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Introduction

Besides the general pattern and ridge characteristics, the chemical composition of latent fingerprints has been of forensic interest. Fingerprints consist of sweat and oil and contain endogenous compounds such as amino acids and fatty acids (Khare *et al.*). The relative abundance of amino acids in fingerprints has been shown to be related to gender (van Helmond *et al.* and Huynh *et al.*); however, practical, accurate and precise analytical methods are required for distinguishing a male fingerprint from a female fingerprint through chemical analysis. A method was developed by previous students in our research group, which successfully identified and semi-quantified eleven amino acids in fingerprints. The current project is focused on application of the developed method in distinguishing between male and female fingerprints based on the amino acid contents of the fingerprints.

Purpose

The first goal of the project was to study amino acid content variations among male and female individuals over time using multiple comparison analysis. Our previously developed sample preparation and instrumentation method was used to analyze the amino acid composition in fingerprints. A total of 25 multivariate fingerprint measurements based on the desired acids were collected from 5 female participants over a 5 weeks period. Similarly, another 25 multivariate fingerprint measurements based on these acids were collected from 5 male participants over the same 5 weeks period.



The second goal was to conduct a discriminant analysis to see whether a fingerprint can be correctly identified as either a male or a female fingerprint based on these multivariate fingerprint measurements. Multiple comparison analysis and discriminant analysis were both performed using SAS (Statistical Analysis System).

Methods

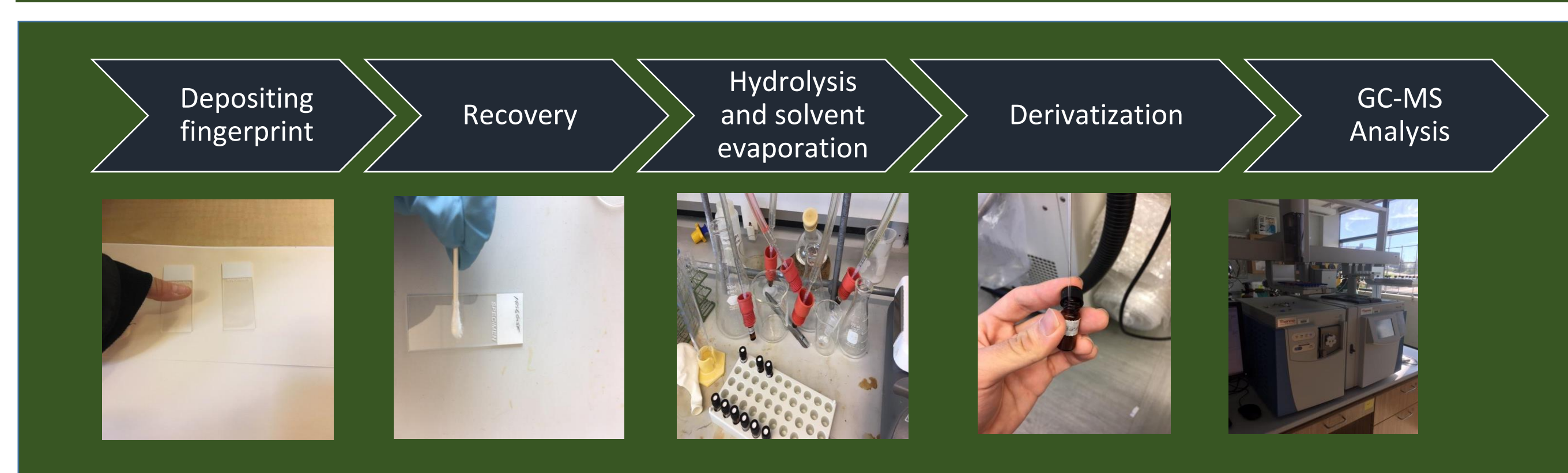


Figure 1: Sample preparation for analysis of amino acids in latent fingerprints.

Sample preparation for latent fingerprints

- Fingerprint was deposited on a glass slide.
- Glass slide was swabbed with a “wet” Q-tip (cotton swab dipped in wash solvent mixture: n-butanol:acetic acid:acetone:toluene:water 35:35:7:11:12).
- Q-tip end was washed twice with 500 μ L of solvent, sonicating the Q-tip for 30 mins each time.
- 10 μ L of each internal standard (deuterated leucine and deuterated glycine) were added to the vial.
- The wash solvents were evaporated using high vacuum system and vial was purged with nitrogen gas and capped.
- For hydrolysis of proteins, 100 μ L HCl 6 M was added to the fingerprint residues in the vial and heated at 120 $^{\circ}$ C for 2 h.
- Water was evaporated and the amino acids were derivatized before GC-MS analysis.

Methods Continued

Derivatization of Amino Acids

BSTFA (*N,O*-Bis(trimethylsilyl)trifluoroacetamide) was used for the derivatization of amino acid:

- 50 μ L of acetonitrile and 50 μ L of BSTFA were transferred into the vial containing the amino acid residues recovered from latent fingerprints.
- The vials were capped, sonicated and incubated at 60 $^{\circ}$ C for four hours before analysis with GC-MS.

Instrumental Analysis

- Thermo Scientific Trace 1310 Gas Chromatograph and ISQ single quadrupole MS
- 5% diphenyl-dimethylpolysiloxane capillary column
- Injection temperature: 280 $^{\circ}$ C
- Temperature program:
 - ✓ 70 $^{\circ}$ C to 170 $^{\circ}$ C at 10 $^{\circ}$ C/min,
 - ✓ Increased to 280 $^{\circ}$ C at 30 $^{\circ}$ C/min,
 - ✓ Held for 3 min,
 - ✓ Total run time: 16.6 min.



