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Familial Aggregation of Fingerprint Patterns: A Systematic Review of Evidence from Mother-Father-Child Triads

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Abstract

The possibility of fingerprint pattern inheritance (dermatoglyphics) within a family has been hypothesized for a long time. However, a quantitative and systematic synthesis of such evidence has remained elusive. The aim of the systematic review was to critically evaluate and consolidate the evidence for fingerprint pattern transmission from parents to offspring through analyzing data from Mother-Father-Child triads. While pictured family fingerprint pattern raw data were taken from key studies comprising one hundred eleven (111) independent triads, additional informative data were also extracted across multiple academic research electronic databases, including PubMed, Scopus, Web of Science, and Google Scholar, via a systematic search. This study has demonstrated a strong and non-random familial aggregation. As a result, high-probability inheritance patterns were identified. Specifically, when both parents exhibited Loop patterns, the offspring also exhibited a Loop pattern in 90.32% of cases (28/31; 95% CI: 74.2–97.7%). Similarly, when both parents exhibited Whorl patterns, the offspring exhibited a Whorl pattern in 91.30% of cases (21/23; 95% CI: 73.2–97.6%). Furthermore, specific parental sub-pattern combinations demonstrated even higher transmission probabilities. For example, when both parents exhibited Loop-Ulnar patterns, the offspring also exhibited a Loop-Ulnar pattern in 100.0% of cases (12/12; 95% CI: 75.8–100.0%). Hence, the present findings provided a quantitative synthesis of Mother-Father-Child fingerprint triad data, generating consolidated transmission probabilities across parental fingerprint pattern combinations for evidence consistent with familial aggregation in dermatoglyphics patterning within a family. This is due to the fact that a clear framework for understanding a pattern-specific inheritance has established to underscore the necessity for standardized methodologies in future familial dermatoglyphics research to enable advanced genetic and forensic applications.

Keywords: Dermatoglyphics, Fingerprint Inheritance, Fingerprint Pattern, Triad Analysis, Nuclear Family

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Introduction

The fingerprint of an individual constitutes a highly stable and biologically informative phenotypic system with multiple applications in human identification (Akpan, 2021; Glover et al., 2023; Maiti et al., 2022; O'Brien & Murphy, 2020; Priyadharshini et al., 2022; Rana et al., 2025; Reynolds & Brundage, 2023; Syarifah et al., 2024). Besides, Slatis et al. (1976) stated that specific genes are responsible for pattern deviation from the baseline of the ulnar loop, and many scientists tried their best to examine fingerprint pattern inheritance, whether it is transmitted from parents to offspring or not, and these suggested that fingerprint morphology has a genetic component, but this component does not translate into a simple or deterministic inheritance pattern. Rather, genetic influences appear to interact with developmental processes during prenatal limb formation, producing familial resemblance while preserving substantial individual variation. Some scholars suggested that fingerprints may carry not only identity but also heredity information (Asen, 2019; Aswini et al., 2025; Heng et al., 2018; Maiti et al., 2022; Sharma, 2022).

This interpretation is consistent with more recent genetic evidence showing that variants near genes involved in limb development, including EVI1, are associated with variation in fingerprint patterns, while experimental evidence indicated these genes influence dermatoglyphics formation through early limb development rather than by directly specifying an exact fingerprint pattern (Li et al., 2022). 91% heritability for arch pattern observed in twins' studies has supported this genetic influence (Reed et al., 2006). While some studies suggested that fingerprints are more genetically determined than environmentally influenced (Aigbougun et al., 2019; Aswini et al., 2025), the mode of inheritance appears complex, potentially involving probabilistic relation rather than a simple Mendelian transmission (Jaiyeoba-Ojigho et al., 2020; Sharma, 2022). Most of the empirical studies agree globally; some of them contradict this familial transmission. Importantly, the apparent contradictions in the literature may partly reflect differences in populations, sample sizes, fingerprint traits examined, classification systems, and analytical definitions of inheritance. Research conducted in Indian population indicated that there is a paternal influence, which is about 28.6% between a father and daughter (Mehra, 2024), while the other argument indicated a significant pattern maternal transmission, with 40% chance of inheritance from mother to offspring (Rena et al., 2025). A reported percentage of similarity or association also does not necessarily represent a genetically determined probability of inheritance. According to a survey conducted in Urhobo, Nigeria, fingerprint patterns were randomly distributed among

their offspring in one study; while study conducted in this place concluded that the parental combination of ulnar loops for the thumb and index finger gives whorls in the offspring fingerprint pattern (Jaiyeoba-Ojigho et al., 2020). It is easily understood from the result of a studies conducted in Himachal Pradesh indicated genetically link within three generation of a family (Verma, 2024). Differences in sample composition and classification criteria may, therefore, contribute to apparently conflicting conclusions.

