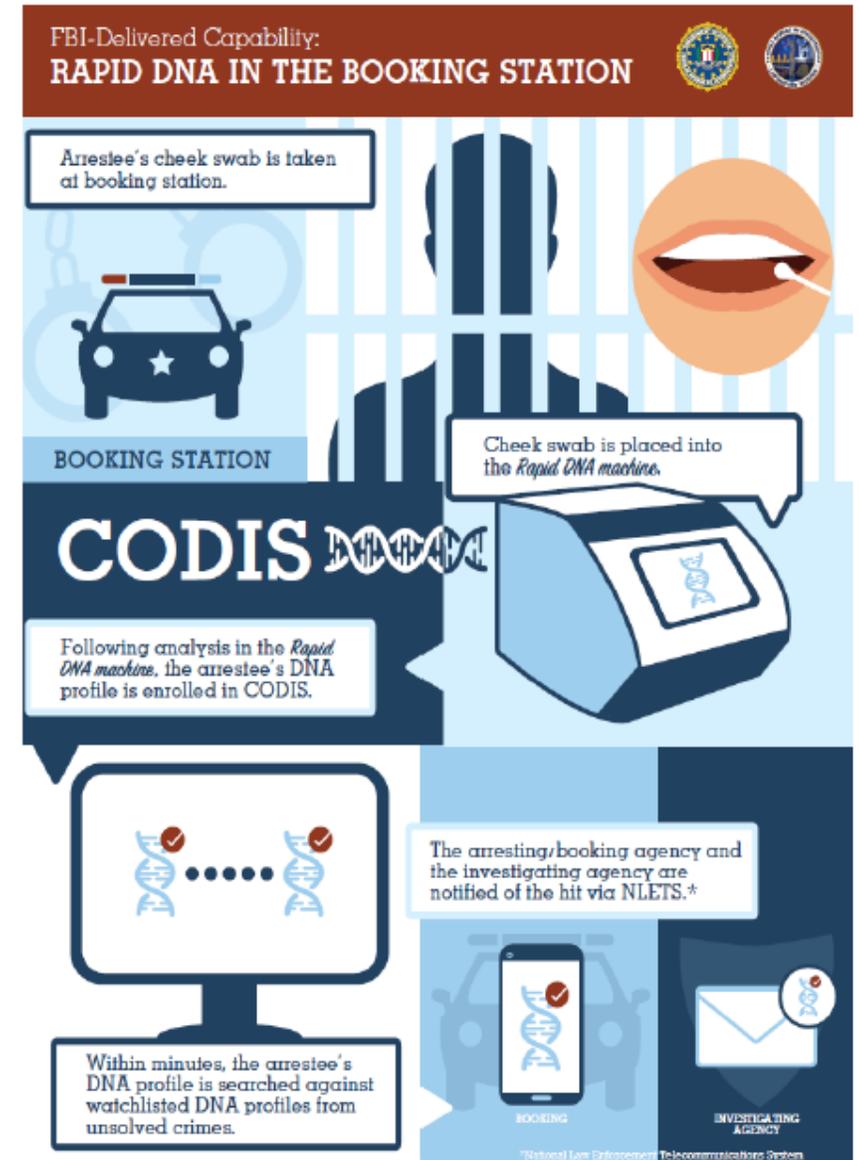
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SHSU was provided instrumentation and kits by Thermo Fisher Scientific, but no remuneration.



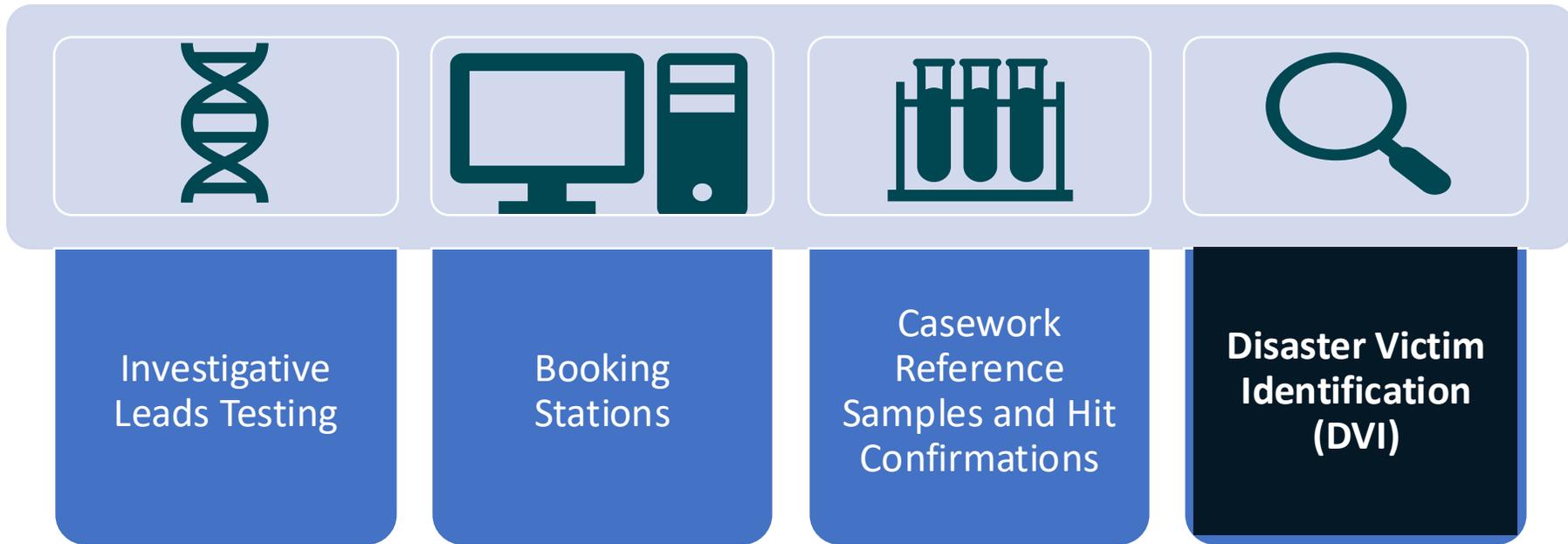
Rapid DNA

- FBI defines Rapid DNA “a fully automated process of developing a DNA profile from a mouth swab. This happens in one to two hours – without the need for a DNA laboratory or DNA intervention and review”¹
- Currently used for booking stations to submit arrestee’s DNA profile to CODIS¹
- July 1, 2025, FBI QAS standards allow for the use of Rapid DNA in forensic casework¹





