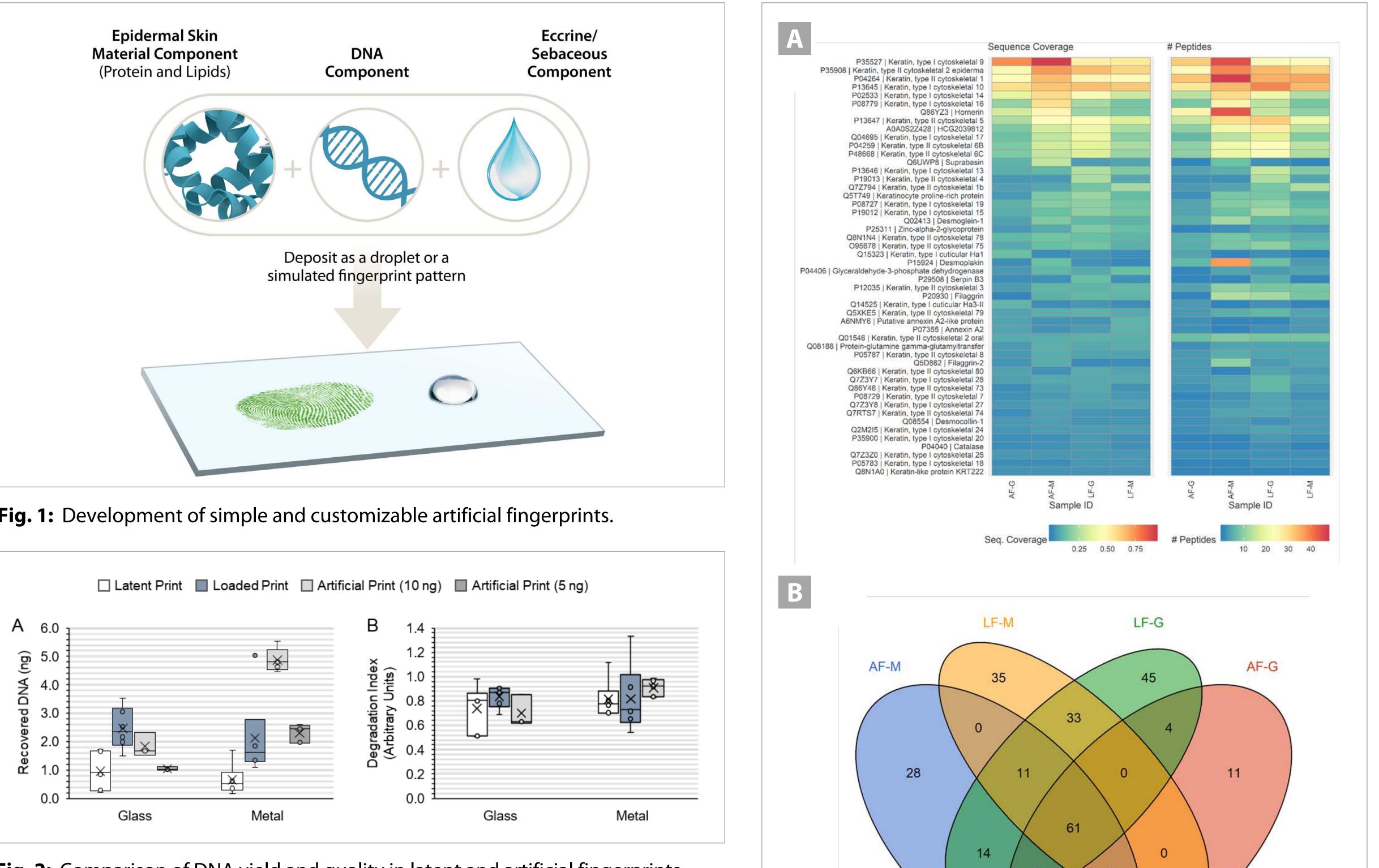
Artificial Fingerprints for Reproducible Development of Touch Sample Analysis Methods

