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Applied Bayesian Analysis of Intergenerational Fingerprint Pattern Similarity

N K Aswini[1], Shukla Rudrank[1], and M C Janaki[1,*]

[1]Department of Forensic Science, Kalasalingam Academy of Research and Education, (Deemed to be University), Krishnankoil, 626126, Tamil Nadu, India.

*Corresponding Author: drjanakimc@gmail.com

Abstract. This research reports on the inheritance of fingerprint types across three generations of families. Uses of Bayesian measures of statistical analysis indicates a moderate transference of loops and whorls between generations (grandfather, father, son), with negligible transference for arches and only joint moderate evidence across all three generations. A total of 150 samples from 50 family trios were analyzed, classified fingerprints as Arch, Ulnar/Radial Loop, Composite, and Whorl. Cross-tabulation showed the highest transference in Ulnar/Radial Loops, followed by Whorls, with minimal transference for Arches and Composites. The Bayesian correlation analysis of father & grandfather and son & father showed strong similarities between generations (father & grandfather - Pearson r = 0.283, BF_{10} = 44.74; Kendall's τB = 0.255, BF_{10} = 4650.48) and substantial evidence for the association between sons and fathers. The analysis showed negligible transference between sons and grandfathers. Bayesian regression and model comparisons supported the null model, with very low R^2 values (0.003–0.012), indicating minimal predictive influence of parental patterns on the son's fingerprint phenotype. Overall, the findings indicate moderate hereditary continuity of fingerprint patterns between successive generations, but weak evidence for transmission across all three generations. This suggests that fingerprint inheritance is complex, influenced by both genetic and developmental-environmental factors affecting dermatoglyphic patterns.

Keyword: Bayesian analysis, fingerprint patterns, inheritance, intergenerational, justice.

1. Introduction

The palmer surface of the hands and the palmer surface of the feet are covered by a layer of corrugated skin to ensure a firmer grip and to resist slippage [1]. The elevated surfaces are known as papillary or friction ridges, while the valleys formed between two ridges are known as furrows or grooves. The reproduction of patterns of the friction ridges on the distal phalanges of the fingers and thumbs are called as fingerprints. Dermatoglyphics is the scientific study of fingerprints and can be traced back to 1892 when one of the most original biologists of his time Sir Francis Galton, a cousin of Charles Darwin, published his now classic work on fingerprints [2]. Fingerprints can be divided into four basic types: arches, loops, whorl, composites and composite patterns comprise lateral pocket loop, central pocket loop, twin loop, accidental [3].

Fingerprint patterns, such as loops, whorls, and arches, are primarily determined by genetic and environmental factors during fetal development [4]. The inheritance of fingerprint patterns is a complex polygenic trait, meaning it is influenced by multiple genes rather than a single gene [5]. Fingerprint ridge patterns and characteristics (e.g., minutiae points) are partially inherited from parents [7].

Studies show similarities in fingerprint patterns among family members, particularly between identical twins [8]. Specific regions of chromosomes, such as those associated with the development of skin andconnective tissue, contribute to ridge formation [9]. Fingerprint patterns are also influenced by conditions in the womb, such as amniotic fluid pressure, blood flow, and fetal movements, making them unique even among identical twins [10]. The field of fingerprint analysis is not newly emerged in forensic science; it has existed for a long time, and lot of transmission have occurred through the innovative research in understanding the fingerprint[11,12], its characteristics[13], development of latent fingerprint[14], genetical inheritance of fingerprint[20], fingerprint formation[21], [22], familial resemblance[23], etc, which can be understood from the extensive research. Whereas, the proposed research work i.e. fingerprints pattern similarity inheritance in the family is not yet explored extensively and data available are with different objectives not related to forensics hence, the present study aims to study the pattern inheritance among the generation.

2. Research Methodology

The study used a cross-generational, comparative design, where data was collected from three generations within a family. This design allows for the examination of patterns in dermatoglyphics (fingerprint patterns) over time and across familial lines. The primary aim is to determine whether certain fingerprint patterns are passed down from one generation to the next.

2.1. Objectives

1. To analyse the distribution of fingerprint pattern types among three generations of family members.
2. To assess the degree of similarity in fingerprint patterns between each generational pair.
3. To evaluate the strength of agreement in fingerprint patterns using statistical tools.
4. To identify whether specific fingerprint patterns show stronger hereditary tendencies across generations.