Over 80% accuracy is achieved using technological advancement for such genetically relation (Maiti & Das, 2023). Despite this versatile evidence, the field is characterized by methodological heterogeneity varying in sample size (Efe et al., 2020; Rohatgi, 2024), classification systems of fingerprint pattern (Aigbogun et al., 2019; Mehra, 2024), fingerprint inheritance (parent-to-offspring) probability (Aswini et al., 2025; Chivukula & Skelly, 2024; Heng et al., 2018; Imran et al., 2021; Priyadharshini et al., 2022; Rana et al., 2025; Reynolds & Brundage, 2023; Sharma et al., 2021; Teicher, 2022), analytical focus on ridge characteristics, creases, or core patterns (Verma, 2024). The existing review literature provides important biological and historical context but does not resolve how consistently particular fingerprint patterns are transmitted between parents and offspring. This diversity makes the synthesis of a clear, quantitative consensus on difficulty in the strength and pathways of fingerprint pattern inheritance. While a strong fingerprint pattern similarity between a related individual than that of the unrelated one (Rana et al., 2025; Sharma, 2022; Swarnaambigaa & Keerthi, 2025), multi-parameter studies confirm some heritability for certain traits in twins (Debta et al., 2018; Heng et al., 2018). Genetic studies identify developmental determinants, whereas familial studies generally examine phenotypic resemblance; these are related but distinct levels of evidence. Therefore, a systematic synthesis that directly evaluates parent-offspring pattern combinations and quantifications of their observed transmission probabilities is needed to bridge the gap. This is because a systematic, quantitative consolidation of evidence from Mother-Father-Child triads that explaining such correlation has remained vague.

To integrate those data from key familial studies across the literature, the present work seeks to move beyond qualitative assertions of heredity by quantifying the probability of pattern inheritance, identifying strong likelihood transmission of major fingerprint pattern and evaluating the predictive effect of specific parental sub-patterns. This systematic review provides a quantitative synthesis of the available evidence on fingerprint pattern inheritance

by integrating findings from published studies with a re-analysis of raw Mother-Father-Child triad data. The study has reflected a pattern-specific parent offspring transmission probability with their respective confidence of intervals rather than establishing a new theory of inheritance and thereby providing a consolidated reference for future familial dermatoglyphics research. The findings could be a significant benchmark in contributing to forensic applications involving kinship assessment and disaster victim identification. It highlights the need for larger and standardized familial datasets to strengthen future genetic and forensic investigations raised from fingerprint heredity.

Therefore, the present systematic review has critically tried to evaluate the available evidence to fill the existing gap and extracted familial fingerprint data to show fingerprint pattern transmission probabilities with 95% corresponding confidence intervals. Specifically, the review aims to (i) determine the fingerprint inheritance probabilities within the families, (ii) assess the evidence for parent-of-origin effects based on specific maternal or paternal sub-patterns, and (iii) critically appraise methodological approaches to provide recommendations for improving the design, analysis, and reporting of future familial dermatoglyphics research.

