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Fingerprint Analysis: Moving Toward Multiattribute Determination via Individual Markers

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**Fingerprint Analysis:
Moving Toward Multiattribute Determination via Individual Markers**

An honors thesis presented to the
Department of Chemistry,
University at Albany, State University of New York
in partial fulfillment of the requirements
for graduation with honors in Forensic Chemistry
and
graduation from The Honors College

Morgan Eldridge

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May 2019

Abstract

Forensic science will be forever revolutionized if law enforcement can identify personal attributes of a person of interest solely from a fingerprint. For the past five years, the goal of the Halánek Lab has been to establish a way to identify originator attributes. Specifically, biological sex has been accomplished and the ultimate goal is to continue to accomplish this using a single analyte for each. To date, an enzymatic assay and two chemical assays have been developed for the analysis of multiple analytes. In this thesis, an additional enzymatic assay has been developed. This time, however, the assay utilizes only one amino acid. The enzymatic assay targets alanine and employs alanine transaminase (ALT), pyruvate oxidase (POx), and horseradish peroxidase (HRP). The assay proved to be capable of accurately differentiating between male and female fingerprints. The ability to target a single-analyte will transform forensic science as each originator attribute can be correlated to a different analyte, leading to the possibility of identifying multiple attributes from a single fingerprint sample. Ultimately, this would allow for a profile of a person of interest to be established without the need for time consuming lab processes.

Acknowledgements

I would first like to thank my parents, for pushing me to be my best self and explore all possibilities ever since I was little. Without them, I would not have ended up at the University at Albany writing this thesis; and I certainly would not have the opportunity to continue to pursue graduate school and beyond. I would also like to thank my friends at the university for being supportive and helping me through the many rough patches and long nights of studying, and of course for volunteering your fingerprints for my causes; I would not have made it this far alone. Another thank you for Dr. Paul Toscano and Brian Gabriel for their patience through my endless stream of questions and scheduling problems, how they were able to sort out every challenge I brought to them still amazes me. Lastly, I must thank everyone I met in the Halámek laboratory, past and present, for taking me in and giving me the opportunity to grow as a student and as a scientist over these past three years. I owe everything I know about research, the laughs and memories made along the way, to you all. A very special thank you to my mentor Erica Brunelle, for dealing with my crazy schedule, my occasional inability to do basic math in the morning, and for helping me to discover my passion for forensic research. Last, but certainly not least, I have to thank Dr. Halámek for seeing my potential and believing in my abilities. The learning and growing I have done as a student and as a researcher over my three years in this lab are unquantifiable; you have encouraged me to go above and beyond what I thought I was capable of accomplishing. I could not imagine my time here any other way, and I am forever grateful.

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Introduction:

Fingerprints have been used since the 19th century in criminal investigations. Dr. Henry Faulds is credited with the first use of fingerprints in criminology after it was decided to be acceptable for use as evidence in court.¹ A system for the classification of fingerprints was created by Francis Galton after he noted the use of fingerprints as a signature marking on important documents. If the origin of the fingerprint was questioned, one only needed to compare it to a fingerprint created on the spot by the supposed originator to confirm the individual's identity.² This classification method, and the numerous identification methods created by others thereafter, have one thing in common: each deals with the ridge patterns and minutiae that create the fingerprint image, not what the print itself is composed of biochemically. Another method explored in fingerprinting is DNA analysis, which could potentially provide significant information about the fingerprint originator. The major setback of this type of analysis is that it can take weeks or even months to process, creating backlogs for cases. Additionally, only a few nanograms of DNA are typically collected, at most, from a fingerprint due to loss during collection and extraction.³ This method is also only useful if the sample is a match to a DNA profile that is already present in the Combined DNA index System (CODIS).⁴ Similarly, the searching of a fingerprint image can only return results if there is a matching fingerprint image already in the latent print national database, named the Automated Fingerprint Identification System (AFIS).⁵

The goal of this thesis project was to determine an attribute of a fingerprint's originator, biological sex specifically, based on the components of the print via an enzymatic assay. With this type of technique, investigators could cut their suspect pool nearly in half with just one test. Perhaps the most beneficial aspect about this technique is that even if there was not a match to the latent print in AFIS, the fingerprint can still be used.