The study will focus on three generations from a single-family group, including grandparents, parents, and children. Ideally, 15 families with multiple members from each generation has been selected a total of 150 samples were selected for data collection from in and around Madurai District of Tamil Nadu.

Fingerprints were obtained manually using the traditional inking technique, which included both rolled and plain impressions to ensure clarity and completeness of ridge details. The collected prints were systematically classified into four major pattern types: whorl, loop, arch, and composite, following standard dactyloscopic classification procedures.

All the participants were male, representing three generations: sons aged between 20 and 30 years, fathers aged between 45 and 65 years, and grandfathers aged above 65 years. This selection enabled the analysis of hereditary similarities in fingerprint traits across generations within a controlled sociodemographic group. Statistical analyses were performed using SPSS and JASP software. Bayesian, Pearson, and Kendall correlation methods were employed to assess the degree of similarity in fingerprint types across generations. Further, Bayesian regression and ANOVA tests were applied to evaluate the frequency distribution of various fingerprint patterns among the three generations.

Participants selected for the study were required to have no history of dermatological or congenital conditions affecting the hands or fingerprint formation, such as eczema or dermatitis. Only families with confirmed participation from all three generations were included. Individuals exhibiting poor fingerprint quality or those affected by medical or procedural alterations of the skin were excluded from the study.