Rapid DNA Applications





Rapid DNA instruments

RapidHIT ID System



- Thermo Fisher Scientific
- 1 sample 90 min
- 2 types of cartridges

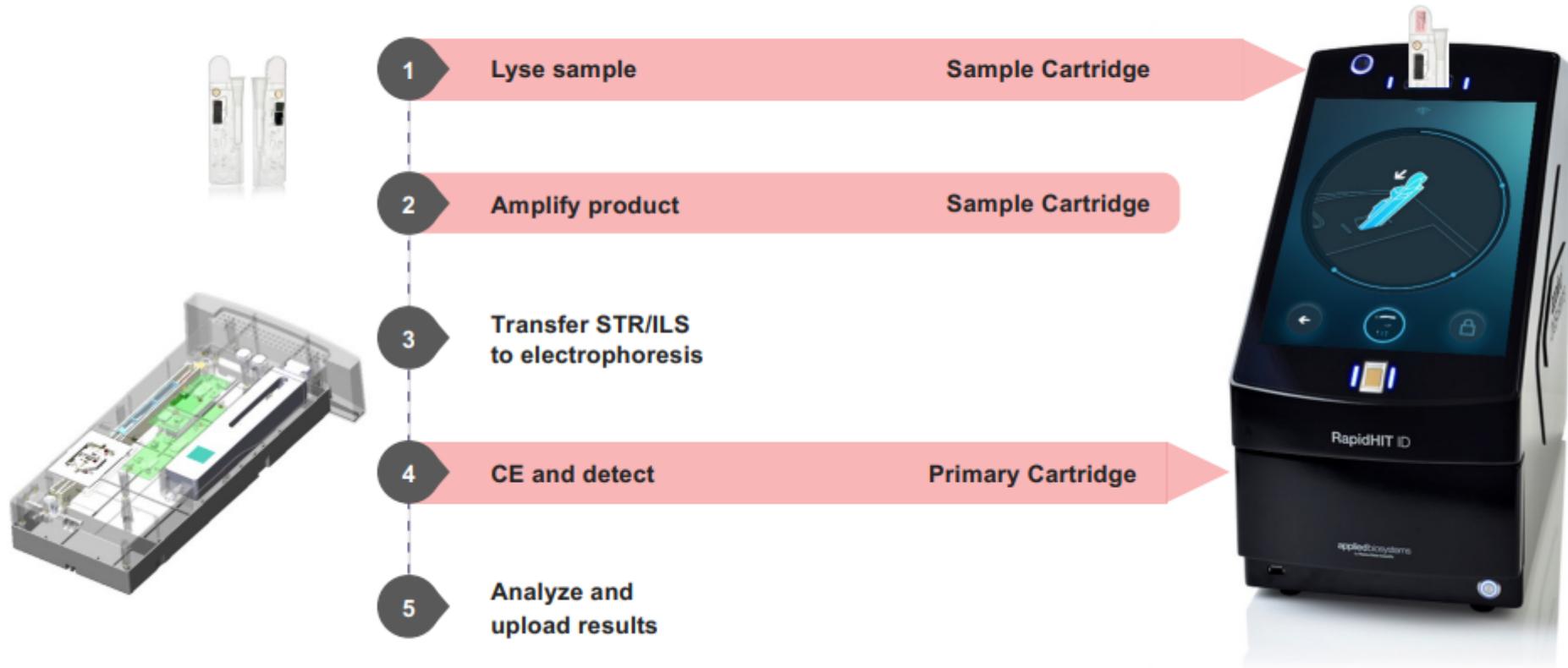
ANDE 6C Instrument



- ANDE
- 5 samples
- Specialized swab and chips

RapidHIT ID System

Lysis and amplification are performed onboard the sample cartridge
 The primary cartridge encapsulates capillary electrophoresis and detection steps



RapidHIT ID System Cartridges

ACE GlobalFiler Express

- Reference Samples
- Booking Station
- 500 μ L lysis buffer
- **28** PCR cycles
- 1 filter paper punch



RapidINTEL™ Plus

- **Moderate to high-yield** crime scene samples
- Investigative Leads
- 500 μ L (general) or 100 μ L (specialized) protocols
- **30** PCR cycles
- Internal Quality Control (IQC) markers
- Quantification markers
- 1 oblong filer punch

Research Objective



Identify the best way to prepare bones by testing different degrees of “fineness” for the RapidHIT ID instrument by using an off-instrument mock rapid CE method



Explore if pretreatment methods would improve results for bones



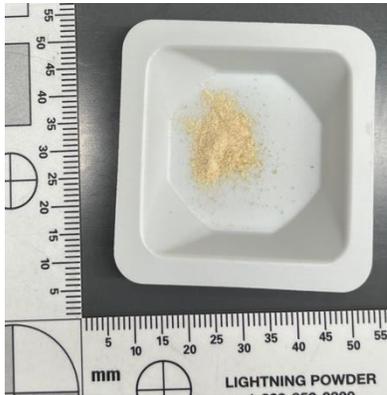
Evaluate cadaveric samples taken at different periods of decomposition to assess when rapid would be the most advantageous.

Workflow

Bone Selection
Good DNA Yield (10ng/ul)
Low DNA Yield (0.0122 ng/ul)

**Quant based on
Quantifiler Trio 50mg**

Powder



Spice Grinder



Chips



Workflow

Bone Selection
 “Good” Bone (10ng/μL)
 “Compromised” Bone(0.0122 ng/μL)

Quant based on Trio 50mg

**Powder
Granule
Chips**

Control Chips:
200mg
General protocol

10 mg

50 mg

100 mg

200 mg

Bone Amounts

25% Prep-n-Go
Buffer

BTA Buffer

Complete
Demineralization
Buffer

Lysis Amounts

Cleanup Step

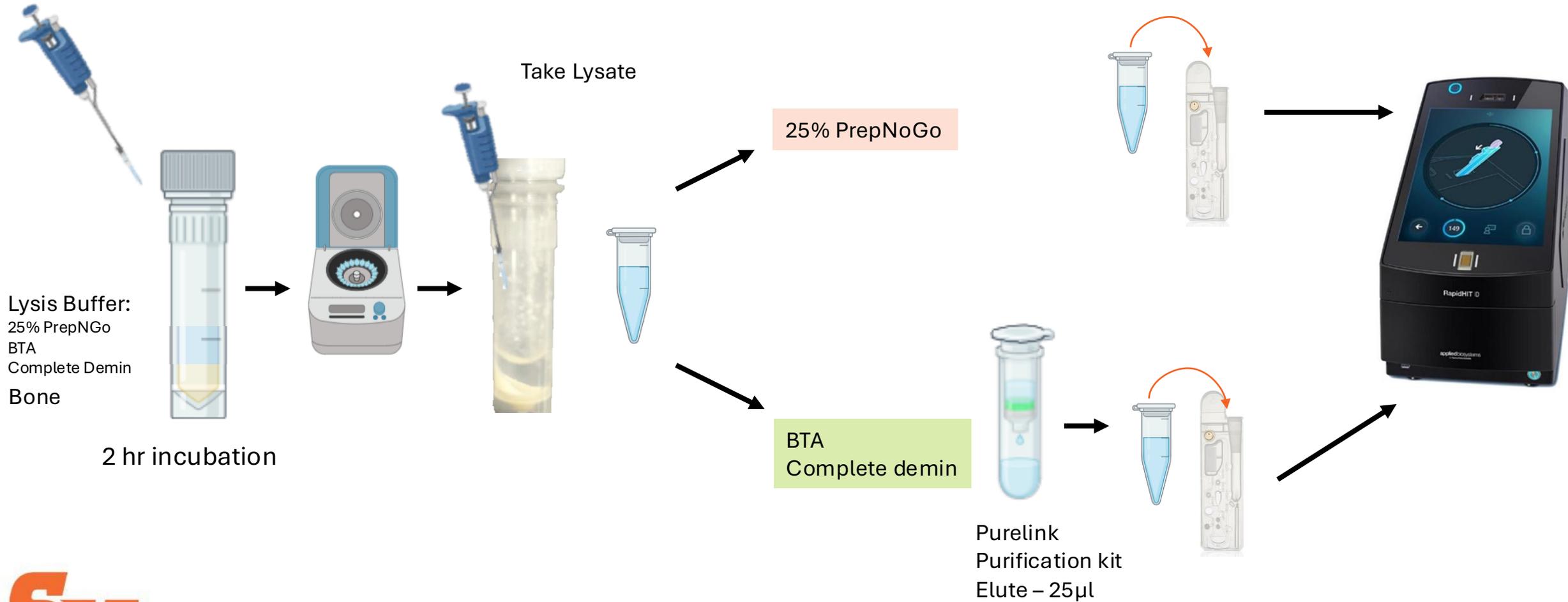
Bone Amount	Powder (μL)	Spice Grinder (μL)	Chips (μL)
10 mg	100	100	N/A
50 mg	200	200	200
100 mg	400	300	300
200 mg	600	400	400