Design of statistical analysis:

- Collected the multivariate fingerprint data. One data point from each male and female was deleted due to missing entries.
- Fitted the probability density function (or logarithm of the probability density function) based on these remaining 24 measurements for both male and female separately.
- Found the discriminant function which is the ratio of the male/female probability density functions (or the difference of the male/female logarithmic probability density functions).
- Used the rule:
 - A person is a female if the discriminant is positive.
 - A person is a male if the discriminant is negative.
- Ran the statistical software program SAS to execute the discriminant analysis.

Results

Table 1: Multiple comparison analysis results presented statistical differences between amino acid contents and week, between amino acid content and gender and between gender and week.

The SAS System

The GLM Procedure

Dependent Variable: y

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	18	1641.555013	91.197501	73.41	<.0001
Error	518	643.506158	1.242290		
Corrected Total	536	2285.061170			

R-Square	Coeff Var	Root MSE	y Mean
0.718386	-293.1563	1.114581	-0.380200

Source	DF	Type I SS	Mean Square	F Value	Pr > F
acid	11	521.064795	47.369527	38.13	<.0001
gender	3	20.939158	6.979719	5.62	0.0009
week	4	1099.551059	274.887765	221.28	<.0001

Source	DF	Type III SS	Mean Square	F Value	Pr > F
acid	11	457.603084	41.600280	33.49	<.0001
gender	3	18.552440	6.184147	4.98	0.0021
week	4	1099.551059	274.887765	221.28	<.0001

Results Continued

Discriminant analysis equations used in SAS for three amino acids:

- $\log_{\text{den_m3}} = 0.5 * (10.901696 * ((x1 - 0.22885) ** 2) - 2 * 1.824282 * (x1 - 0.22885) * (x2 - 1.50899) - 2 * 9.466251 * (x1 - 0.22885) * (x3 - 0.74799) + 2.8498471 * ((x2 - 1.50899) ** 2) + 2 * 0.1743283 * (x2 - 1.50899) * (x3 - 0.74799) + 9.2946763 * ((x3 - 0.74799) ** 2)) + 0.5 * \log(0.1226849);$
- $\log_{\text{den_f3}} = 0.5 * (26.503751 * ((x1 + 0.29141) ** 2) - 2 * 2.168984 * (x1 + 0.29141) * (x2 - 1.26331) - 2 * 25.37466 * (x1 + 0.29141) * (x3 - 0.27192) + 1.4740383 * ((x2 - 1.26331) ** 2) + 2 * 1.3075273 * (x2 - 1.26331) * (x3 - 0.27192) + 25.089362 * ((x3 - 0.27192) ** 2)) + 0.5 * \log(0.0857142);$
- $\text{disc3} = \log_{\text{den_m3}} - \log_{\text{den_f3}};$
- if (disc3 > 0 and _N_ le 24) or (disc3 < 0 and _N_ > 24) then id3='correct'; else id3='incorrect';

Table 2: Discriminant analysis results based on three amino acids. Male: Correct Identification = 67 %, Female: Correct Identification = 62 %

Number of Obs	Female		Male	
	Disc3	Id3	Disc3	Id3
1	7.50278	Correct	-5.17914	Correct
2	2.22926	Correct	0.68510	Incorrect
3	0.21904	Correct	0.44615	Incorrect
4	0.29703	Correct	-5.01719	Correct
5	0.90517	Correct	0.42200	Incorrect
6	0.46856	Correct	-0.03063	Correct
7	0.57676	Correct	-0.03670	Correct
8	0.41910	Correct	-0.61945	Correct
9	0.53770	Correct	-1.39152	Correct
10	-0.44364	Incorrect	-0.38073	Correct
11	-0.26811	Incorrect	-0.40826	Correct
12	-0.40541	Incorrect	-0.30271	Correct
13	-0.19353	Incorrect	-0.45555	Correct
14	-0.29239	Incorrect	-0.60937	Correct
15	-0.38963	Incorrect	0.30799	Incorrect
16	0.19324	Correct	0.34043	Incorrect
17	0.31620	Correct	2.85351	Incorrect
18	0.08362	Correct	-0.06270	Correct
19	-0.20320	Incorrect	0.48007	Incorrect
20	-0.78279	Incorrect	-3.69327	Correct
21	0.19811	Correct	-0.49538	Correct
22	0.54239	Correct	-0.00989	Correct
23	0.01089	Correct	0.56353	Incorrect
24	-1.69903	Incorrect	-0.03507	Correct

Conclusion

- The multiple comparison analysis revealed significant differences between individual amino acid signals in both male and female fingerprints, between signals for the total amino acids from one week to the next, and for signals obtained for total amino acids between male and female subjects.
- The discriminant analysis performed based on three amino acids showed that correct gender identification can be made for male and female, with the accuracy of 67% and 62%, respectively.

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References

- Khare, V.; Singla, A. A Review on the Advancements in Chemical Examination of Composition of Latent Fingerprint Residues. *Egyptian Journal of Forensic Sciences* 2022, 12 (1), 6.
- van Helmond, W.; van Herwijnen, A.W.; van Riemsdijk, J.J.H.; van Bochove, M.A.; de Poot, C.J.; de Puit, M. Chemical profiling of fingerprints using mass spectrometry. *Forensic Chem.* 2019, 16, 100183. DOI: 10.1016/j.forc.2019.100183.