

Recovery of Human DNA from Maggots

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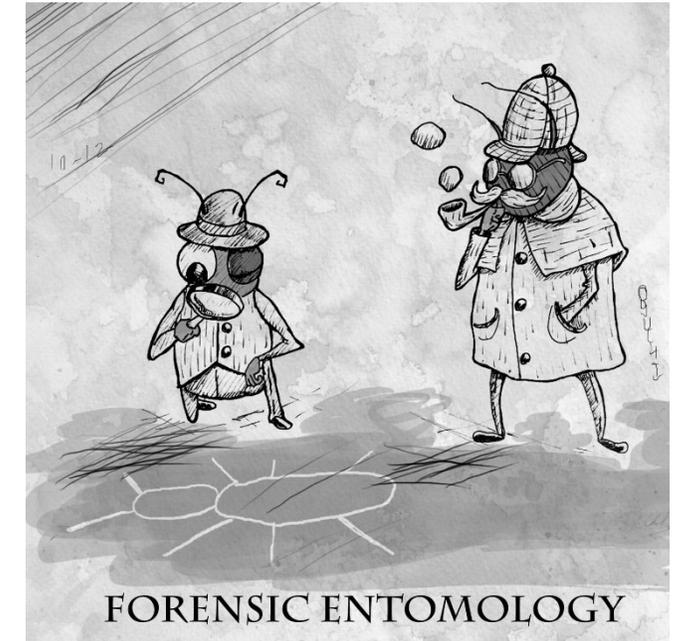


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Forensic Entomology

- Application of insects to criminal and civil investigations
- Post-mortem Interval (PMI)
 - Insect Succession
 - Accumulated Degree Hour (ADH)
- DNA Analysis
 - Insect Species Identification
 - **Human DNA^[1,2]**



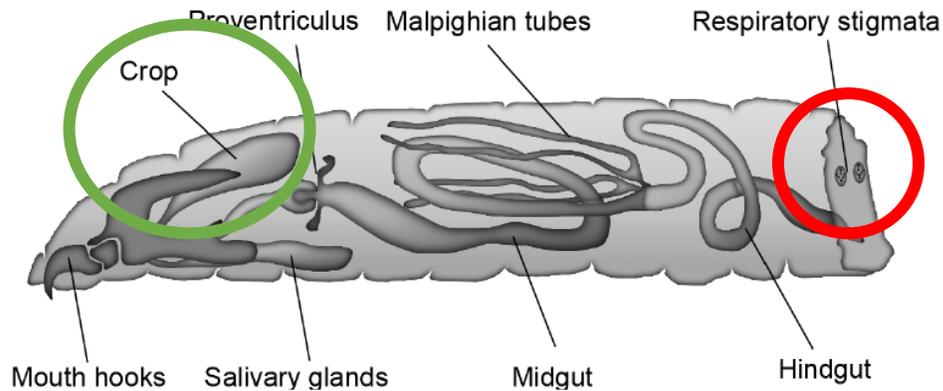
Forensic Entomology (Student Magazine Illustration). Oguchi Anyaele. (n.d.). <https://oguchiart.artstation.com/projects/3oIm22> (accessed February 5, 2021).