RapidHIT ID System

**Straight into:
RapidHIT ID System**

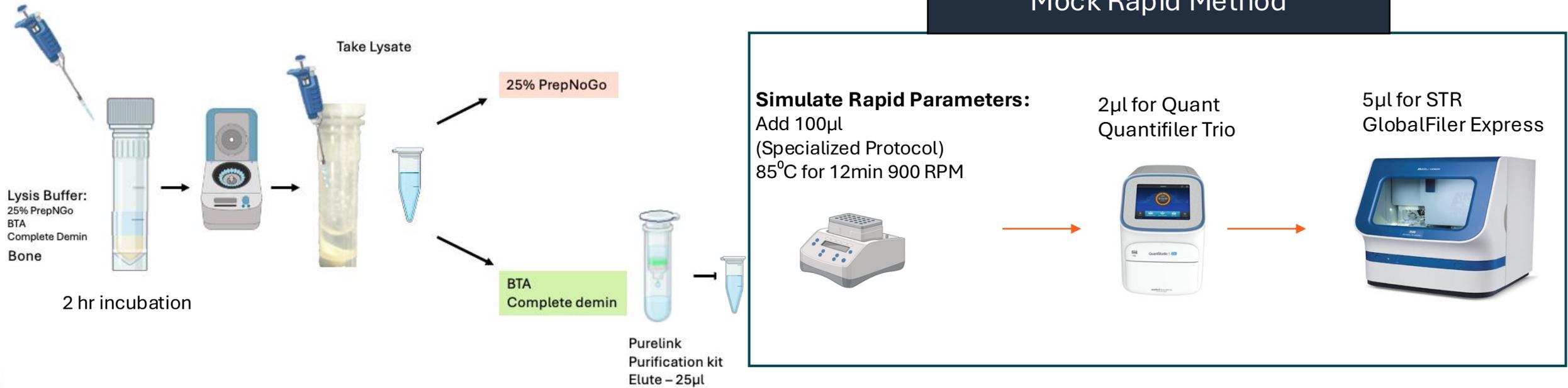


Rapid Workflow



Mock Rapid Workflow

RapidHIT ID System Parameters Mock Rapid Method



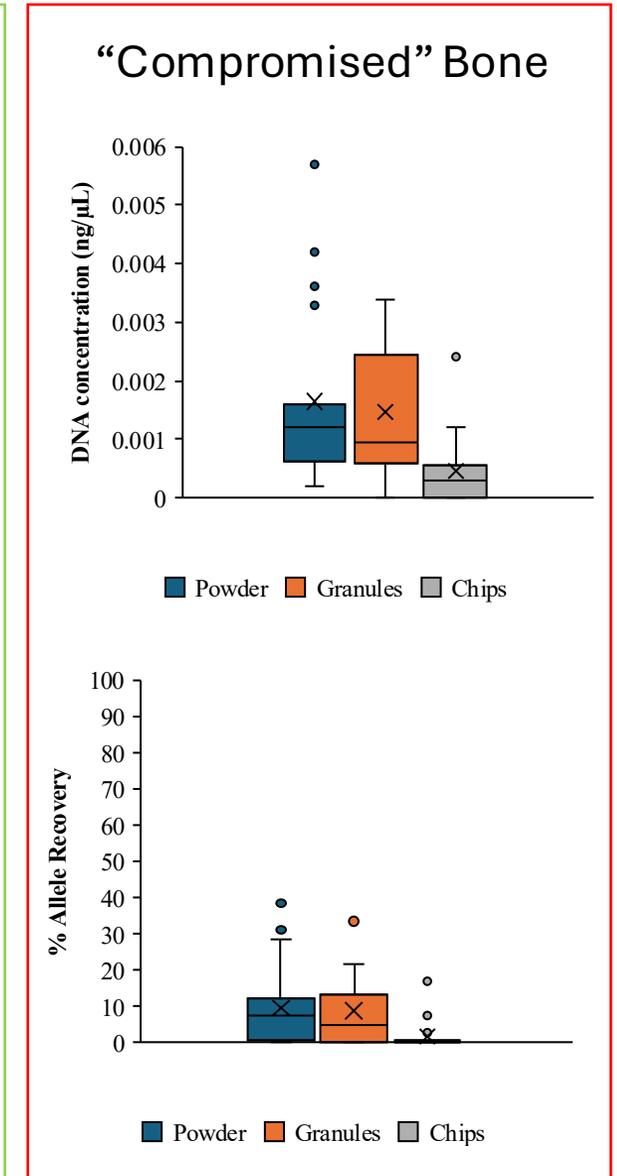
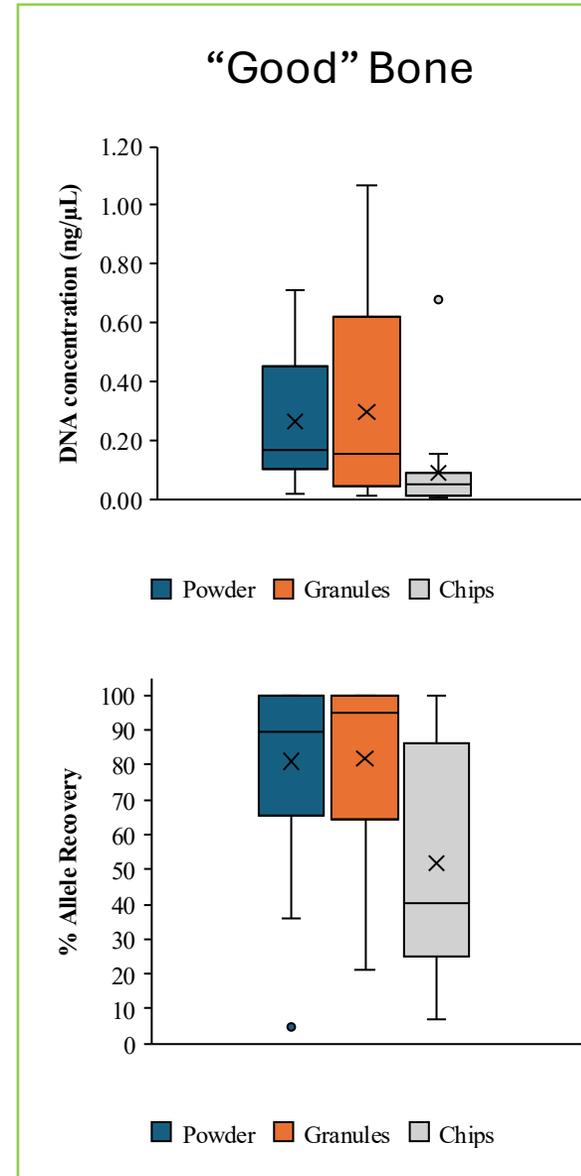
Comparison of Bone Consistencies