The concentrations of different amino acids in sweat have been proven to be more than just an extension of the levels in blood.⁶ These concentrations are, however, variant depending on a person's metabolism, a complex system of body functions involving hormone-based control mechanisms.⁷ Metabolism itself is dependent on factors such as age, health, biological sex, and ethnicity. Due to the fact that fingerprints are made of mostly sweat and some fatty oils, the concentrations of the biochemical components that make up a fingerprint would correlate to metabolic factors. Previous research reported this to be true; according to Croxton et al., the concentrations of amino acids in female sweat are higher than in male sweat.⁸ These findings are summarized in Table 1. Based on this research, bioanalytical assays for the detection and quantification of these metabolites could be developed. With regard to this project specifically, alanine was the metabolite of interest utilized for with the concept of biological sex identification.

Table 1: Average concentrations (mM) of amino acids (AA) for females and males derived from sweat

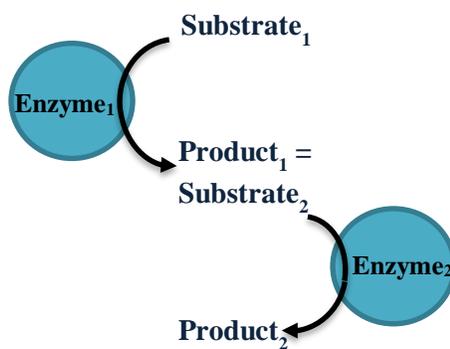
Amino Acid	Female Concentration (mM)	Male Concentration (mM)
Thr	0.2090	0.1121
Ser	0.9840	0.5208
Glu	0.1780	0.1109
Gly	0.6463	0.3418
Ala	0.3870	0.1968
Cit	0.1967	0.1267
Asp	0.1196	0.0638
Asn	0.0380	0.0161
Gln	0.0178	0.0120
Pro	0.0728	0.0349
Val	0.0919	0.0459
Cys	0.0012	0.0009
Met	0.0085	0.0034
Iso	0.0494	0.0229
Leu	0.0625	0.0324
Tyr	0.0559	0.0303
Phe	0.0378	0.0172
β -ala	0.0128	0.0034
Orn	0.1361	0.0684
Lys	0.0528	0.0285
Trp	0.0151	0.0071
His	0.1790	0.0804
Arg	0.0948	0.0540

There are two main categories of bioaffinity-based enzyme assays: single-enzyme systems and multi-enzyme systems. Each type of assay has strengths and weaknesses depending on the target analyte. Single enzyme bioaffinity-based assays are already well established in the medical field, such as glucometers, which measure the concentration of glucose in a blood sample for those with diabetes.⁹ These types of assays are simple and straightforward, with few moving parts. However, these assays are limited with respect to specificity and the ability to reduce background noise in the response. Due to the limited adjustment factors, these systems are difficult to fine tune. Multi-enzyme assays are more complex and form a cascade system. In order to proceed, all parts

of the assay must be present. For example, if there is no substrate for the first reaction to occur, the second reaction will not begin, and, therefore, there will be no response from the system. In the system shown in Scheme 1, the reaction between Enzyme₁ and Substrate₂ must occur to create Product₁, which then acts as the substrate for Enzyme₂. This then generates the final product, Product₂. It is this series of reactions that allows one to fine tune certain parts of the system, adjusting the rate of the reaction and the sensitivity of the initial detection. The weakness of the multi-enzyme assay is that since there are multiple enzymes and substrates involved, it can be more difficult to target one specific analyte. Furthermore, the additional products could interfere with the overall cascade response.