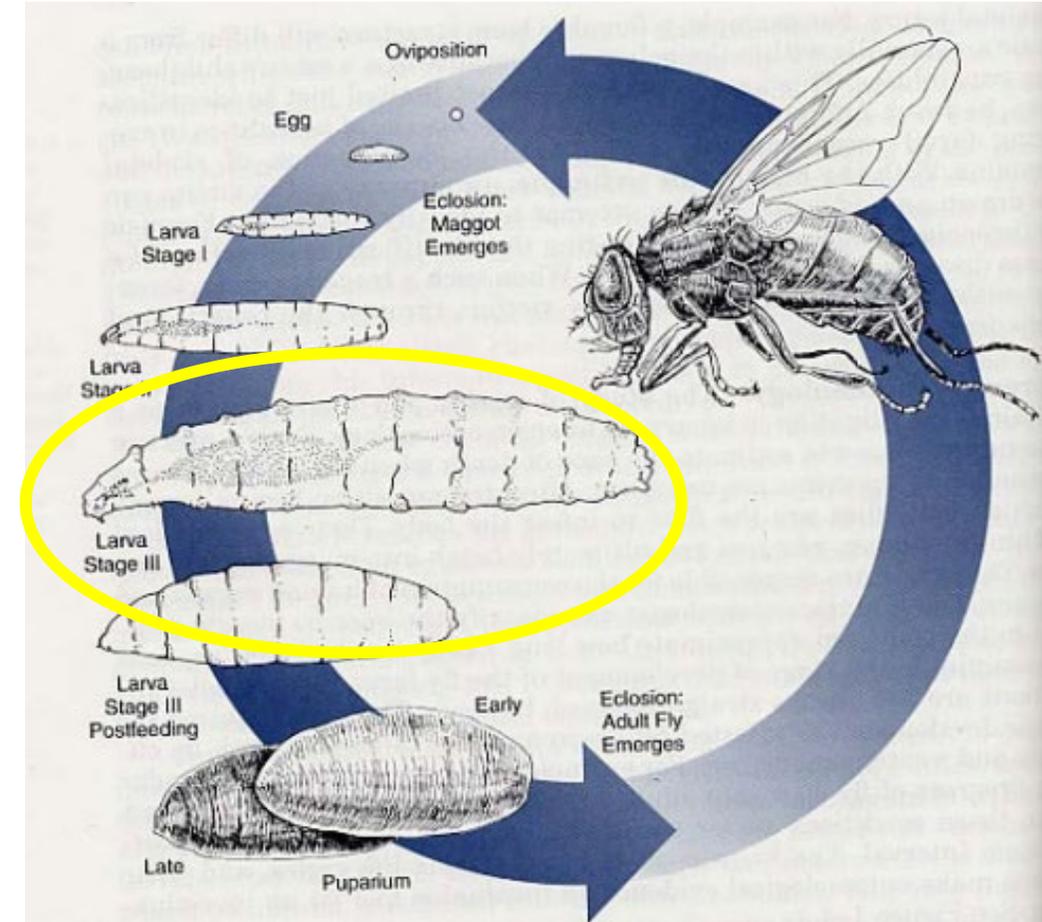
O'Brien, Jennifer. "Smell That? It's Forensic Entomology At The Body Farm." Science Friday, <https://www.sciencefriday.com/educational-resources/forensic-entomology-body-farm/>. Accessed 3 Nov. 2020.

Fly Larvae

- Family Calliphoridae
 - Blow flies
 - Forensically relevant
- Morphological Identification
 - Posterior spiracles
- Crop: food storage with little to no digestion



A. Baumann, New tools for maggot debridement therapy research: From the establishment of qRT-PCR to the characterization of *Lucilia sericata* Urate Oxidase, (n.d.) 90.



Cannon K, Cannon M. Analysis of Entomological Specimens Recovered Under Ancient Bison Carcasses and Recent Dead Large Animal Carrion from the Salmon River Bison Jump Area in Eastern Idaho June, 2007. 2015.

Recovery of human DNA from maggots

- Possible to recover human DNA from maggots^[1-9]
 - Criminal cases in China and Mexico^[4,10]
- Uses:
 - Identification of a victim
 - Link deceased to a scene^[11]
- Studies have shown:
 1. Crop preferred^[2]
 2. Preservation method^[5]
 3. Third instar maggots^[2]
 4. Purification of extract^[12]



Goal: Determine best extraction method and forensic genotyping methods for analysis of human DNA recovered from a maggot

Methods

Collection and Dissection

Southeast Texas Applied Forensic Science (STAFS) Facility

DNA Extraction

DNeasy® Powersoil® Pro (QIAGEN) (n=10)
Crops and Whole Fly Larvae

EZ2™ DNA Investigator® (QIAGEN) (n=10)

QIAcube® Connect (QIAGEN) (n=10)

Postfeeding (n=5)
Whole Fly Larvae

Burned (n=5)

Human DNA Quantification
Quantiplex® Pro (QIAGEN)