“Good” Bone

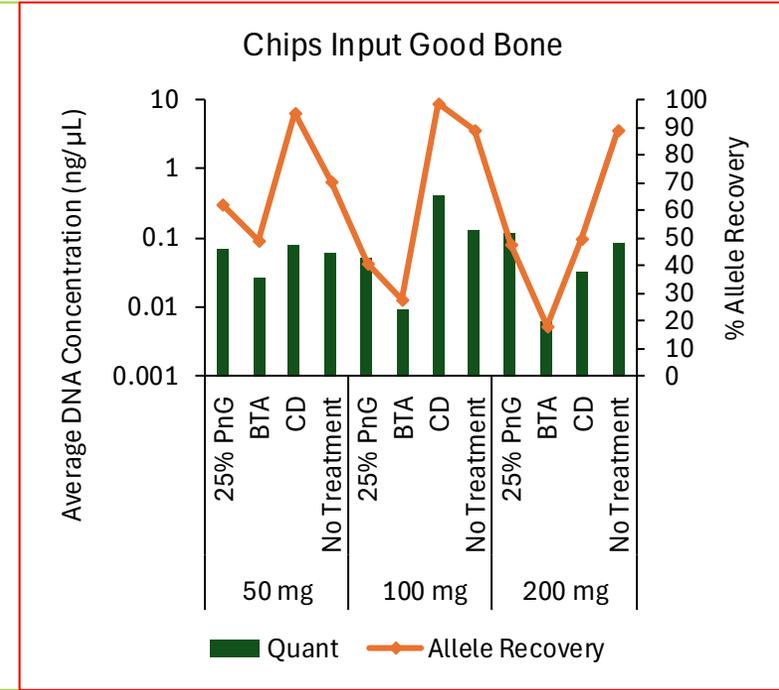
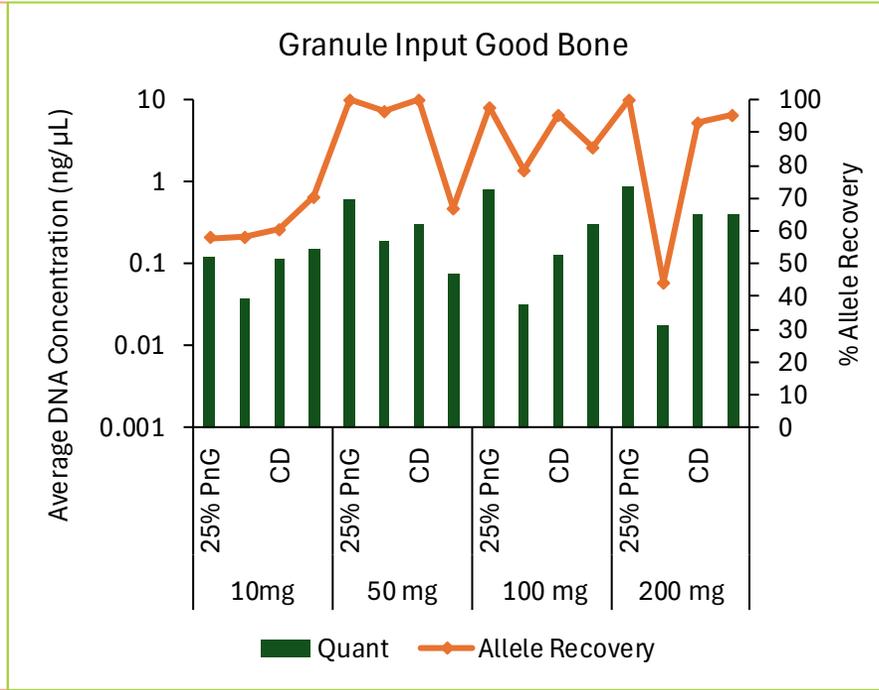
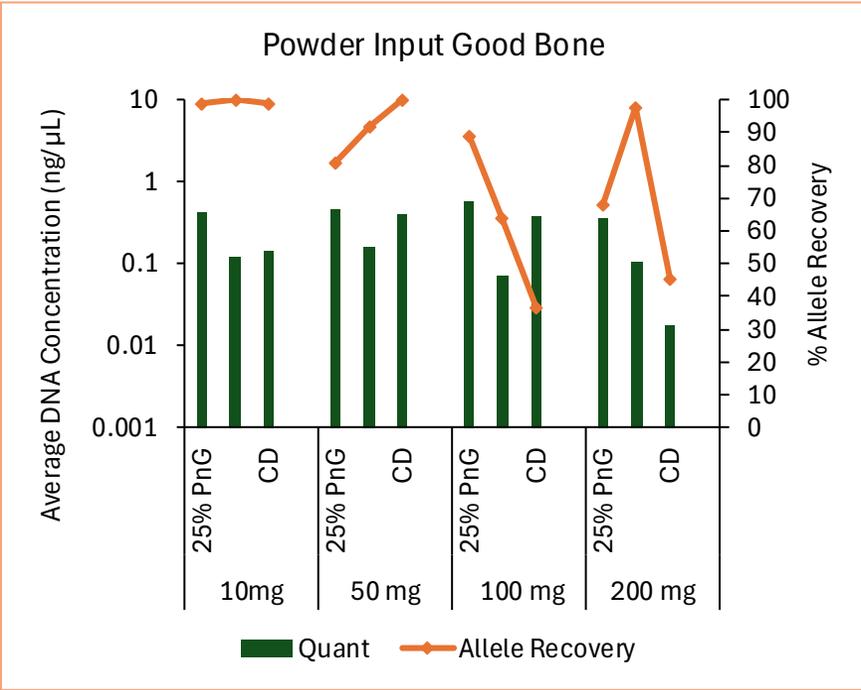
- Bone consistency had a significant effect on DNA concentration ($p < 0.05$)

“Compromised” Bones

- Low quantities and partial STR profiles
- Chips were the least successful



Bone Consistency Comparison



10 mg Powder performed most consistently among all pretreatments

Granules performed the most consistently with 50 mg or more input for DNA yield and STR recovery