Material and Methods

The study has been designed to analyze and critically evaluate the evidence related to the inheritance of fingerprint patterns within family triads. To outline the search strategy, eligibility criteria, and analytical approach a prospective review protocol was followed before any conclusive commencement that ensure methodological rigor. Throughout this review work Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) model was conducted. A systematic literature search was performed across multiple academic research electronic databases, including PubMed, Scopus, Web of Science, and Google Scholar, to identify recent relevant studies published up to May 2025. The search strategy utilized and combined medical subject headings, controlled vocabulary, and free-text keywords related to fingerprints, inheritance, and family studies, such as (fingerprint or dermatoglyphics) and (inherit or family or heredity or parent). While this strategy was adopted for all electronic databases, the reference lists were also manually examined to identify additional relevant publications not captured by the electronic database search, resulting in 12 additional records. No dedicated search of unpublished or grey literature was undertaken. Only studies published in English were considered for inclusion, and the retrieved records were sent to a reference management system. Hence, the studies were selected based on predefined eligibility criteria. Duplicate records were removed before the

two-stage screening process. Studies were considered eligible if they were original and involved sufficient data. Data were extracted through a standardized extraction form that included the first author, publication year, country of study, study design, sample characteristics, number of family triads, fingerprint classification system, analytical methods, and principal findings. For each numerical fingerprint pattern frequency reported, the original data were extracted directly from published tables to permit secondary quantitative analysis. The population of interest was human nuclear families involving at least one biological parent and child. The exposure was biological relatedness, and the outcome was any reported measure of fingerprint pattern similarity or inheritance between parents and offspring.

The methodological quality of the studies included in the quantitative synthesis was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Analytical Cross-Sectional Studies. This checklist tried to evaluate key sources of bias, including participant selection and statistical analysis. Since only two studies met the eligibility criteria, both were individually appraised. The assessment was used to support interpretation of the findings rather than as an exclusion criterion.