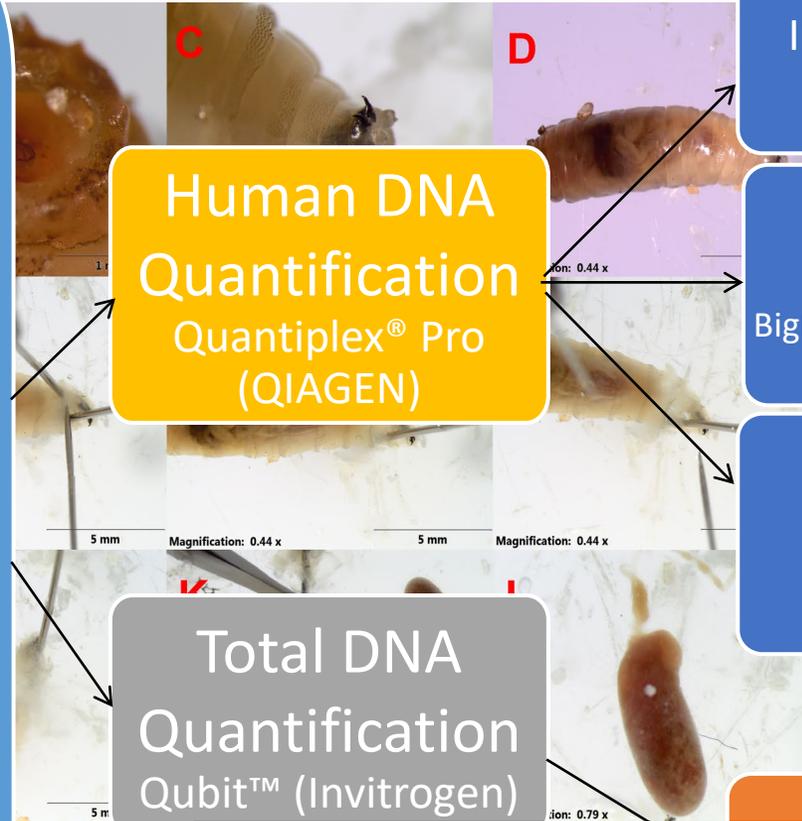
Total DNA Quantification
Qubit™ (Invitrogen)

STR
Investigator® 24plex (QIAGEN)

mtDNA
HV1 and HV2
BigDye Direct Cycle Sequencing Kit (Applied Biosystems)

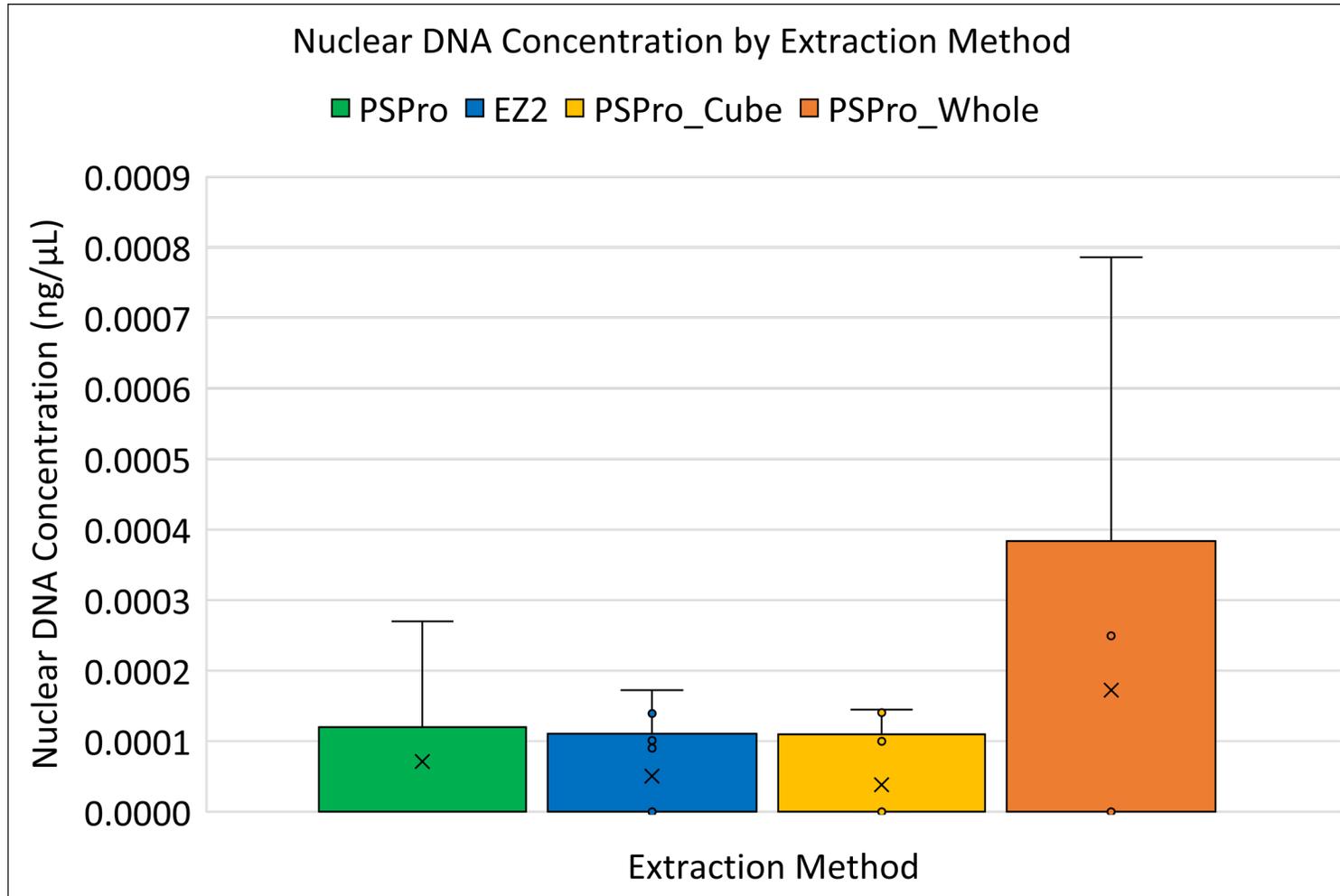
NGS
Mainstay SE (Verogen)