3. Results and Discussion

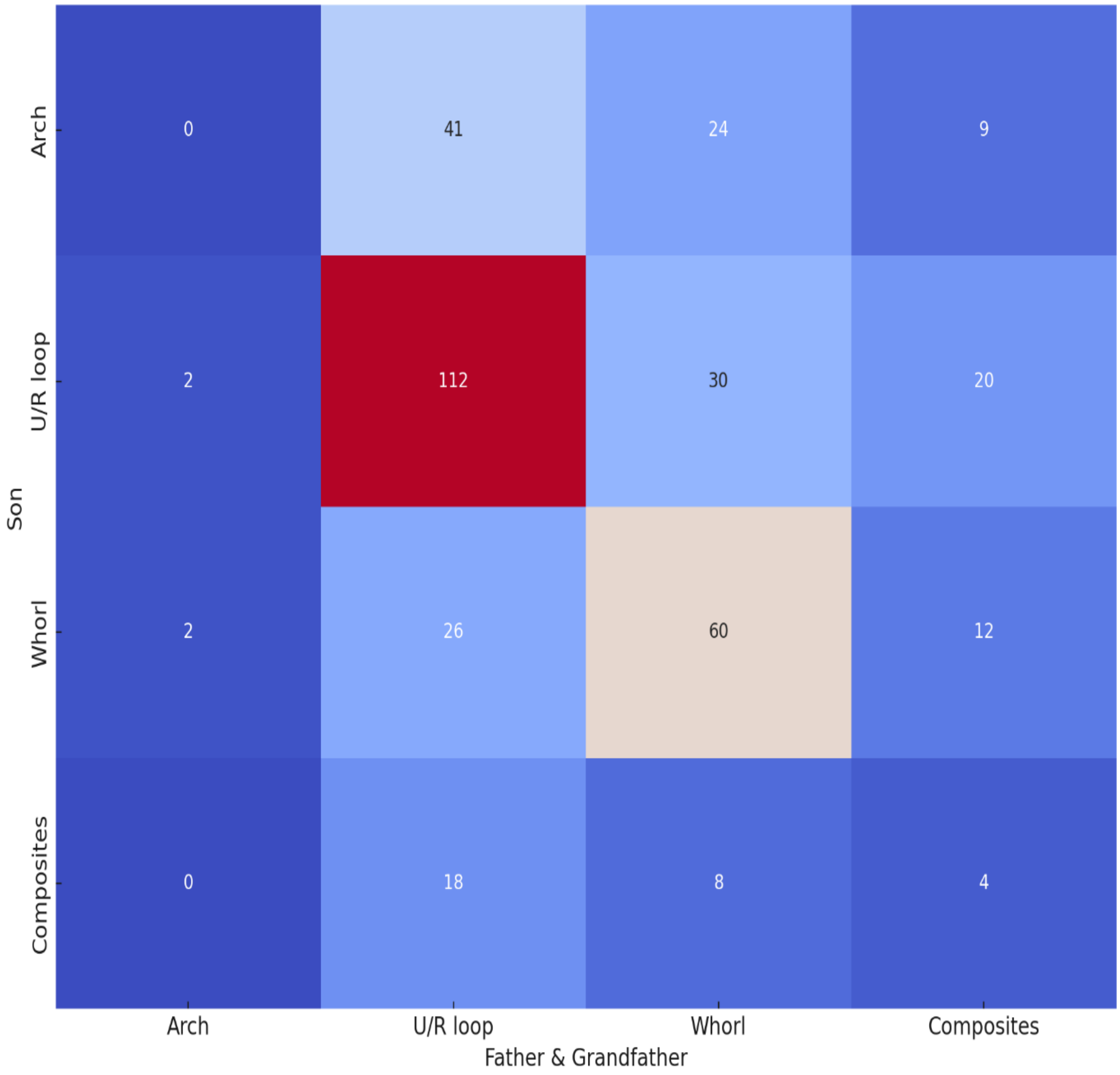

Figure 1. Heatmap indicating cross tabulation of fingerprint pattern inheritance.

The data suggests that inheritance of fingerprint type varies across types. The Ulnar/Radial loop type has the strongest conditional inheritance with the highest incidence when fathers/grandfathers pass on any fingerprint pattern to sons as did fathers/grandfather. The Whorl type demonstrates a moderate conditional inheritance relationship with lower incidence rates when compared to the loops. The Composite pattern is rare, although present, but little systematic inheritance may be seen. The Arch pattern appears entirely absent, with no cases of systematic inheritance on a three-generation scan, suggesting these patterns are both rare and weakly inherited in this present sample.

Also, evidence of inter-pattern transitions was noted. Some sons with Whorl patterns came from loop pattern parents, and vice versa, loops came from Whorl or Composite (parent) patterns. So, while we may see a relation of inherited patterns-especially with Ulnar/Radial loops and Whorls-some transitions to a different fingerprint type seem not to be outside the realm of possibility indicating a variability of dermatoglyphic trait expression across generations.

Table 1. Percentage Distribution of Fingerprint Patterns.

Pattern	Son	Father	Grandfather
Arch	2.0	1.3	0.00
U/R loop	54.7	53.3	47.3
Whorl	33.3	32.7	34.0
Composites	10.0	12.7	18.7
Total	100%	100.0%	100.0%
Mean	2.5133	2.5667	2.7133

The results indicate that the U/R loop pattern predominates across all three generations, accounting for 54.7% among sons, 53.3% among fathers, and 47.3% among grandfathers. Whorl patterns remain comparatively stable (32.7–34.0%), suggesting moderate hereditary consistency. Composite patterns exhibit a gradual increase from 10.0% in sons to 18.7% in grandfathers, indicating possible generational variation. In contrast, arch patterns show a clear decline from 2.0% to 0.0%, reflecting minimal inheritance. The mean values (2.51 for sons, 2.57 for fathers, and 2.71 for grandfathers) demonstrate a slight upward trend, implying subtle intergenerational differences in fingerprint pattern distribution.

Table 2. Statistical Analysis of Degree of Similarity of fingerprint patterns inheritance.

Bayesian Correlation Table

Models	n	Pearson		Kendall	
		r	BF_{10}	tau B	BF_{10}
Son - Father	150	0.149	0.531	0.208***	126.250
Son - Grandfather	150	-0.149	0.532	-0.109	0.733
Father - Grandfather	150	0.283**	44.739	0.255***	4,650.476

* $BF_{10} > 10$, ** $BF_{10} > 30$, *** $BF_{10} > 100$

Bayesian correlation analysis showed strong intergenerational similarity between Father and Grandfather fingerprints (Pearson r = 0.283, $BF_{10} = 44.74$; Kendall's τB = 0.255, $BF_{10} = 4650.48$). Son–Father comparisons yielded weak Pearson correlation (r = 0.149, $BF_{10} = 0.53$), but Kendall's τB indicated a small yet reliable association (τB = 0.208, $BF_{10} = 126.25$). No meaningful correlation was found between Son and Grandfather fingerprints (r = –0.149; τB = –0.109, $BF_{10} < 1$). Overall, results suggest stronger fingerprint pattern similarity across one generation (Father–Grandfather) than across two generations (Son–Grandfather), with mixed evidence for the Son–Father link.

Table 3. Regression Model Summary Analysis.