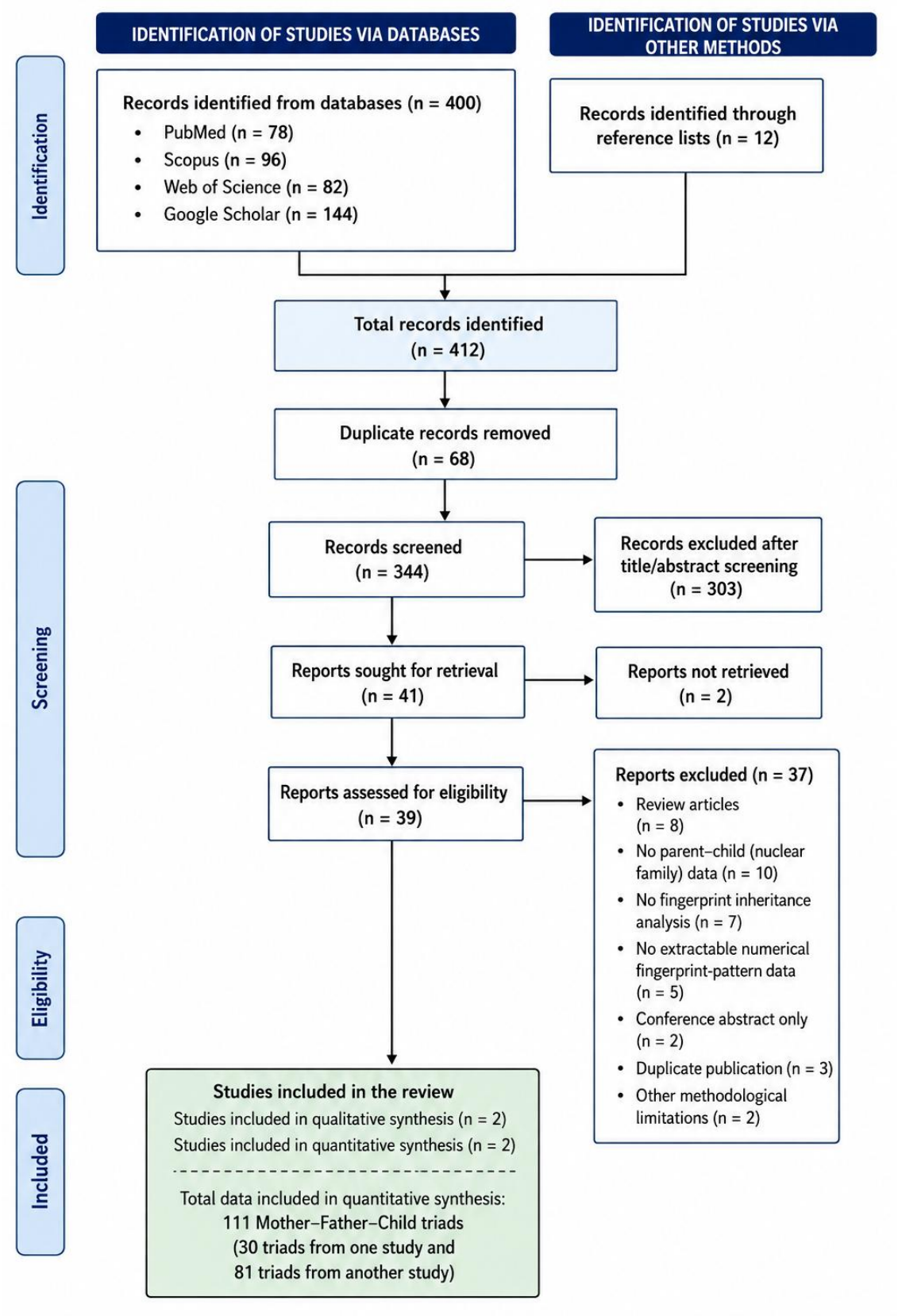


Figure 1: PRISMA Flow Diagram.

The present study mainly incorporated a detailed re-analysis of raw fingerprint pattern picture-based data from two primary familial studies that offered granular, triad-level

information, which gave a novel probabilistic result. According to the JBI checklist (Table 1), both included studies were of moderate methodological quality. Both studies clearly described their study populations, fingerprint classification methods, and statistical analyses. However, none of the studies adequately addressed the potential confounding factors or reported inter-observer reliability. Rather, the studies were found to be highly limited by relatively small sample sizes. These limitations were considered when interpreting the findings.

Table 1: Joanna Briggs Institute Critical Appraisal Checklist for Analytical Cross-Sectional Studies.

JBI Criterion	**Study 1 (30 Triads)**	**Study 2 (81 Triads)**
Inclusion criteria clearly defined	Yes	Yes
Participants and setting described	Yes	Yes
Exposure measured validly and reliably	Yes	Yes
Standard criteria used for outcome measurement	Yes	Yes
Confounding factors identified	No	No
Strategies to deal with confounding	No	No
Outcomes measured validly and reliably	Yes	Yes
Appropriate statistical analysis	Yes	Yes
Overall quality	Moderate	Moderate

The JBI appraisal indicated that both included studies were of moderate methodological quality. Although both studies employed appropriate fingerprint classification methods, there was still a limitation in sample sizes, reporting of confounding variables, and absence of reliability assessment. That is why the reported transmission probabilities should be interpreted cautiously until validated in larger, standardized family studies.

The first dataset comprised 30 Mother-Father-Child triads sourced from a published study with exact 90 fingerprints while the second dataset originally included 100 triads which mean 100 families fingerprint images with an exact 1500 fingerprints. But from the second dataset, a subset of 81 triads was selected for analysis based on stringent quality criteria for print clarity and interpretability. Based on these combined 111 triads, fingerprint pattern transmission probabilities among the triads were calculated. Since descriptive statistics were used to summarize the inheritance patterns of the fingerprint, for each parental fingerprint combination, the proportion of offspring exhibiting the fingerprint pattern was also calculated and reported as observed frequency, n/N. The Wilson score method was used to quantify the precision of these estimated proportions based on a 95% confidence level. This review distinguished between high-confidence major transmission supported by adequate sample sizes and minor associations that were suggestive but might require further validation for a better result.

Results and Discussion

The results obtained from quantitative analysis were combined to suggest a probabilistic framework for pattern inheritance. Table 2 presented a unified analysis extracted from the two major independent familial fingerprint studies (111 triads) (maternal to paternal). The data have been summarized to highlight the hereditary transmission probabilities of major and minor fingerprint patterns relation (Loop, Whorl, and their sub-patterns) from parents to offspring. Based on the findings, the genetic transmission of certain fingerprint sub-patterns demonstrated a strong observed association. For instance, when both parents possess the Loop-Ulnar sub-pattern, the child inherits it in 100% of observed cases (12/12; 95% CI: 75.8–100%).If a Loop-Ulnar Father is paired with a Loop Mother, the child also inherits a Loop pattern in 100% of observed cases (14/14; 95% CI: 78.5–100%) (Table 3). Another finding suggested that the Ulnar allele acts as a potentially influential factor that may contribute to the observed pattern association. This possible influence is supported by the 94.12% of observed cases (16/17; 95% CI: 73.0–99.0%) of a Loop child when a Loop-Ulnar Mother is paired with a general Loop Father. Besides, the significance of sub-patterns extends beyond these strong probabilities. For example, a Mother with Whorl-Plain sub-pattern and a Father with Whorl general pattern yield a Whorl child 84.62% of the time (11 out of 13; 95% CI: 57.8–95.7%). While the same Whorl-Plain sub-pattern in a Father with a Whorl Mother increases the probability to 94.44% (17 out of 18; 95% CI: 74.2–99.0%) as of Table 3. This pattern may be consistent with a possible familial or Mendelian-like