Multi-analyte assays give a signal that is due to the overall sum of the responses generated by the target analytes. This makes the assay beneficial when working with lower concentrations; in the case of this project, concentrations of amino acids. Generally speaking, if there is only a small amount of amino acid 1 - a result of

having attribute A - and a large amount of amino acid 2 - resulting from having attribute B - the combined signal would have an overall higher response than the signal of just amino acid 1 alone. This makes the multi-analyte assay unreliable for attribute identification because you do not know which attribute is causing the assay's response to increase. Single-analyte enzymatic assays, however, have a signal that is generated only by the analyte of interest. This is ideal for attribute identification, as no other substrates or metabolites will contribute to the overall signal. With this type of assay, however, low concentrations can be problematic since there is no way to boost the overall signal with the addition of another response.

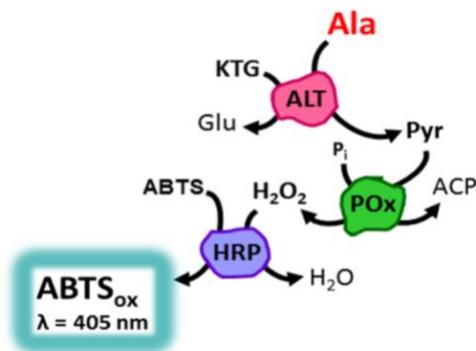


Scheme 1: Multi-enzyme system. Substrate₁ produces Product₁, which is consumed by Enzyme₂ to create the final Product₂. This reaction results in a color change when a redox dye is present. This color change can be read using a spectrophotometer.

In order to study the biochemical composition of a fingerprint with an enzyme cascade, the water-soluble compounds, amino acids, in this case – must be isolated to prevent interference from the lipids and other contaminants present in sweat. In 2015, the Halámek Laboratory developed an extraction procedure that allowed for the lipophobic, biochemical components of a fingerprint to be extracted. This process separates the water-soluble amino acids from the lipid contents, allowing for further examination of the differences in the biochemical makeup of fingerprints between diverse groups, such as the differences between males and females. The extraction process was coupled with a multi-enzyme bioaffinity-based assay to determine biological sex via amino acid concentrations in a latent fingerprint. This assay used L-amino acid oxidase (L-AAO).¹⁰ L-AAO represents approximately 30% of the total venom of some snake species, mainly rattlesnakes.¹¹ Within the multi-enzyme assay category, there are multi-analyte and single-analyte assays. L-AAO is part of the multi-analyte category, meaning that the assay is not specific to one analyte and instead generates a signal based on the concentrations several amino acids. This dual-enzyme cascade is initiated when the L-AAO reacts with 23 amino acids that are present in the fingerprint sample, converting the O₂ present into H₂O₂. It is important to note that L-AAO does not react with each amino acid equally. HRP then consumes the H₂O₂ and oxidizes the oxidation/reduction (redox) dye added to the assay. In this case, *o*-dianisidine (OD) was used, which can be observed spectrophotometrically at a maximum wavelength (λ_{\max}) of 436 nm. However, this assay is a multi-analyte assay that targets all amino acids known to be in a fingerprint, rendering it unable to explicitly connect the response to a single originator attribute. The concept of this study was the basis for several projects in the Halámek Lab, including the project discussed here.

The use of single-analyte assays as reliable attribute identifiers has been discussed previously, and the goal of the research presented in this thesis has been to move from a multi-

analyte to single-analyte assay that can be used to target a specific amino acid and correlate it to a specific originator attribute. The multi-enzyme, single-analyte assay that was utilized here consists of alanine transaminase (ALT), pyruvate oxidase (POx), and horseradish peroxidase (HRP). ALT has an affinity for one specific amino acid, alanine, so it reacts with the alanine present in the fingerprint to start the reaction. The reaction is depicted in Scheme 2. The product of



Scheme 2: *ALT/POx/HRP Cascade.* ALT reacts with alanine in the fingerprint, producing pyruvate. Pyruvate is consumed by POx to produce H₂O₂, which is then consumed by HRP. This results in the oxidation of ABTS, which turns a blue color, and is measured spectrophotometrically at $\lambda = 405$ nm.

this reaction is pyruvate (Pyr), which then is converted to hydrogen peroxide (H₂O₂) via the enzyme POx. The final step is the consumption of H₂O₂ by HRP in order to oxidize the present redox dye, 2, 2'-azino-bis (3-ethylbenzthiazoline-6-sulfonic acid) diammonium (ABTS). After this process, a visible blue/green color is present, which is spectrophotometrically measurable at a λ_{max} of 405.¹² Ultimately, just as with the L-

Table 2: Average concentrations of alanine in sweat for females and males.