No general trends observed



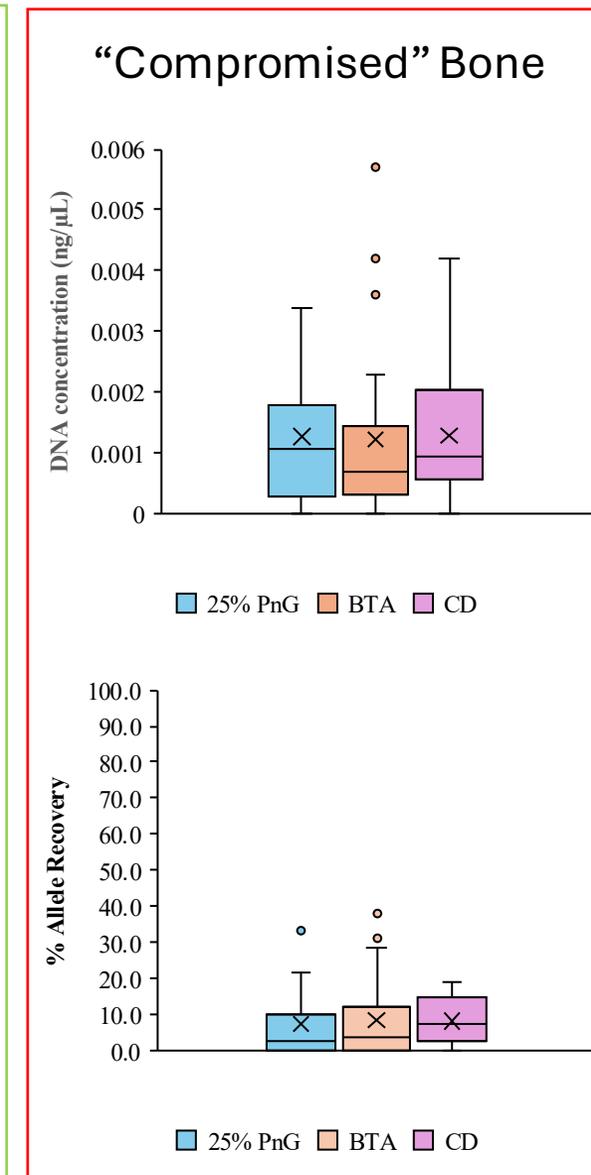
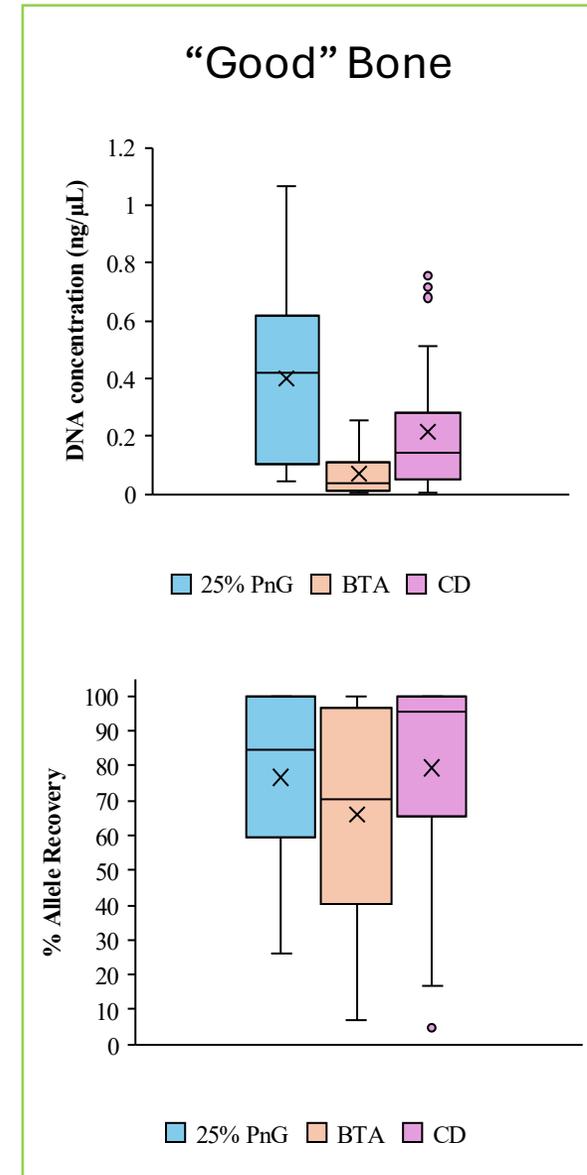
Comparison of Pretreatments

“Good” Bone

- DNA concentrations were significantly different with 25% Prep-n-Go buffer compared to other methods ($p < 0.05$)

“Compromised” Bone

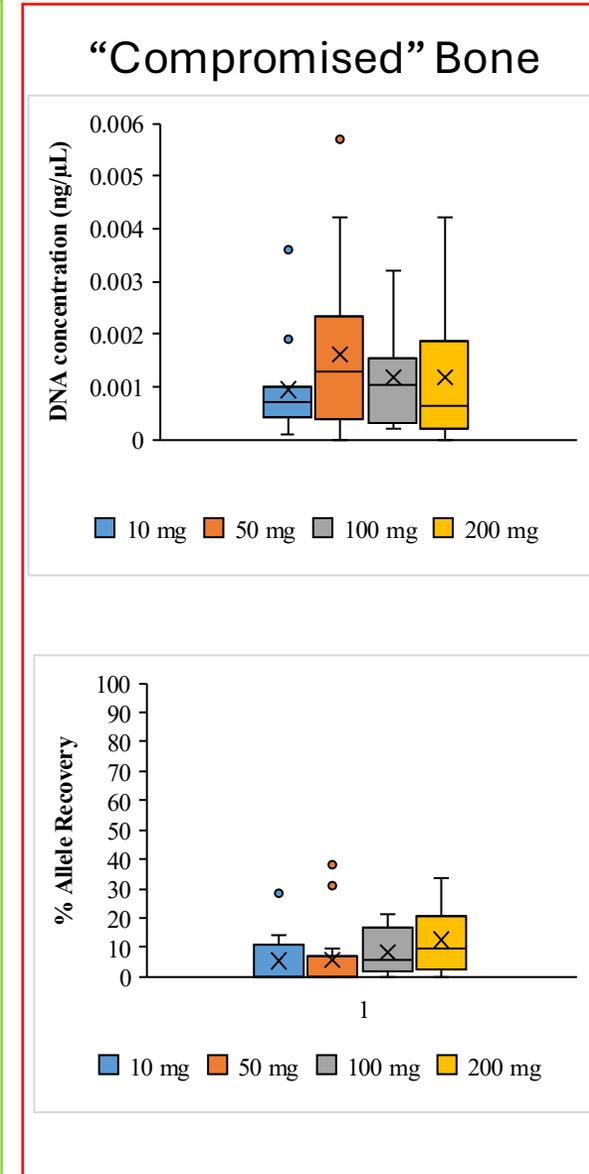
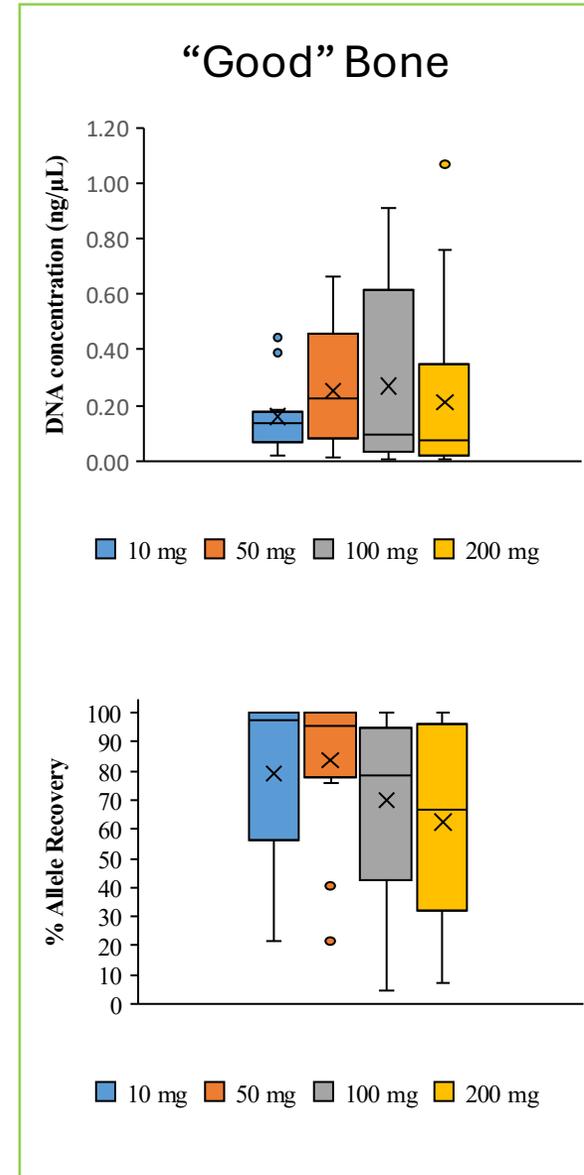
- No significant difference was observed between pretreatments ($p > 0.05$)