relationship, although the present data alone cannot establish a Mendelian mode of inheritance.

Similarly, a Loop-Radial sub-pattern Mother with a Loop Father produces a Loop child 85.71% of the time (12 out of 14; 95% CI: 60.1–96.0%), and a Whorl-Plain sub-pattern Mother with a Loop Father results in a Loop child 81.82% of the time (18 out of 22; 95% CI: 61.5–92.7%). Not only this, but also, the findings indicated possible parent-of-origin differences in the observed probabilities, where the same sub-pattern confers different probabilities depending on which parent transmits it. While a maternal Whorl-Plain transmission holds an 84.62% probability from Table 2 (11/13; 95% CI: 57.8–95.7%), the paternal Whorl-Plain transmission from Table 3counts 94.44% for producing a Whorl child (17/18; 95% CI: 74.2–99.0%) due to their parental source.

Table 2: Compiled relation from the one hundred eleven (111) triads (maternal to paternal) (M→F)

Mother pattern	Father pattern	Child pattern	Observed frequency (n/N)	Probability (%)	Wilson 95% CI
Loop	Loop	Loop	28/31	90.32	74.2–97.7%
Whorl	Whorl	Whorl	21/23	91.30	73.2–97.6%
Loop-Ulnar	Loop	Loop	16/17	94.12	73.0–99.0%
Loop-Ulnar	Loop-Ulnar	Loop-Ulnar	12/12	100.00	75.8–100.0%
Whorl-Plain	Whorl	Whorl	11/13	84.62	57.8–95.7%
Whorl-Plain	Loop	Loop	18/22	81.82	61.5–92.7%
Loop-Radial	Loop	Loop	12/14	85.71	60.1–96.0%
Whorl-Plain	Whorl-Plain	Whorl-Plain	11/12	91.67	64.6–98.5%
Loop	Loop	Whorl	3/31	9.68	3.4–24.9%

Note: “Father X Mother” and “Mother X Father” do not have a similar result

1: Following a Mendelian theory, take first mother’s side pattern allel then the father’s fingerprint alell.

Finally, the present study has underscored some high-probability outcomes for fundamental patterns, such as two Loop parents producing a Loop child 90.32% of the time 28 out of 31 and 91.30% of the time 21 out of 23 Whorl child is born for a Whorl Mother and Father. The present study has also highlighted rare exceptions like the 9.68% (3 out of 31) occurrence of a Whorl child from two Loop parents, which may represent low-penetrance recessive traits. Since the major general patterns set the foundation, the specific sub-patterns strongly regulate the result and generallyindicate that fingerprint inheritance is a complex but predictable trait. This finding revealed that fingerprint inheritance follows strict probabilistic rules and is also supported by independent studies employing different methodological frameworks. Offspring have shown patterns similar to their parental combinations, with high frequencies ranging from 76% for the index finger to 92% for the little finger (Aigbogun et al., 2019).