	Female	Male
Concentration (mM)	0.387	0.1968

AAO/HRP system, the reason this cascade can determine the biological sex of the fingerprint originator is because of the alanine concentration differences in concentration of alanine between females and males. Female concentrations of alanine in sweat are known to be much greater than male concentrations, stated by Coltman, et al., as shown in Table 1.¹³

Experimental Procedure:

Assay Components

Water used in the experiment was ultrapure (18.2 M Ω -cm) water from PURELAB flex, an ELGA water purification system. EMD hydrochloric acid, manufactured by Fisher Scientific, was used for the amino acid extraction procedure. The following reagents were purchased from Sigma-Aldrich: glutamic-pyruvic transaminase from porcine heart (also known as alanine transaminase; ALT, E.C. 2.6.1.2), pyruvate oxidase (POx, E.C. 1.2.3.3), horseradish peroxidase Type VI (HRP, E.C. 1.11.1.7), 2,2'-azino-bis (3- ethylbenzthiazoline-6-sulfonic acid) diammonium (ABTS), α -ketoglutaric acid sodium salt (KTG), thiamine pyrophosphate (TPP), flavin adenine dinucleotide disodium salt hydrate (FAD), magnesium chloride (MgCl₂), dipotassium phosphate, monopotassium phosphate, L-aspartic acid, L-threonine, L-serine, L-glutamic acid, L-asparagine, L-glutamine, L-proline, glycine, L-valine, L-cystine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, β -alanine, L-ornithine, L-lysine, L-tryptophan, L-histidine, L-arginine, and L-citrulline. and L-alanine. A Molecular Devices UV-Vis spectrophotometer/plate reader, SpectraMax Plus 384 containing a Xenon flash lamp, was used to take optical measurements of the samples at $\lambda = 405$ nm after a 4-minute incubation period at 37 °C. All measurements were carried out at 37 °C in 96-well microtiter polystyrene plates (PS, Thermo Scientific).

Rationale

The study began with a statistical analysis of data from studies previously conducted on amino acid concentrations in sweat. These studies showed a trend of positively skewed data that was consistent with a log-normal distribution, rather than normally distributed data. This data was only available for overall amino acid concentrations. The existing parameters for a normal distribution were modified for a log-normal distribution. Then statistically generated values

agreeing with the recalculated parameters for the log-normal distribution in males and females were established using R-project software.¹⁰ This created 1150 different amino acid concentrations, 575 for each biological sex. These concentrations were then statistically grouped together in order to establish 25 male and 25 female buffer-based samples used to mimic fingerprints. These mimicked samples are representative of an expected amino acid distribution in the general population.

Fingerprint Extraction

The process of amino acid extraction from authentic fingerprint samples separates the amino acids from the other components of a fingerprint, lipid-based components such as triglycerides, wax esters, free fatty acids and squalene.¹⁴ For this research, this was achieved using elevated temperature and mildly acidic conditions. In order to remove the water-soluble amino acids from the fingerprint content, the fingerprints are deposited onto a portable lipophilic surface, the polyethylene film (PEF). An area of 2 cm × 1 cm was cut away from the sample, in order to minimize the error resulting from deviation in fingerprint size, and placed into a 1.5 mL microcentrifuge tube, followed by the addition of 120 µL of 10 mM HCl. Once the PEF is completely submerged, the sample was vortexed for 2 minutes followed by a brief centrifugation. It is important to note that the piece of PEF must remain completely submerged during the incubation period. The microcentrifuge tube was subsequently placed in a heat block at 40 °C for 20 minutes. During this process, the lipid-based content remains on the lipophilic PEF during incubation while the amino acids migrate into the aqueous acidic solution. Following the incubation period, the PEF was removed from the aqueous acidic solution, spread along the inside wall of the centrifuge tube, and then quickly centrifuged to pull all of the sample to the bottom to minimize the amount of sample lost. Of this sample, 100 µL is collected and used for analysis.