DNA Barcoding
COI



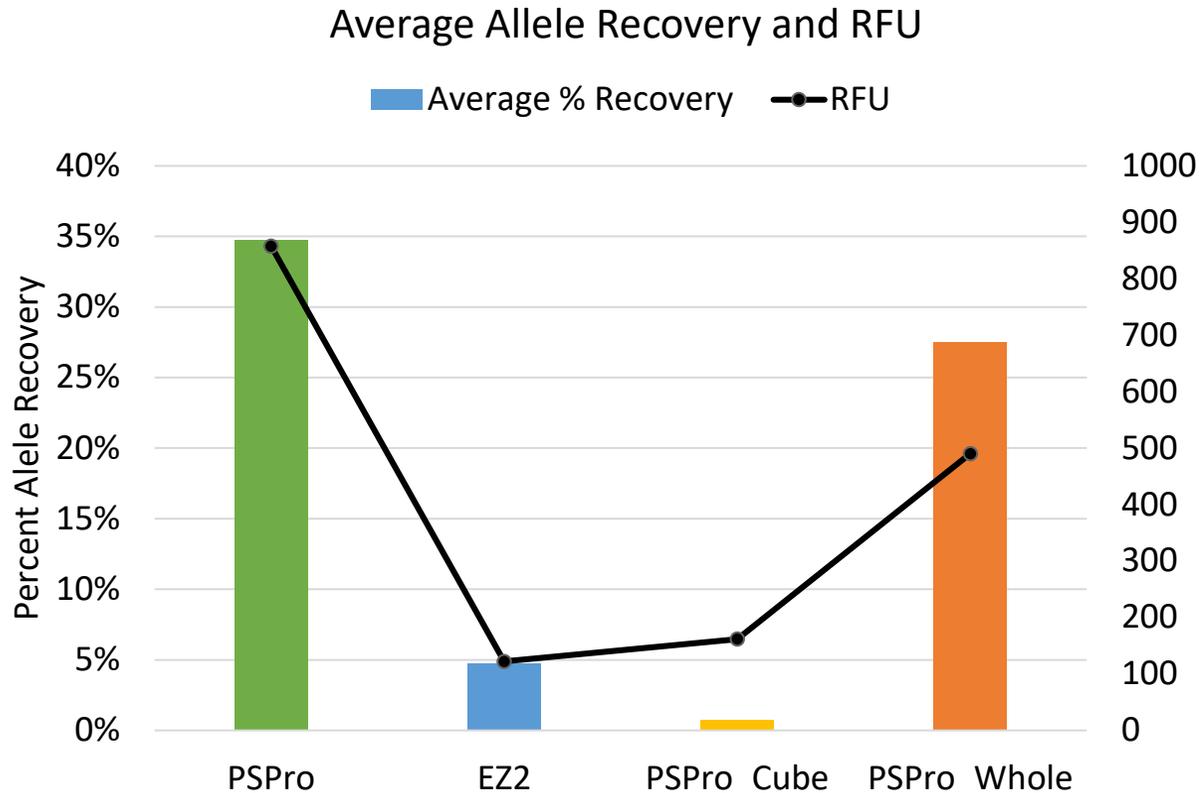
Cantu C, Bucheli S, Houston R. Comparison of DNA extraction techniques for the recovery of bovine DNA from fly larvae crops. JFS 2022;67(4):1651-9. <https://doi.org/10.1111/1556-4029.15010>