Model Comparison

Models	P(M)	P(M|data)	BF_M	BF_{10}	R^2
Null model	0.250	0.736	8.355	1.000	0.000
Father	0.083	0.073	0.869	0.298	0.008

Grandfather	0.083	0.054	0.622	0.218	0.003
Son	0.083	0.052	0.598	0.210	0.003
Son + Father	0.083	0.025	0.284	0.103	0.012
Son + Father + Grandfather	0.250	0.024	0.075	0.033	0.012
Father + Grandfather	0.083	0.020	0.229	0.083	0.009
Son + Grandfather	0.083	0.016	0.178	0.065	0.005

Bayesian model comparison showed that the null model- representing the baseline scenario in which generational factors (Father, Grandfather, or Son) are assumed to have no effect on fingerprint pattern variation (P(M|data) = 0.736) was overwhelmingly favored over models including Father, Grandfather, or Son as predictors (all P(M|data) < 0.08). Bayes Factors indicated that all predictor models were substantially less likely than the null ($BF_{10} \leq 0.30$). Consistently low R^2 values (0.003–0.012) suggest that intergenerational predictors explained virtually no variance in fingerprint similarity. Thus, the analysis provides strong evidence that fingerprint patterns are not significantly transmitted across generations in this sample.

Table 4. Result of ANOVA.

Model Comparison

Models	**P(M)**	**P(M|data)**	**BFM**	**BF10**	**error %**
Null model (incl. Grandfather, Father)	0.500	0.611	1.569	1.000	
Son	0.500	0.389	0.637	0.637	6.272

Note. All models include Grandfather, Father.

Bayesian model comparison indicated that the model including Grandfather and Father (P(M|data) = 0.611) was more supported than the model that also included the Son (P(M|data) = 0.389). The Bayes Factor ($BF_{10} = 0.64$) suggested weak evidence against including Son, implying that intergenerational fingerprint similarity may be primarily explained by Grandfather and Father without requiring additional contribution from the Son.

4. Over all Discussion

This study aimed to explore the intergenerational inheritance of fingerprint patterns (dermatoglyphics) across three generations-grandfather, father, and son-within families. A combination of cross-tabulation, Bayesian analysis including correlation- Pearson and Kendal models for testing degree of similarity whereas, regression and ANOVA modelling was used to examine the patterns inheritance.

Table 1 shows that U/R loops are the most prevalent fingerprint pattern across all generations, while arches are the least common, disappearing entirely in grandfathers. Whorl patterns remain relatively stable, and composite patterns gradually increase from sons to grandfathers. The mean values of all fingerprint patterns (2.51 in sons, 2.56 in fathers, and 2.71 in grandfathers) show a slight upward trend, indicating minor intergenerational variation in overall fingerprint distribution. These results suggest that certain patterns, like loops, are consistently expressed, while others, such as composites and arches, vary slightly across generations.

4.1. Heat Map (Fig.1)

- Ulnar/Radial Loop is the most dominant and consistently inherited fingerprint pattern across generations.
- Whorl patterns also show moderate levels of inheritance, with 22 father-son and 15 grandfather-grandson matches.
- Composite and Arch patterns were far less likely to be directly inherited, with composites showing variability and arches being nearly absent in direct matches.

This reflects a possible inherited dominance of loop and whorl patterns, while arches and composites may be more influenced by developmental or polygenic factors [25], [26].

4.2. Bayesian Analysis

Bayesian correlation analysis (Table 2) revealed definitive differences between generations in associations. A pathway of moderate and robust correlation occurred between Fathers and Grandfathers, and we found compelling Bayes Factor evidence for similarity in fingerprint patterns. The Son–Father pair had a weaker connection between generations—Pearson's correlation revealed no evidence, and Kendall's τB indicated a small but-useable ordinal connection. By comparison, Son–Grandfather connections were trivial, and did not have enough Bayesian evidence to support. All together, these results suggest strongest fingerprint similarity with one generation (Father–Grandfather), weaker for Son–Father, and virtually absent association for Son–Grandfather. Some combination of dilution, or generation variable, may surface from these effects(2).

Bayesian regression model (Table 3) comparisons clearly favoured the null model over models with Father, Son, or Grandfather predictors. Very low R^2-values (0.003–0.012) provide little support for generation predictors and fingerprint similarity, despite some weak descriptive models support of hereditary patterns. Bayesian ANOVA-style model comparison (Table 3) compared the Grandfather + Father to the model including Son—comparatively showing similar evidence in support of Grandfather + Father. Overall, both models found evidence to support the Fathers and Grandfathers relationship, with little incremental evidence of Son variable [27], [28].