For each analysis, sets of five (n=5) authentic fingerprints from each volunteer, all taken from the right thumb, were analyzed.¹⁵

Mimicked and Authentic Fingerprint Assay

The three-enzyme cascade, depicted in Scheme 2, for the analysis of both mimicked and authentic fingerprints was designed and optimized in 0.1 M potassium phosphate buffer pH 7.6 containing 5 U ALT, 1 U PO_x, 3 U HRP, 1 mM KTG, 5.5 μM FAD, 11 μM TPP, 7 mM MgCl₂, and 1 mM ABTS. This cascade system is activated when ALT reacts with the alanine present in the sample, which produces pyruvate. Subsequently, pyruvate is then converted to H₂O₂ via PO_x, which is then consumed by HRP and converted to H₂O. In the presence of this conversion, ABTS is oxidized and observed spectrophotometrically at $\lambda = 405$ nm. All components of the assay were added to and mixed in 96-well microtiter plate prior to the addition of either the mimicked fingerprint or the extracted fingerprint sample, which initiated the reaction. Before measurement, there was a 4-minute incubation period at 37 °C. In this reaction, the rate of color production (oxidation of ABTS) is proportional to the concentration of alanine present in the sample.

Surface Experiment

Following the analysis of the authentic fingerprints on the PEF, authentic fingerprints from one male and one female that were taken from five different surfaces – a brass door knob, a laminate desktop, a chemical resin lab benchtop and a glass computer screen – were analyzed. The PEF that was also used for the initial experiments was the fifth surface, acting as the control. These analyses were performed following the same conditions that were used for the authentic fingerprints. The only difference was that the fingerprints were placed on a surface and transferred to the PEF, instead of being placed directly on the PEF.

Statistical Analysis

Receiver operating characteristic (ROC) analysis was used to evaluate the performance of the assay when using both mimicked and real fingerprints. The purpose of the ROC analysis is to estimate the probability of correctly classifying a fingerprint as either male or female when an unknown sample is used. Using this method of statistical analysis, the threshold at which the absorbance changes correspond only to female samples that yielded the maximum accuracy was determined. ROC analysis involves changing the threshold and observing the effect on the predictive power of the model used to produce a ROC curve. The area under the ROC curve (AUC) is a single measurement that summarizes the overall discriminating ability of the assay. It represents the probability that the diagnostic test will correctly distinguish between the male and female samples when an unknown sample is analyzed. Ultimately, the higher the AUC, the greater the probability that the sample will be classified correctly.¹⁰

Results and Discussion:

Preliminary Analysis

This assay was developed specifically to address the potential issue of an enzyme having a varying affinity for all amino acids, such as in the case of L-AAO.¹⁰ Such an issue would prevent the enzymatic assay from identifying specific attributes, as the signal generated is an overall sum of several responses from multiple amino acids. This is the first time that biological sex identification from a fingerprint was attempted

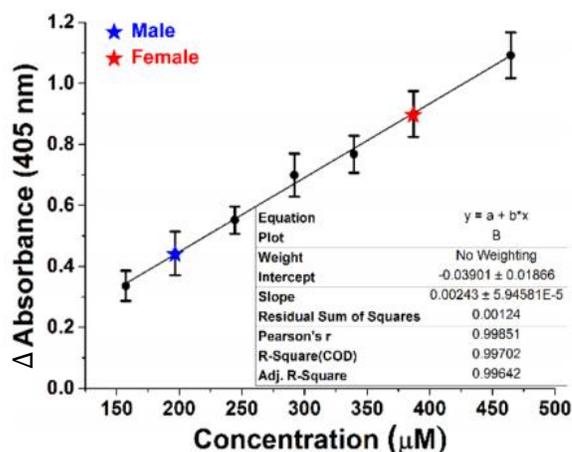


Figure 1: ALT/POx/HRP enzymatic assay calibration curve. This curve represents the positive, linear correlation between the concentration of alanine and the change in absorbance at 405 nm. The textbook values for male and female alanine concentrations are denoted with blue and red stars, respectively.