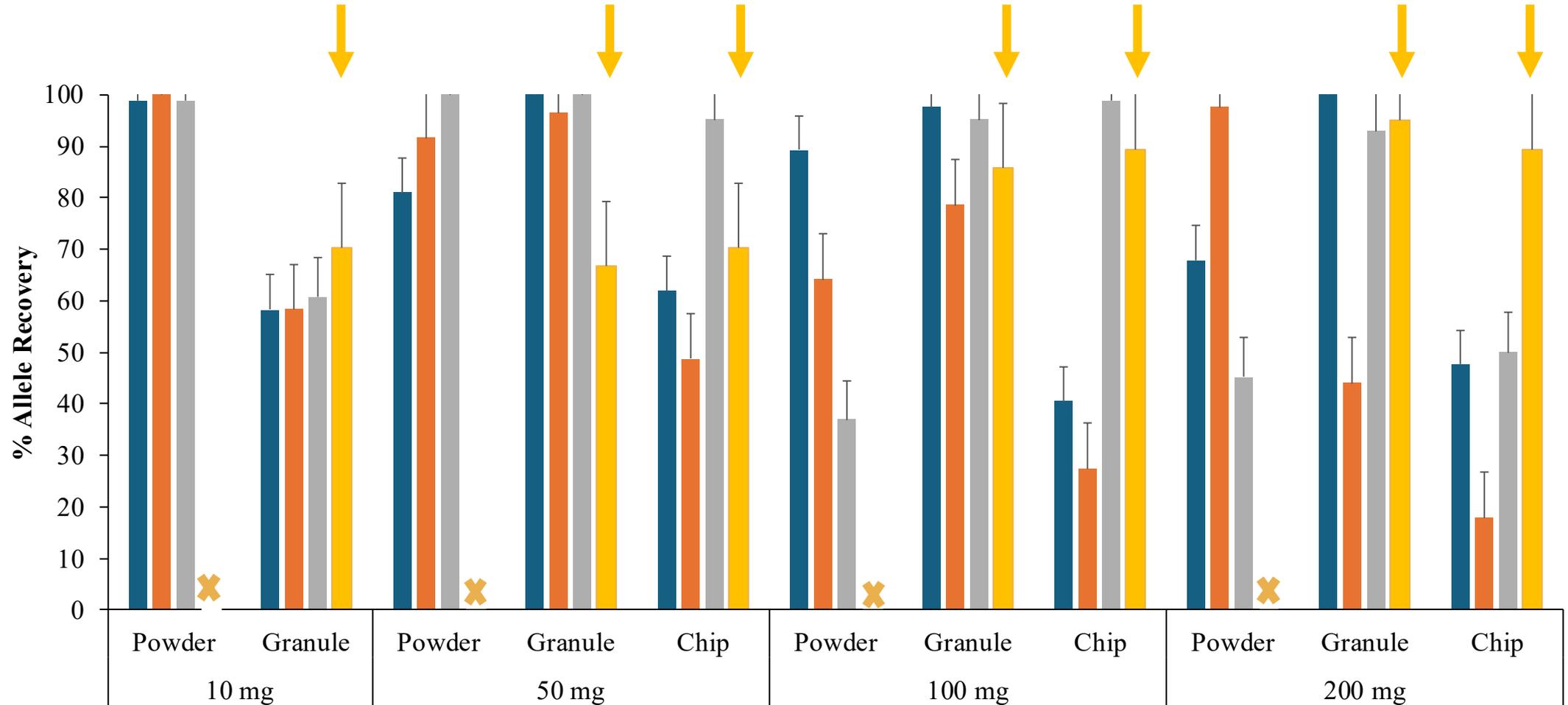
Comparison of Bone Inputs

- Regardless of pretreatment, the amount of starting bone mass did not make any statistically significant difference to DNA yield or STR recovery
- Only 5 μL was inputted into our mock rapid method

Bone Amount	Powder (μL)	Spice Grinder (μL)	Chips (μL)
10 mg	100	100	N/A
50 mg	200	200	200
100 mg	400	300	300
200 mg	600	400	400



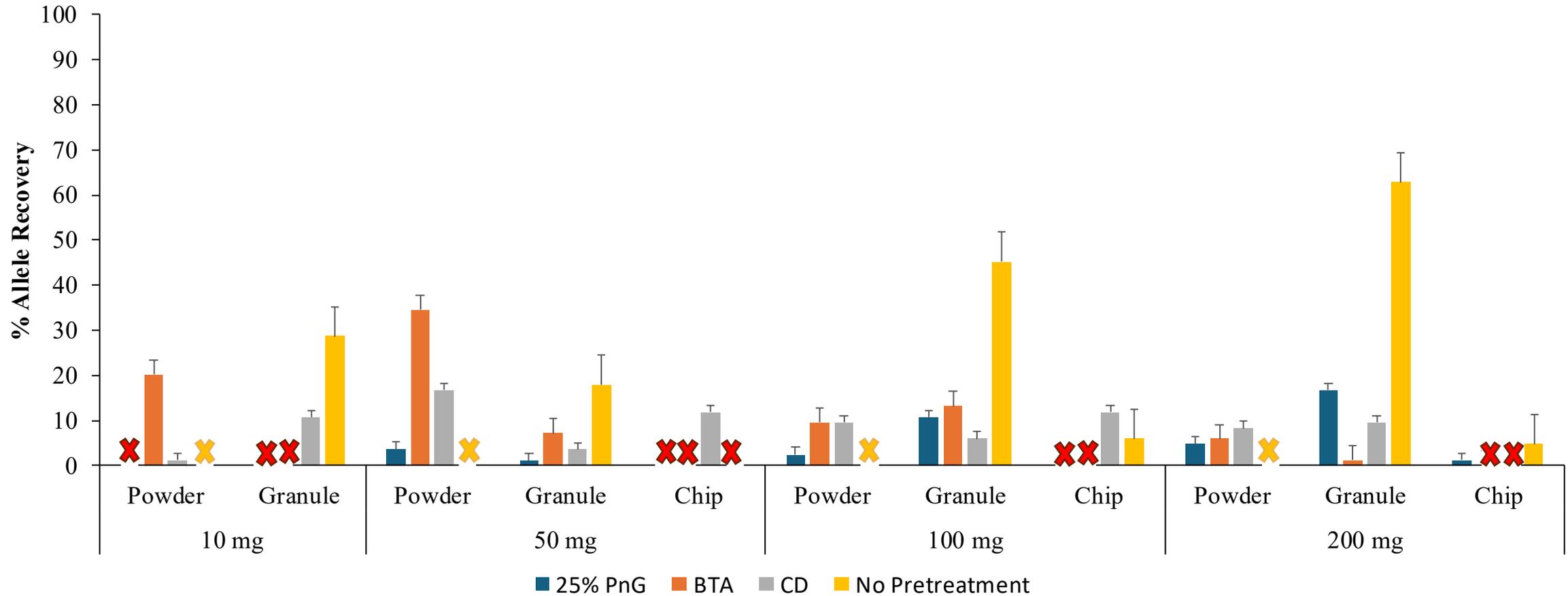
Allele Recovery Summary for “Good” Bone



No powder tested for no treatment
 Performed in duplicate; error bars represent standard error

No pretreatment samples yielded only near-complete profiles

Allele Recovery Summary for “Compromised” Bone



No powder tested for no treatment
 Performed in duplicate, error bars represent standard error