The range aligns closely with the high-probability pathways identified in the present analysis: 90.32% for a parent with both Loop-Loop pattern, 91.30% for a parent with both Whorl-Whorl pattern. Furthermore, the observation that offspring from two Loop parents can occasionally exhibit a Whorl pattern 9.68% in the present study agrees with the complex inheritance model proposed by Aigbogun et al. (2019). The complementary evidence from ridge-level analysis also supports a measurable familial correlation (Jaiyeoba-Ojigho et al., 2020). Such results across methodologies, from summarized pattern probabilities to heritability coefficients, refute notions of purely random distribution and indicate a strong heritable transmission, aligning with old classical genetic theories of dermatoglyphic inheritance (Slatis et al., 1976). From the consolidated probabilities and separating the data by inheritance direction (maternal versus paternal) and pattern category (general versus specific), the analysis has revealed distinct hereditary interpretations. These consistent results across methodologies and geographies refute notions of purely random distribution and underscore a strong heritable component, aligning with classical novel twin-study evidence (Heng et al., 2018; Rana et al., 2025; Slatis et al., 1976). The following sub-sections present each of these key relations with its supporting data and specific interpretation.

Table 3: Compiled Relation from the one hundred eleven (111) triads (paternal to maternal) (F→M)

Father pattern	Mother pattern	Child pattern	Observed frequency (n/N)	Probability (%)	Wilson 95% CI
Loop-Ulnar	Loop	Loop	14/14	100.00	78.5–100.0%
Loop-Radial	Loop	Loop	14/17	82.35	59.7–93.6%
Whorl-Plain	Whorl	Whorl	17/18	94.44	74.2–99.0%
Loop-Ulnar	Whorl	Loop	13/15	86.67	62.1–96.3%
Whorl-Plain	Loop	Whorl	11/13	84.62	57.8–95.7%

The data in Table 3 indicated that there is a directional (non-commutative) inheritance pattern, where the outcome of paternal-to-maternal (F→M) analysis is not equivalent to maternal-to-paternal (M→F) analysis. Such asymmetry may reflect differences in the observed transmission probabilities between paternal and maternal combinations, where the contribution of parental traits is not equally interchangeable. However, this observed asymmetry does not by itself establish a Mendelian inheritance mechanism, dominance, or parent-specific gene expression, given the polygenic nature of fingerprint development. Mother-to-Father inheritance analysis is completely different in result from Father-to-Mother inheritance result, which might indicate the presence of Mendelian rule in fingerprint genetics. The paternal-to-maternal (from Father to Mother) inheritance analysis also displayed high predictability with slight differences compared to M→F results.

Moreover, the analysis of the present study indicated that the paternal sub-patterns, particularly Loop-Ulnar (100%) and Whorl-Plain (94.4%), revealed higher predictive consistency in offspring compared with their maternal counterparts. This directional tendency finds interesting collateral in the broader literature. A study reported a significant association between children's fingerprint patterns and those of their mother, indicating a 40% probability of inheritance from the mother to both children, whereas similarity with the father was lower and more variable (30% for the first child and 10% for the second child) (Rana et al., 2025). Similar results were observed on fingerprint pattern inheritance from both parents to offspring, showing a, more pronounced result among daughters than sons, which suggested a possible gender-based influence on fingerprint inheritance (Mehra, 2024). In contrast, Aswini et al. (2025) identified a strong inherited similarity between fathers and their sons,

while Priyadharshini et al. (2022) reported a noticeable similarity between fathers and daughters. These different findings suggest that parental influence may be complex and potentially regulated by specific pattern types. The possibility of such differential contributions is further supported by the work of Jaiyeoba-Ojigho et al. (2020), whose quantitative heritability analysis showed varying percentages between offspring and each parent, which indicated that the strength of genetic transmission is not uniform.

This concept reflected that inheritance is not a simple probabilistic blend, which aligns with the complex genetic models proposed by researchers like Aigbogun et al. (2019), who inferred a mode of inheritance "closer to co-recessive with complex expressivity". Besides, Sharma (2022 concluded that the pattern of inheritance was more complex than simple co-dominance. This allows for scenarios where the expression of an allele may be influenced by its parental origin. The evidence, including the present finding of paternal sub-pattern, underscores the presence of potential parental redirection in fingerprint inheritance that highlights the importance of independently evaluating maternal and paternal contributions as well as considering specific pattern classes individually.

Minor Pattern Inheritance

Minor fingerprint patterns resulted from these less frequent patterns and being observed but revealed consistent hereditary trends. Table 4 has presented these inheritance trends for less frequent fingerprint pattern observed. Accordingly, although inheritance probabilities for these minor patterns are lower than those observed for major categories it indicated that parent-child effect remains evident.