F. Curtis Hewitt, Danielle S. LeSassier, Myles W. Gardner Kathleen Q. Schulte, Tara E. Manley, Alan R. Smith, Megan L. Powals, Nicolette C. Albright, Benjamin C. Ludolph, Katharina L. Weber

Background

Quantitative evaluation of human latent fingerprint depositions represents a major challenge within the forensic field due to high variability in the amount of DNA and protein deposited with each touch.¹



Objective

To better assess the effectiveness of collection and analysis methods for touch depositions, we present a method to produce simple and customizable artificial fingerprints. These artificial fingerprints include the primary components of a typical latent fingerprint, specifically sebaceous fluid, eccrine perspiration, extracellular DNA, and proteinaceous epidermal skin material (ESM) (i.e., shed skin cells).^{2,3,4,5,6}

Technical Approach

A commercially available emulsion of sebaceous and eccrine material provides a chemically-relevant suspension solution for fingerprint deposition, simplifying artificial fingerprint production. Extracted human genomic DNA is added to accurately mimic the extracellular DNA content of a typical latent print and we demonstrate comparable DNA yields from our artificial prints to both latent and loaded prints across multiple surface types. Capitalizing on recent advancements in the use of protein sequence identification for human forensic analysis, these samples also contain a representative quantity of protein, originating from ESM collected from the fingers and palms of volunteers.^{2,7,8,9}

Fig. 1: Development of simple and customizable artificial fingerprints.

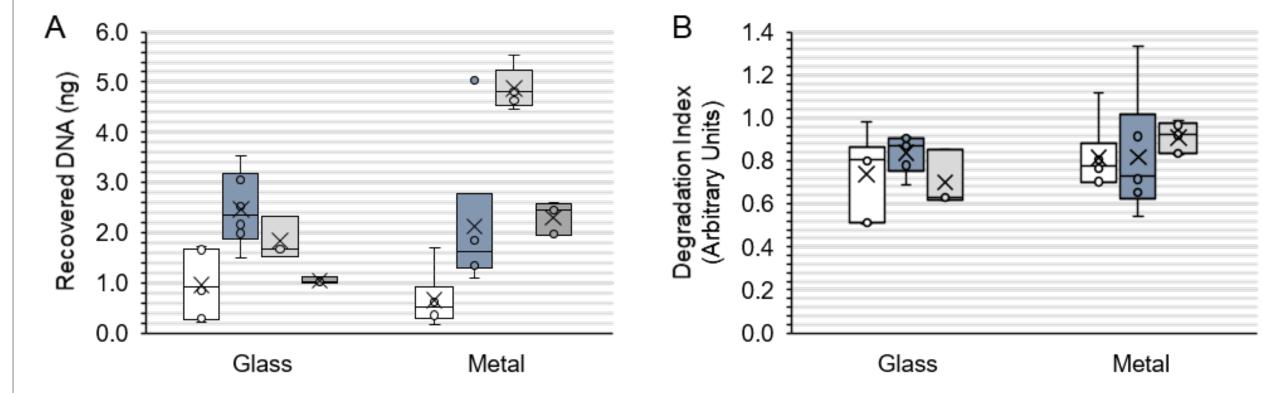


Fig. 2: Comparison of DNA yield and quality in latent and artificial fingerprints.