using only one analyte. As such, a calibration curve was generated by varying the concentration of alanine, shown in Figure 1. The known reported averages for male and female concentration of alanine, as seen in Table 1, were included in this curve, as well as several points above, below, and between these two concentrations. The male concentration is denoted by the blue star and the female concentration is denoted by the red star. The linearity of the responses in this calibration curve supported the hypothesis that the ALT/POx/HRP assay could distinguish between male and female samples using only one amino acid.

Mimicked Sample Analysis

Following this confirmation, the ALT/POx/HRP assay was tested using 50 mimicked samples consisting of statistically grouped male and female amino acid concentrations. The mimicked samples were prepared using the aforementioned process and were used to optimize the assay prior to analyzing the authentic fingerprint samples. Figure 2 shows the responses for the

ALT/POx/HRP assay when analyzing mimicked fingerprint samples. Here, in the presence of alanine, ABTS is oxidized, producing a blue/green color change. As shown, the female responses (red) were generally higher than the male responses (blue); however, there were some overlapping traces. This was to be expected, since the responses from the mimicked samples were the result of specifically alanine concentrations for a large general population, as

opposed to the sum of all of the amino acids. ROC analysis was then performed, which produced

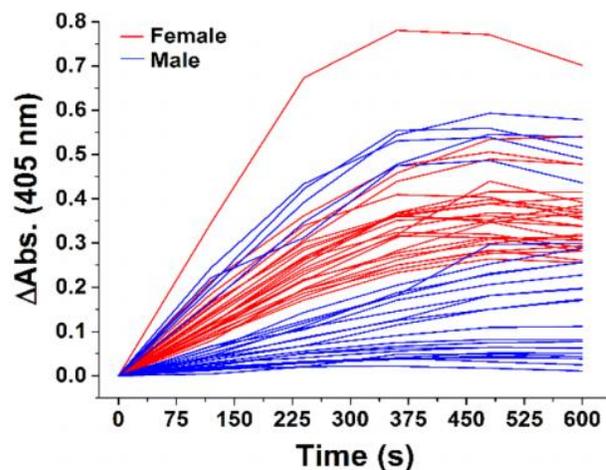


Figure 2: Change in absorbance (ΔAbs) of mimicked fingerprint samples upon the reaction with the ALT/POx/HRP assay at 405 nm. There was an incubation period of 4 minutes at 37 °C before measurement began. All blue traces indicate male samples, and all red traces indicate female samples.

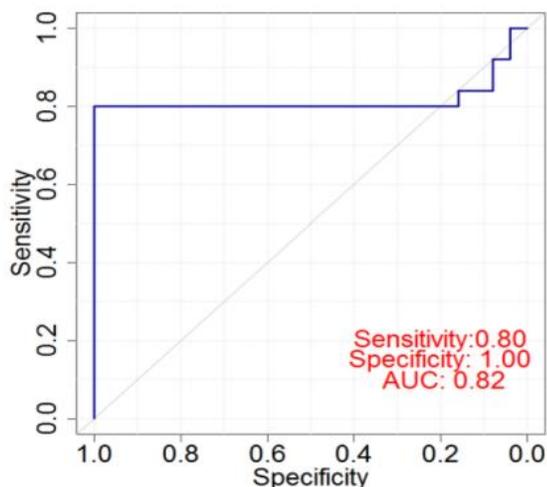


Figure 3: ROC analysis curve for the ALT/POx/HRP enzymatic assay using mimicked fingerprint samples. The AUC is 0.82, or 82%, as denoted by the area encompassing the space beneath the blue line. The diagonal line denotes random choice, or 50% probability.

value, there was potential for authentic fingerprints to improve the ROC/AUC. This is due to the fact that the alanine concentrations were statistically generated based on the average amino acid concentrations of the total population, which is expected to vary. Additionally, this assay only targets one amino acid, which removes any potential interference of using the sum of the responses of several amino acids as seen in a multianalyte assay such as L-AAO.¹² The response of the assay displayed here is solely the result of the single analyte, alanine.