Pretreatment did not improve STR recovery

Testing the “Mock Rapid” Method

Mock Rapid

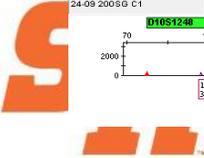
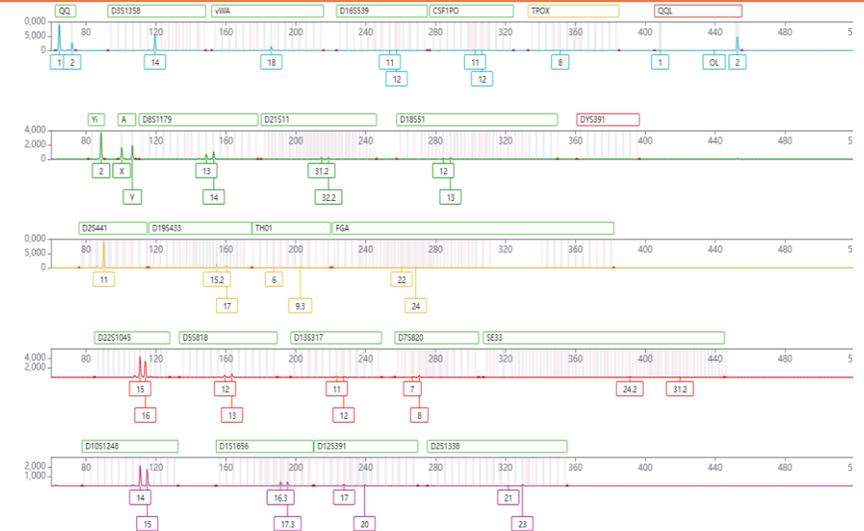
- Allele Recovery: 97.6%
- DNA input from Trio: 1.93 ng
- DI value: 126