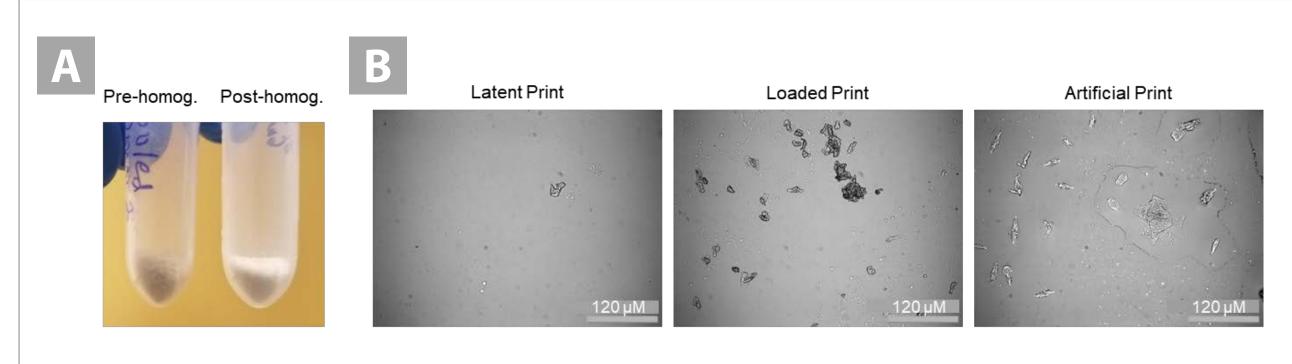
Results

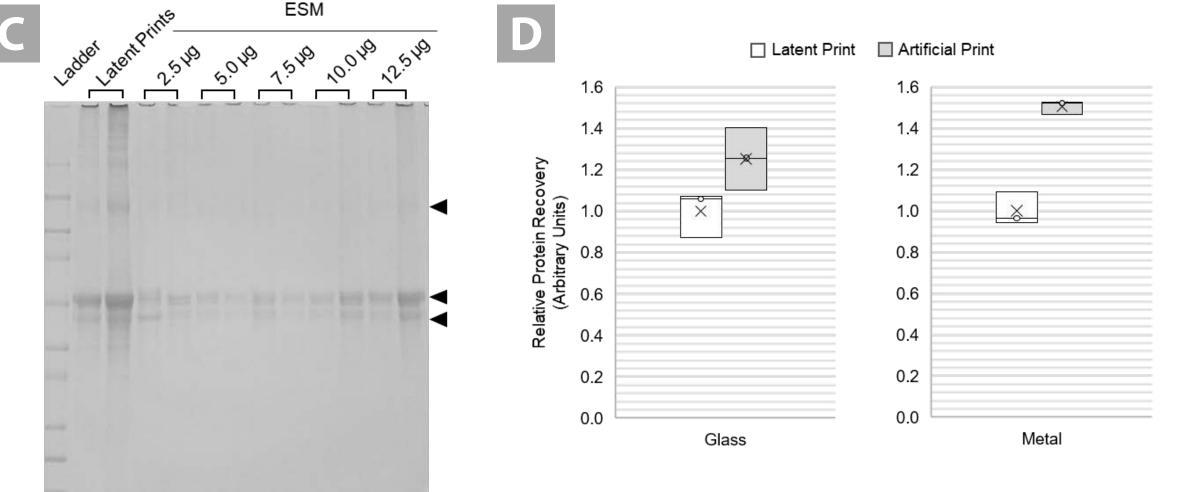
DNA analysis (DNA quantification and STR analysis) demonstrates similar reproducibility, quality, and overall DNA yield comparing between artificial and latent fingerprints. Liquid chromatographytandem mass spectrometry (LC MS/MS) analysis indicates a high level of protein similarity between artificial and latent prints. DNA and protein loadings into artificial prints can be precisely adjusted to mimic high or low "shedders."

Conclusions

Collectively, these artificial fingerprints produce samples that accurately represent typical human latent prints. By depositing known quantities of DNA and protein into each artificial print, this method enables total DNA and protein recovery to be quantitatively assessed across different sample collection and extraction methods to better evaluate extraction efficiency.

(A) Latent, loaded, and artificial fingerprints were deposited on various surfaces and then the DNA was extracted to evaluate the total yield. (B) Comparison of DNA degradation index across fingerprint deposition on multiple surface types (a value of > 1.0 indicates DNA degradation).