Authentic Fingerprint Analysis

Ultimately, the next step was to analyze authentic fingerprints. For this study 25 authentic female and 25 authentic male samples were collected on PEF and extracted according to the method stated previously, followed by analysis via the ALT/POx/HRP assay. The authentic fingerprints show significantly less overlap than the mimicked samples, as denoted in Figure 4. This can be attributed to the notion that the mimicked samples cannot capture all the factors of the actual samples, and the fact that the actual samples are drawn from a different population – a much

the best absorbance threshold of 0.073, representing the best balance between sensitivity and specificity. In Figure 3, the ROC curve shows the optimal cut off point of 100% specificity with 80% sensitivity. The AUC was approximated to be 0.816 using the trapezoidal integration method at a 95% confidence interval. This indicated that the ALT/POx/HRP assay had an 82% probability of correctly categorizing an unknown sample as male or female under mimicked conditions. Even with this low

smaller one – than the mimicked samples. Following analysis, ROC/AUC statistical analysis was repeated using the data generated by the authentic fingerprint samples, shown in Figure 5.

Based upon the ROC analysis of the authentic fingerprint samples, the best absorbance threshold was identified as 0.9984. The AUC was determined to be 0.998 with a 95% confidence interval. This means that the ALT/POx/HRP enzymatic assay has a 99.8% probability of correctly classifying an unknown sample as male or female.

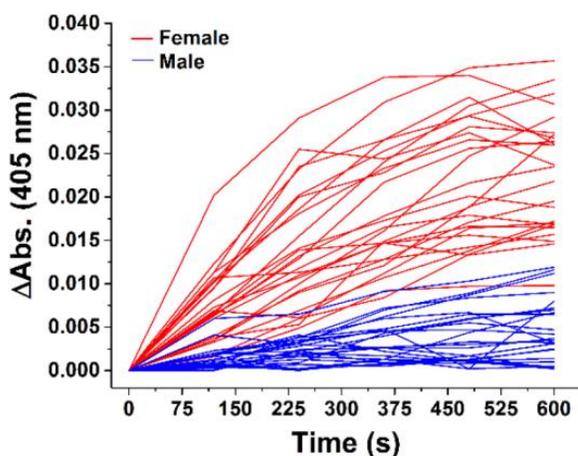


Figure 4: Change in absorbance ($\Delta Abs.$) of authentic fingerprint samples upon the reaction of ALT/POx/HRP at 405 nm. There was an incubation period of 4 minutes at 37 °C before measurement began. Blue traces indicate male samples, and the red traces indicate female samples.

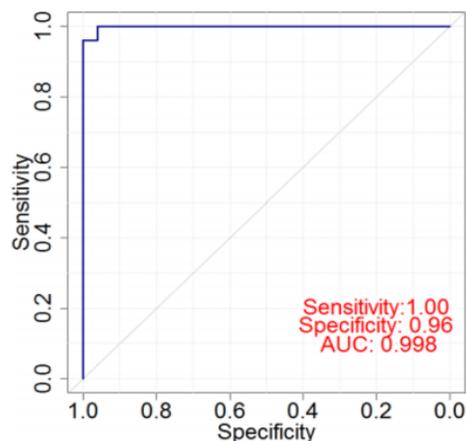


Figure 5: ROC analysis curve for the ALT/POx/HRP enzymatic assay using authentic fingerprint samples. The AUC is 0.998, or 99.8%. The diagonal line denotes random choice, or 50% probability.

Surface Analysis

After the assay had proven itself to be able to distinguish the difference between male and female authentic fingerprints on PEF, it was necessary to relate the study to more real-world conditions. Fingerprints from one male and one female were placed on various surfaces that could be found at a crime scene. For this experiment, fingerprints were placed on various surfaces including: a brass doorknob, a laminate desktop, a chemical resin laboratory benchtop, and a glass computer screen. Ultimately, the PEF from the initial study was to be used as the control surface.