Extraction Method Results



- No significant difference between human DNA recovered
- Powersoil Pro with manual purification was more consistent in recovering human DNA
- No trend observed between crop weight (g) and DNA concentration^[2]

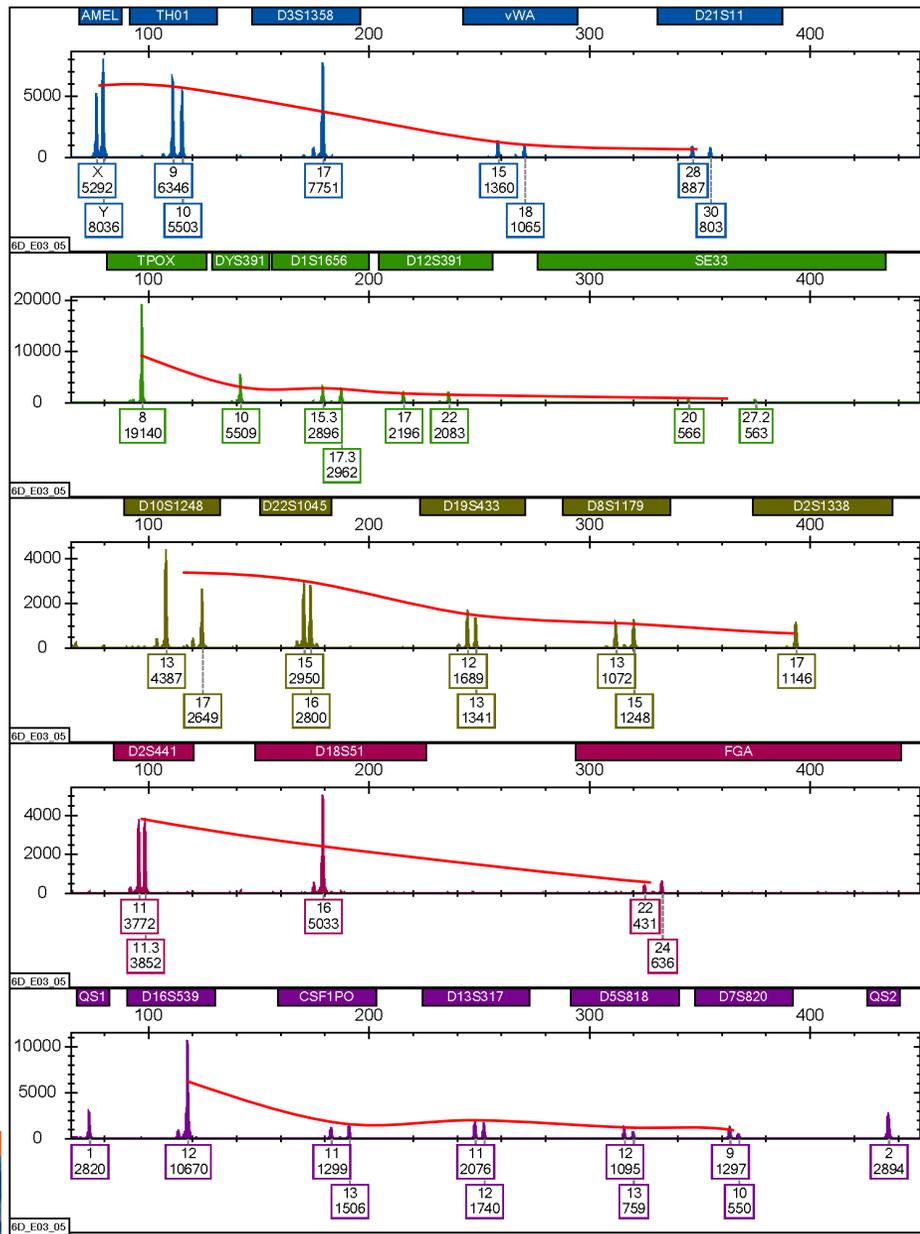