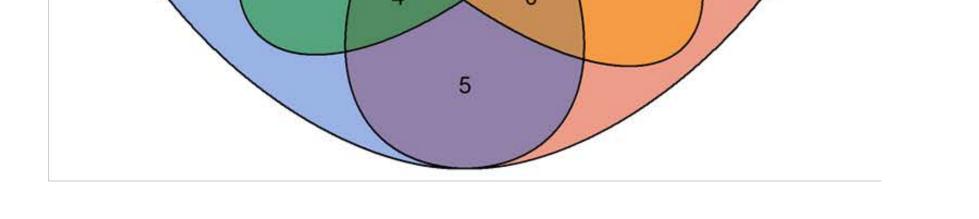


Fig. 4: Comparison of proteome composition between artificial and latent fingerprints. (A) Protein sequence coverage (left) and number of peptides (right) in the 50 most common proteins detected in artificial or latent fingerprint samples. (B) Overlap of total peptides detected among proteins in artificial (AF) or latent (LF) fingerprint samples on metal (M) or glass (G) surfaces.

Acknowledgements

This research is based upon work supported in part by the Office of the Director of National Intelligence (ODNI), Intelligence Advanced Research Projects Activity (IARPA), via contract number 2018-18041000003. The views and conclusions contained herein are those of the authors and should not be interpreted as necessarily representing the official policies, either expressed or implied, of ODNI, IARPA, or the U.S. Government. The U.S. Government is authorized to reproduce and distribute reprints for governmental purposes notwithstanding any copyright annotation therein.

References

- 1. Burrill J, Daniel B, Frascione N. A review of trace "Touch DNA" deposits: Variability factors and an exploration of cellular composition. Forensic Sci Int Genet. 2019 Mar;39:8–18
- 2. Oonk S, Schuurmans T, Pabst M, de Smet LCPM, de Puit M. Proteomics as a new tool to study fingermark ageing in forensics. Sci Rep. 2018 Dec;8(1):16425.
- 3. Sisco E, Staymates J, Schilling K. A chemically relevant artificial fingerprint material for the cross-comparison of mass spectrometry techniques. Can Soc Forensic Sci J. 2015 Oct 2;48(4):200–14.
- 4. Hong S, Hong I, Han A, Seo JY, Namgung J. A new method of artificial latent fingerprint creation using artificial sweat and inkjet printer. Forensic Sci Int. 2015 Dec;257:403-8. 5. Staymates JL, Staymates ME, Gillen G. Evaluation of a drop-on-demand micro-dispensing system for development of artificial fingerprints. Anal Methods. 2013;5(1):180-6. 6. Stanciu CE, Philpott MK, Kwon YJ, Bustamante EE, Ehrhardt CJ. Optical characterization of epidermal cells and their relationship to DNA recovery from touch samples. F1000Research [Internet]. 2015 Nov 26 7. Mason KE, Anex D, Grey T, Hart B, Parker G. Protein-based forensic identification using genetically variant peptides in human bone. Forensic Sci Int. 2018 Jul;288:89–96. 8. Mason KE, Paul PH, Chu F, Anex DS, Hart BR. Development of a Protein-based Human Identification Capability from a Single Hair. J Forensic Sci. 2019 Feb 8; doi:10.1111/1556-4029.13995

fingerprints. (A) Comparison of ESM pre-homogenization (left) or following sievebased homogenization (right) shows reduction in the overall skin particle size. (B) Evaluation of ESM size in deposited latent (left), loaded (middle), or artificial (right) fingerprints on glass by light microscopy. (C) Range-finding of ESM amount for artificial fingerprints to determine the corresponding protein amount in typical latent fingerprints. Arrowheads indicate prominent bands found in both latent and artificial fingerprints. (D) Protein recovery measured by a fluorometric assay between latent and artificial fingerprint samples across two surface types. The amount of protein recovered was quantitated and the relative amount normalized to the surface-specific latent print average.

9. Parker GJ, Leppert T, Anex DS, Hilmer JK, Matsunami N, Baird L, et al. Demonstration of Protein-Based Human Identification Using the Hair Shaft Proteome. Calafell F, editor. PLOS ONE. 2016 Sep 7;11(9):e0160653.



www.signaturescience.com