RHID

- Allele Recovery: 95.2%
- DNA input: 4.99 ng
- Degradation flagged

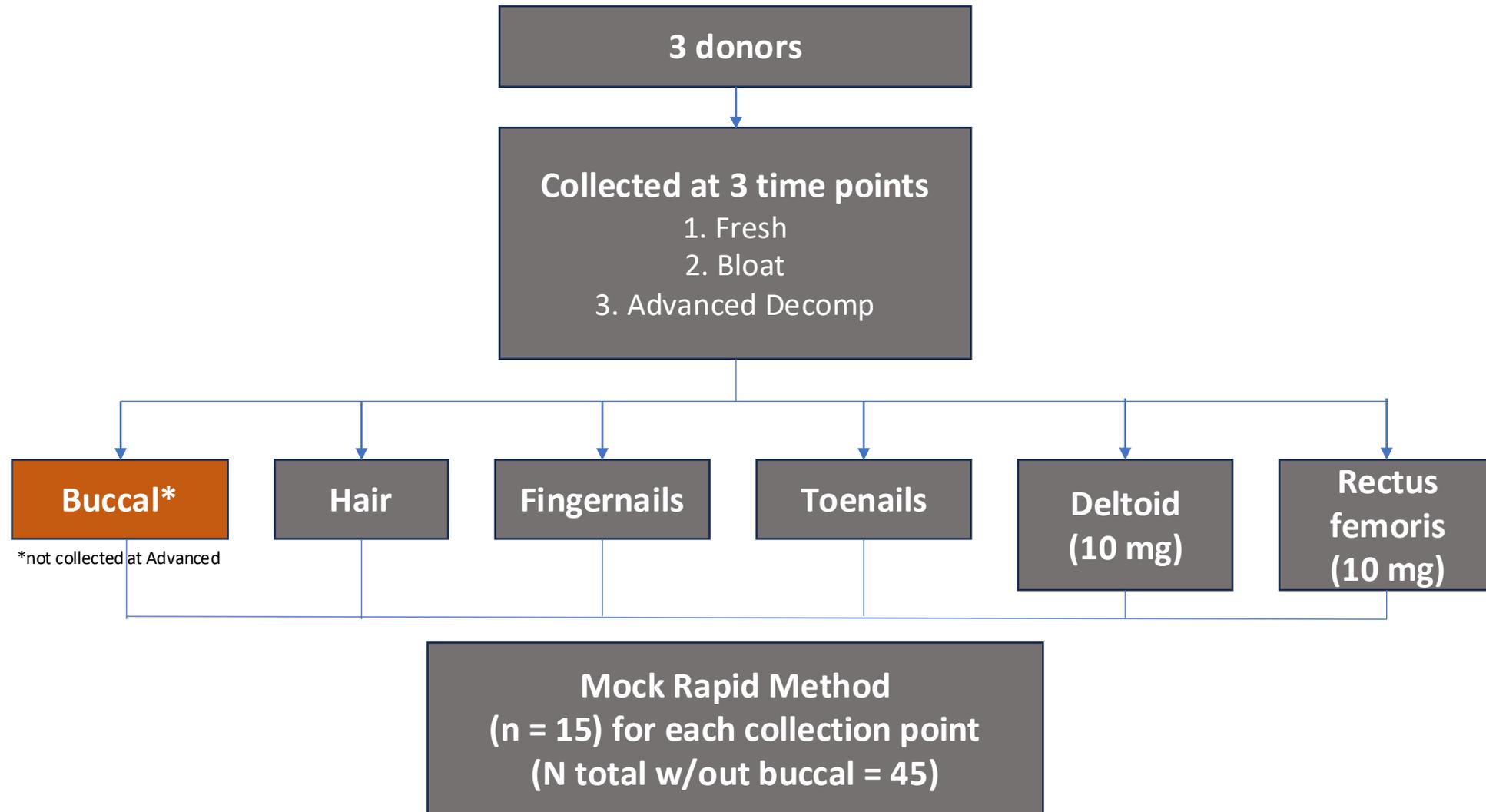


■ SQ: 1
 ● CGQ
 ● STO
 ▲ DEG
 | QTS: 4990 pg | QTL: 68 pg



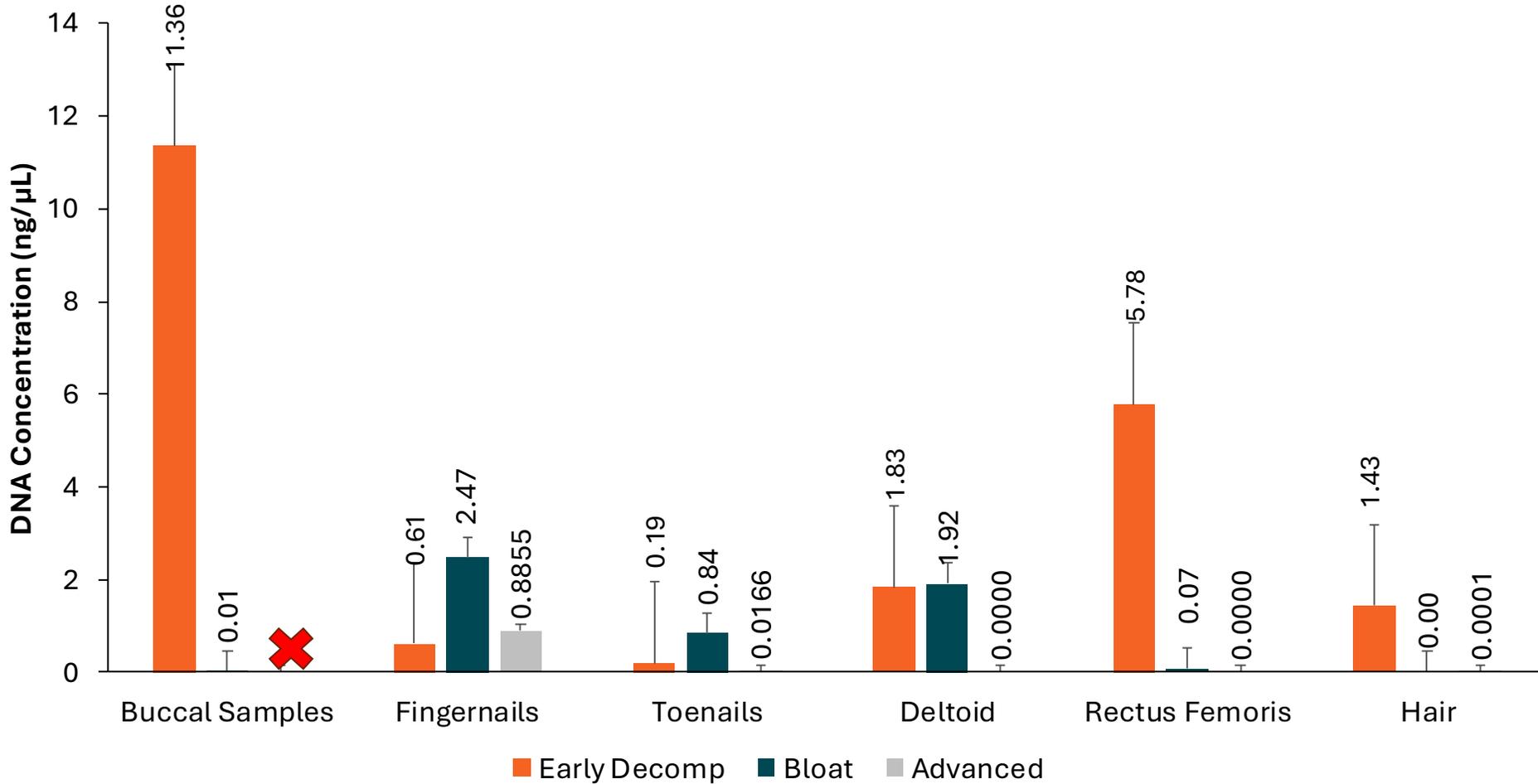


Workflow Cadaveric Samples



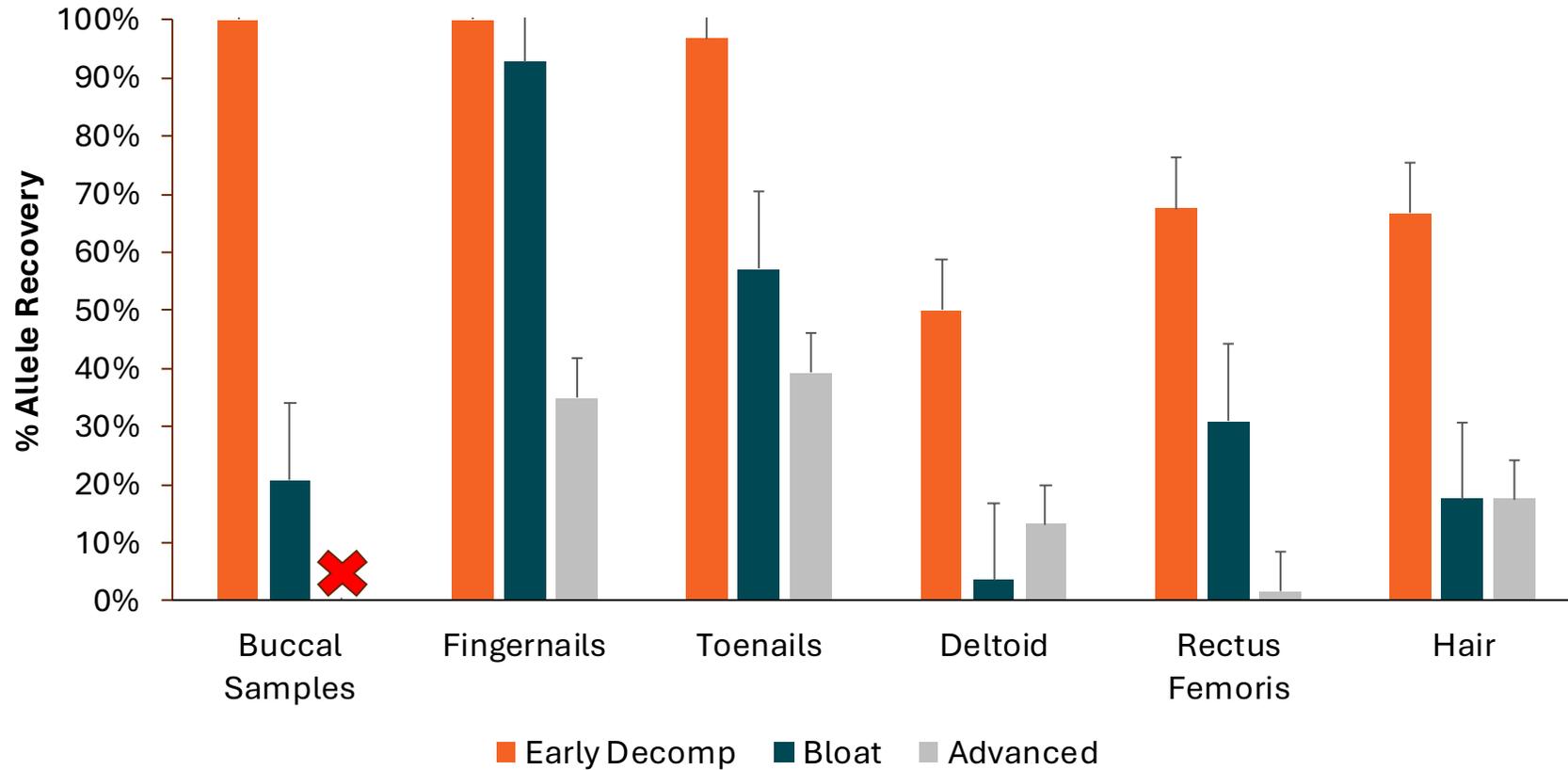


Quantification Data for Cadaveric Samples Mock Rapid Method





CE Results for Cadaveric Samples Mock Rapid Method



Nails best for Bloat



Conclusions

Bone Pretreatment

- Spice grinder is the way to go
 - Saves time and resources compared to powdering
- May increase recovery with 25% Prep-n-Go buffer, but pretreatment may not always be necessary

Cadaveric Samples

- Buccal samples and nails are viable options for up to the Bloat phase
- Future work should test more samples
- Once in the Advanced phase, traditional methods should be performed
- Rapid is a valuable tool, but traditional methods might be the best

Mock rapid method serves as an option for triaging samples to save time and cost



References

1. Law Enforcement Resources. FBI. <https://le.fbi.gov/science-and-lab/biometrics-and-fingerprints/codis/rapid-dna#:~:text=Rapid%20DNA%2C%20or%20Rapid%20DNA,any%20human%20intervention%20and%20review>
2. Guide to All Things Rapid DNA. FBI. <https://le.fbi.gov/file-repository/rapid-dna-guide/view>
3. Ramos, Erica, Moreno, Liliana, and Hares Douglas. Results of the 2023 Rapid DNA Multi-laboratory Study – RapidINTEL Plus Sample Cartridge. <https://doi.org/10.1016/j.fsir.2024.100396>

Thank you!

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Questions

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