Five fingerprints from each sex were placed on each surface. The fingerprints were then lifted from each of the surfaces using the PEF. Once again, the same extraction protocol was followed for extracting the amino acids from the fingerprint followed by enzymatic analysis of the extracted samples. As seen in Figure 6, there were no results generated for the male samples from the four new surfaces. This is because these samples did not generate a usable signal when tested. As shown, there is a significant decrease in the change in absorbance between the female fingerprints from the PEF and the remaining surfaces.

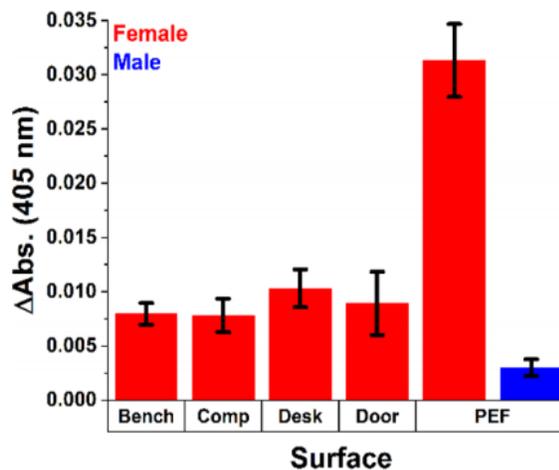


Figure 6: A bar diagram of the average absorbance ($n=5$) for each surface and each sex at $\lambda = 405 \text{ nm}$. The red bars correspond to female authentic fingerprint samples and the blue bar corresponds to male authentic fingerprint samples. Error bars have been included to demonstrate the efficacy of this experimental procedure. The abbreviation ‘Comp’ represents computer.

This is likely due to the addition of the transfer step. As such, it would be expected that the male samples would follow the same trend. However, in this case, the male samples from the PEF already generated a relatively low optical response. When the surface transfer step was added, there was not enough alanine that transferred, thus reducing the already low signal to noise. However, even though the female surface fingerprints displayed a significant reduction in response, it was still possible to differentiate a female surface fingerprint from a fresh male fingerprint. Furthermore, the error bars included in Figure 6 also demonstrate the extraction of the fingerprints is consistent and efficient despite the potential loss of sample due to the added transfer step.

Conclusion:

The hypothesis that a single amino acid can be correlated to biological sex has been proven true by the research presented here. The concept that it is possible to find one biological marker that can be directly correlated to one originator attribute other than biological sex is entirely feasible in the future based on the results shown here. The mimicked fingerprint analysis resulted in a trend of higher alanine concentrations in female (red) samples than male (blue), with some overlap between the two groups. The authentic fingerprint analysis followed the same trend of having higher alanine concentrations in female than males, however, this data showed less overlap between the two groups due to the use of a smaller sample group. The ROC/AUC analysis for the determination of biological sex from mimicked fingerprint samples using the ALT/POx/HRP system produced an 82% chance of correct classification of an unknown fingerprint, while the authentic fingerprints produced a 99.8% chance of correct classification. This was taken one step further in the surface phase of the experiment, where it was again proven that the assay can differentiate between authentic male and female fingerprints regardless of the surface that the fingerprints were taken from. This is a crucial factor given that fingerprints at a crime scene are not in a controlled environment nor are they on a specific surface. The surface experiment proved that this assay can be translated into a real crime scene scenario to help provide law enforcement with more information about a fingerprint's origin, especially if there isn't a visual match for that fingerprint in AFIS or a DNA match in the Combined DNA Index System (CODIS).¹⁶

The ALT/POx/HRP assay demonstrates the future possibility of creating a system that is capable of identifying multiple originator attributes from a single fingerprint to aid in establishing a profile of a person of interest. This could establish a breakthrough in the forensic science world where fingerprints are more useful than just their visual context and minutiae. With the development of other assays to identify other key originator attributes, a series of tests can then be

performed to provide a much clearer picture of a perpetrator, especially if the print has no direct visual matches or is smudged and cannot be imaged at all.

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