STR Profiling Success



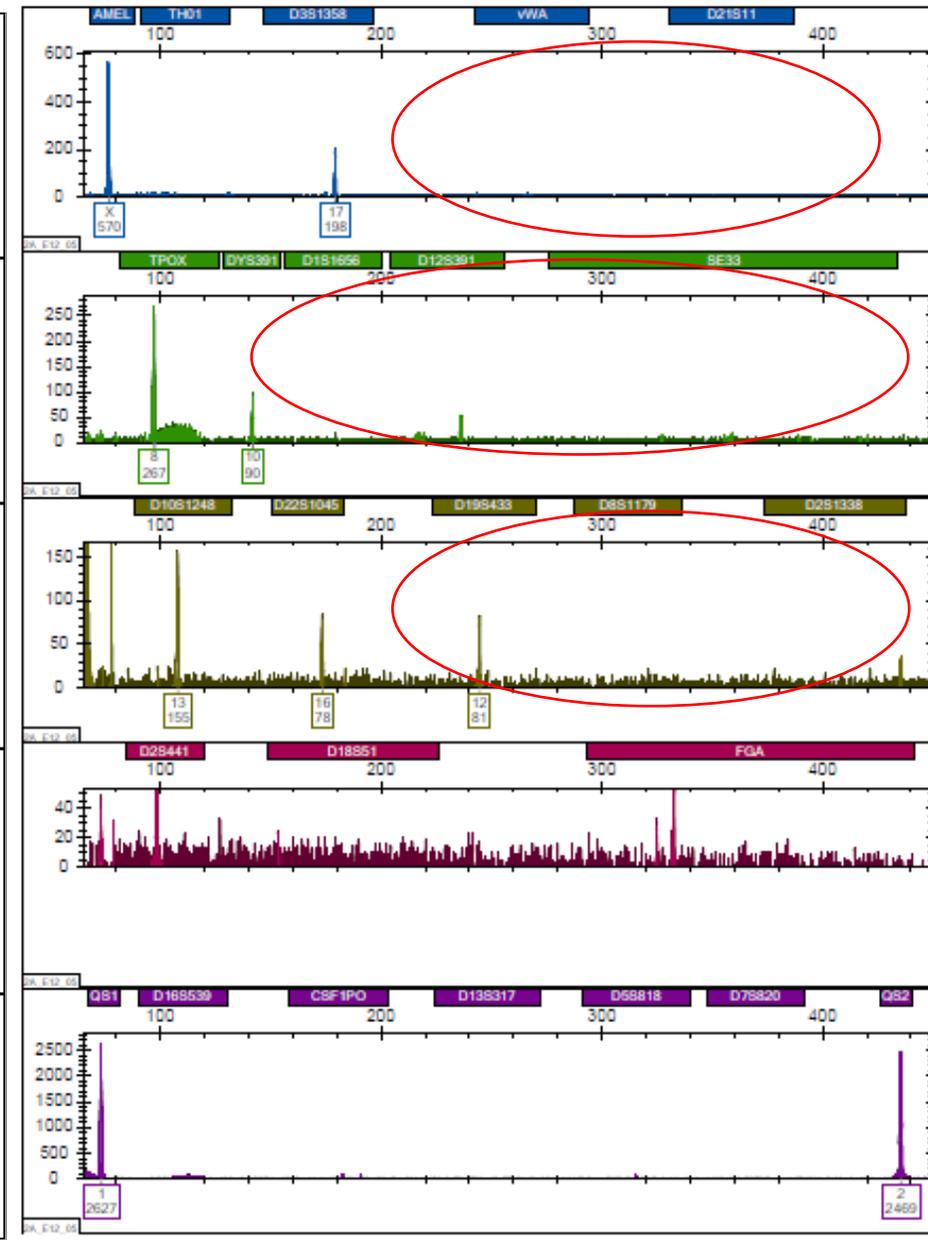
- CODIS eligible samples produced by PowerSoil Pro extractions
 - Crop, Whole, and Post-feeding samples
- Automation could be detrimental to human DNA recovery
- Degradation
 - Consumption by fly larvae and decomposition