5. Conclusion

This study examined the intergenerational inheritance of fingerprint patterns across grandfather–father–son trios by employing a suite of statistical tools, including Bayesian Pearson and Kendall correlations to assess similarity, and Bayesian regression and ANOVA models to compare fingerprint pattern frequencies across generations. The results revealed that Ulnar/Radial loop and Whorl patterns demonstrated the strongest evidence of hereditary continuity, with loops emerging as the most consistently inherited trait. In contrast, Composite and Arch patterns were rare and showed little to no systematic inheritance. Bayesian correlation highlighted a moderate and reliable similarity between father–grandfather dyads, whereas son–father pairs showed only weak agreement, and son–grandfather pairs exhibited negligible inheritance links. Regression and ANOVA analyses consistently favored the null model, suggesting minimal explanatory contribution of generational predictors and highlighting weak overall transmission of fingerprint traits.

References

[1] R. Romero Reverón, "Marcello Malpighi (1628-1694), Founder of Microanatomy," *Int. J. Morphol.*, vol. 29, no. 2, pp. 399–402, June 2011, doi: 10.4067/S0717-95022011000200015.

[2] M. Kücken and A. C. Newell, "Fingerprint formation," *J. Theor. Biol.*, vol. 235, no. 1, pp. 71–83, July 2005, doi: 10.1016/j.jtbi.2004.12.020.

[3] J. R. Miller, "Dermatoglyphics," *J. Invest. Dermatol.*, vol. 60, no. 6, pp. 435–442, 1973.

[4] K. Wertheim, "Embryology and morphology of friction ridge skin," in *The Fingerprint Source Book*, NIJ, 2011.

[5] A. Teicher, "Kristine Bonnevie's theories on the genetics of fingerprints, and their application in Germany," *Stud. Hist. Philos. Sci.*, vol. 92, pp. 162–176, Apr. 2022, doi: 10.1016/j.shpsa.2022.01.006.

[6] G. Temaj, T. Škarić-Jurić, A. Butković, E. Behluli, M. Zajc Petranović, and A. Moder, "Three Patterns of Inheritance of Quantitative Dermatoglyphic Traits: Kosovo Albanian Twin Study," *Twin Res. Hum. Genet.*, vol. 24, no. 6, pp. 371–376, Dec. 2021, doi: 10.1017/thg.2021.56.

[7] B. Karmakar, I. Malkin, and E. Kobyliansky, “Inheritance of finger pattern types in MZ and DZ twins,” *HOMO*, vol. 62, no. 4, pp. 298–306, Aug. 2011, doi: 10.1016/j.jchb.2011.02.002.

[8] T. Reed, R. J. Viken, and S. A. Rinehart, “High heritability of fingertip arch patterns in twin-pairs,” *Am. J. Med. Genet. A.*, vol. 140A, no. 3, pp. 263–271, Feb. 2006, doi: 10.1002/ajmg.a.31086.

[9] A. R. Hale, “Morphogenesis of volar skin in the human fetus,” *Am. J. Anat.*, vol. 91, no. 1, pp. 147–181, July 1952, doi: 10.1002/aja.1000910105.

[10] W. Babler, “Prenatal development of dermatoglyphic digital patterns: Associations with epidermal ridge, volar pad and bone morphology,” *Coll. Antropol.*, vol. 11, no. 2, pp. 297–303, 1987.

[11] R. D. Oslen, *Scott’s Fingerprint Mechanics*. Charles C Thomas: Springfield, IL, 1978.

[12] C. Huynh and J. Halámek, “Trends in fingerprint analysis,” *TrAC Trends Anal. Chem.*, vol. 82, pp. 328–336, Sept. 2016, doi: 10.1016/j.trac.2016.06.003.

[13] H. J. Kobus, K. P. Kirkbride, and M. A. Raymond, “Identification: Fingerprints a Key Identification Parameter – Detection, Identification, and Interpretation,” in *Encyclopedia of Forensic and Legal Medicine*, Elsevier, 2016, pp. 65–73. doi: 10.1016/B978-0-12-800034-2.00208-1.