Table 4: Minor pattern inheritance probabilities

Pattern Combination	Child Pattern	Observed frequency (n/N)	Probability (%)	Wilson 95% CI
Tented Arch (F)×Loop (M)	Loop	7/9	77.78	45.3–93.7%
Double-Loop Whorl (F)×Whorl (M)	Whorl	7/8	87.50	52.9–97.8%
Composite Loop (F)×Loop-Radial (M)	Loop	6/7	85.71	48.7–97.4%
Accidental (M)×Loop-Ulnar (F)	Loop	5/6	83.33	43.6–97.0%

These findings asserted that certain patterns particularly arches are less common and may follow distinct inheritance rules that agreed with the work of Reed et al. (2006), and Omuruka et al. (2019) stated that the presence of an arch pattern on at least one fingertip

showed a significant heritability. These concepts also aligns with the observations of Aigbogun et al. (2019) whose novel fingerprint classification system allowed for the study of combined patterns that led to the conclusion fingerprint inheritance involves "complex expressivity." The inherent variability of less common patterns is also suggested by population-level data; for example, in the study by Aigbogun et al. (2019), arch patterns (A) were the least prevalent (<22%), and their distribution was not entirely consistent, mentioning at more stochastic developmental outcomes. The interpretation is further supported by genetic research of Li et al. (2022), which showed that fingerprint patterning is influenced by genes involved in general limb development.

These findings significantly had addressed the existence of non-random familial similarity in fingerprint patterns by demonstrating that fingerprint pattern inheritance should be interpreted probabilistically rather than deterministically interpretation. The estimated transmission probabilities presented in this study provide a quantitative summary of familial pattern distributions and may inform future research on dermatoglyphics, population variation, and the potential forensic relevance of fingerprint inheritance.

Conclusion

According to the present study, fingerprint pattern is inherited with a quantifiable and non-random familial phenomenon between familial triads. When both parents exhibited Loop patterns, the offspring also exhibited a Loop pattern in 90.32% of cases (28/31; 95% CI: 74.2–97.7%). Some specific parental pattern combinations have shown strong probabilistic resemblance on the offspring from their respective parents which is the major finding of the present work. Particularly Loop-Ulnar and Whorl-Plain specific pattern often revealed a high degree of resemblance exceeding 90% of probabilistic similarity of the offspring. When both parents exhibited Loop-Ulnar patterns, the offspring also exhibited a Loop-Ulnar pattern in 100.0% of cases (12/12; 95% CI: 75.8–100.0%). These findings have also tried to raise constructive suggestion that further methodological consistence of genetic contribution of fingerprint inheritance is significant parametric point for future researches. Furthermore, the quantitative findings of the present study affirmed that biological mechanisms need further investigation rather than being used as only confirmatory processes like genomic imprinting. Hence, prioritizing a standardized and high-resolution parameter in a fingerprint classification is suggested to the upcoming research for a better result. Ultimately, integrating these phenotypic patterns with modern genomic approaches such as DNA profiling may help identify the specific genetic variants that contribute to these heritable traits.

Methodological Appraisal and Recommendations for Future Directions

For having a better genetic dermatoglyphics with a forensically applicable discipline, future research should adopt standardized methodological frameworks that unified fingerprint classification scheme through capturing both major patterns and sub-patterns. The digital fingerprint with high image resolution should be prioritized while reporting practices should be standardized to include pattern frequencies at individual and digit level and inheritance probabilities expressed with appropriate confidence intervals.

Furthermore, future studies should integrate a multi-parametric analytical approach for a better modeling of inheritance mechanisms including potential parent-of-origin differences (Table 5).

Table 5: Data reproducibility

Comparison	Successful outcome	Probability	Wilson 95% CI
Maternal Whorl-Plain X paternal Whorl → Whorl	11/13	84.62%	57.8–95.7%
Paternal Whorl-Plain X maternal Whorl → Whorl	17/18	94.44%	74.2–99.0%

Accessible for open science principles like data sharing should be encouraged for a better transparency and reproducibility including generalizability for future studies. Through such systematicc addressing and adaptation of standardized research practices, the future studies can move beyond descriptive pattern inheritance and strengthened forensic applications.

Conflict of Interest

All authors declare no potential conflicts of interest.

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