STR Profiling Success

Full Profile
Powersoil Pro



Partial Profile
Powersoil Pro

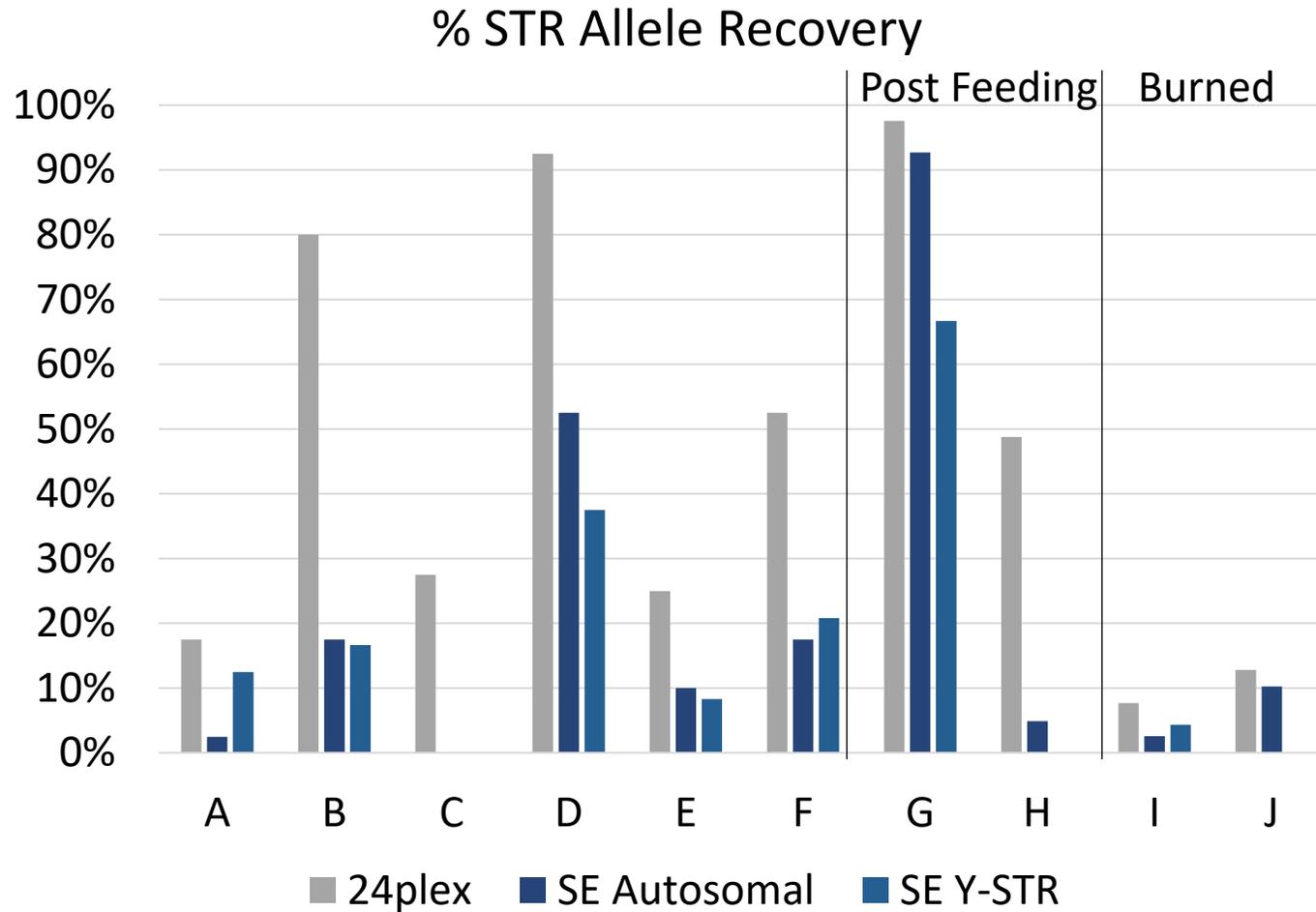


mtDNA

Sample	Extraction	Type	Small Target Quant	% STR Allele Recovery	Haplotype
1	PSPPro	Crop	0.0001	2.5	U4b1+146+152
2	PSPPro	Crop	0.0011	80	U4b1+146+152
3	PSPPro	Crop	0.0003	27.5	U4b1+146+152
4	PSPPro	Crop	0.0000	2.5	U4
5	EZ2	Crop	0.0001	0	U4b1+146+152
6	EZ2	Crop	0.0000	7.5	U4b1+146+152
7	EZ2	Crop	0.0002	27.5	U4b1+146+152
8	PSPPro_Cube	Crop	0.0001	5.0	U4b1+146+152
9	PSPPro_Cube	Crop	0.0001	0	R8
10	PSPPro_Cube	Crop	0.0001	2.55	U4b1+146+152
11	PSPPro	Whole	0.0000	2.5	U4b1+146+152
12	PSPPro	Whole	0.0002	0	U4b1+146+152
13	PSPPro	Postfeeding	-	4.9	V+@16298
14	PSPPro	Postfeeding	-	0	H2a2a
15	PSPPro	Postfeeding	0.0003	0	H2a2a
16	PSPPro	Burned	0.0003	7.7	H7d2
17	PSPPro	Burned	0.0001	12.8	H7d2
18	PSPPro	Burned	0.0002	5.1	H7d2
19	PSPPro	Burned	0.0003	12.8	H7d2