[14] Krushnai. J. Parkale and Manjushri. S. Bagul, “A Review of Latent Fingerprint Developed Powder from using Natural Materials,” *Int. J. Sci. Res. Sci. Technol.*, vol. 11, no. 2, pp. 715–717, Apr. 2024, doi: 10.32628/IJSRST24112115.

[15] P. Boonyaras, S. Boonpang, and K. Dangudom, “Latent fingerprint detection using fluorescent powder dusting technique,” *J. Phys. Conf. Ser.*, vol. 2653, no. 1, p. 012075, Dec. 2023, doi: 10.1088/1742-6596/2653/1/012075.

[16] H.-S. Jung, K.-J. Cho, S.-J. Ryu, Y. Takagi, P. A. Roche, and K. C. Neuman, “Biocompatible Fluorescent Nanodiamonds as Multifunctional Optical Probes for Latent Fingerprint Detection,” *ACS Appl. Mater. Interfaces*, vol. 12, no. 5, pp. 6641–6650, Feb. 2020, doi: 10.1021/acsami.9b19245.

[17] R. Vadivel, M. Nirmala, and K. Anbukumaran, “Commonly available, everyday materials as non-conventional powders for the visualization of latent fingerprints,” *Forensic Chem.*, vol. 24, p. 100339, June 2021, doi: 10.1016/j.forc.2021.100339.

[18] Q. A’yuni *et al.*, “Development of silica gel from Lapindo volcanic mud as fluorescent fingerprint powder based on methyl orange,” *South Afr. J. Chem. Eng.*, vol. 50, pp. 143–151, Oct. 2024, doi: 10.1016/j.sajce.2024.08.002.

[19] J. D. James, C. A. Pounds, and B. Wilshire, “Flake Metal Powders for Revealing Latent Fingerprints.,” *J Forensic Sci*, vol. 36, no. 5, pp. 1368–1375, 1991.

[20] J. Devi, B. Das, and J. Das, “Study on Inheritance of Fingerprint Pattern and its Association with ABO Blood Groups at Nagaon, Assam,” *Indian J. Sci. Technol.*, vol. 16, no. 23, pp. 1694–1701, June 2023, doi: 10.17485/IJST/v16i23.1941.

[21] Lee，Young Ho, “Study on Medical Significance and Mechanism of Fingerprint Formation,” *Anat. Biol. Anthropol.*, vol. 34, no. 4, pp. 105–110, Dec. 2021, doi: 10.11637/ABA.2021.34.4.105.

[22] J. D. Glover *et al.*, “The developmental basis of fingerprint pattern formation and variation,” *Cell*, vol. 186, no. 5, pp. 940-956.e20, Mar. 2023, doi: 10.1016/j.cell.2023.01.015.

[23] E. O. Aigbogun, Jr, C. P. Ibeachu, and A. M. Lemuel, “Fingerprint pattern similarity: a family-based study using novel classification,” *Anatomy*, vol. 13, no. 2, pp. 107–115, Aug. 2019, doi: 10.2399/ana.19.065.

[24] A. Rana, D. Siwan, A. Vashisht, and K. Krishan, “Understanding familial resemblance of fingerprints: Forensic and anthropological aspects,” *Ann. Anthropol. Pract.*, p. e12231, Jan. 2025, doi: 10.1111/napa.12231.

[25] Y. Y. W. Ho *et al.*, “Common Genetic Variants Influence Whorls in Fingerprint Patterns,” *J. Invest. Dermatol.*, vol. 136, no. 4, pp. 859–862, Apr. 2016, doi: 10.1016/j.jid.2015.10.062.

[26] J. Li *et al.*, “Limb development genes underlie variation in human fingerprint patterns,” *Cell*, vol. 185, no. 1, pp. 95-112.e18, Jan. 2022, doi: 10.1016/j.cell.2021.12.008.

[27] V. Patil and D. R. Ingle, “An association between fingerprint patterns with blood group and lifestyle based diseases: a review,” *Artif. Intell. Rev.*, vol. 54, no. 3, pp. 1803–1839, 2021, doi: 10.1007/s10462-020-09891-w.

[28] N. Rivaldería, A. Moreno-Piedra, A. Álvarez, and E. Gutiérrez-Redomero, “Study of the fingerprints of a Spanish sample for the determination of the hand and finger,” *Sci. Justice*, vol. 64, no. 2, pp. 216–231, Mar. 2024, doi: 10.1016/j.scijus.2024.01.005.