- mtDNA typing successful for samples with little to no quantifiable nuDNA
- Alternative method when STR typing yields no results

NGS-Mainstay SE



- Significant difference between autosomal STR recovery ($p < 0.05$)
- Required minimum DNA input could not be met for NGS

Species ID Barcoding

Sample	Month Collected	Extraction	Sample	Stage	BLAST Result
20	April				
21	April				
22	April	Powersoil Pro			
23	April				
24	April				
25	Apr				
26	Apr				
27	Apr	EZ2			
15	Septem				
17	June/				

ate species ID

an mtDNA did not
any interference

concordance with
ells et al. (2001)

time *Phormia regina*
been used for the
ry of human DNA

mples resulted in
quality sequencing
equence was still
ible

Post-mortem Interval Estimation

- Species specific development rates can be used for PMI estimation
 - *Phormia regina*
 - Minimum PMI estimation of 5-9 days
 - Actual PMI= 11 days
 - Improve PMI estimation with more data

Stage	ADH	
	Byrd et al.(2001) ⁺	Núñez-Vázquez et al. (2013)*
First Instar	380	800
Second Instar	720	1,480
Third Instar	1,240	2,040
Prepupa [^]	1,600	3,880
Pupa	3,760	6,000
Adult	7,160	10,520

+ Byrd et al. reported a range in hours

[^]Prepupa include postfeeding/wandering fly larvae

*Prepupa combined with third instar

	Date	Average Temperature (°C)	ADH
1	4/1/2022	17.50	180.00
2	3/31/2022	15.56	313.33
3	3/30/2022	19.17	533.33
4	3/29/2022	25.00	893.33
5	3/28/2022	22.78	1,200.00
6	3/27/2022	23.06	1,513.33
7	3/26/2022	20.28	1,760.00
8	3/25/2022	18.06	1,953.33
9	3/24/2022	13.61	2,040.00
10	3/23/2022	14.17	2,140.00
11	3/22/2022	15.83	2,280.00

Byrd et al. { 1-6 }
 Núñez-Vázquez et al. { 7-11 }

Conclusion

- Use of crops and whole fly larvae can yield investigative information
 - Whole fly larvae benefits: gross dissection and post-feeding fly larvae
- STR and mtDNA results in agreement with other studies^[4-7,9,10,15,16]
 - Recovery of full and CODIS eligible partial profiles only from Powersoil Pro
- First time in which NGS has been attempted on human DNA recovered from fly larvae
 - Hindered due to low DNA input

Conclusion

- First report of *Phormia regina* in the recovery of human DNA from fly larvae
- Post-feeding fly larvae can be used, even if no crop is visible
 - Digestive tract could have human DNA that can be recovered
- Future work includes reattempting NGS with better samples



HUMAN

- Identity- STR or NGS
- Ancestry- mtDNA or NGS
- Phenotype- SNPs



SPECIES
IDENTIFICATION

- Aid Post-mortem Interval Estimation
- Geographical Origin

Acknowledgements

We would like to acknowledge the Southeast Texas Applied Forensic Science Facility and the donors and their loved ones, without whom this research would not be possible.

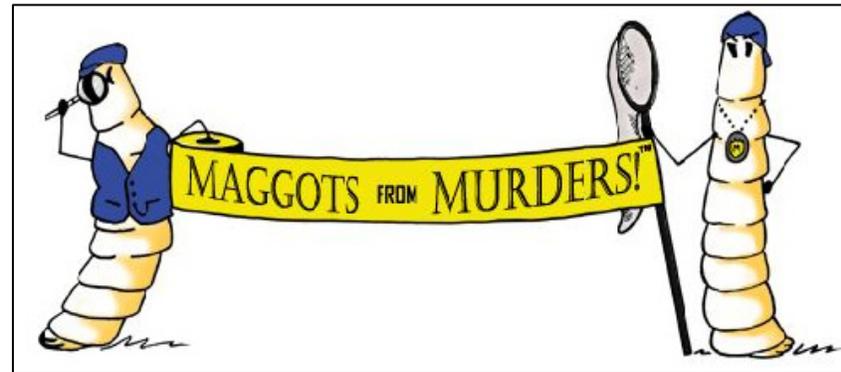


Thanks to the Department of Forensic Science and the Department of Biological Sciences at Sam Houston State University.

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Questions?



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