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Beyond the Ridge: Exploring Fingerprints to Determine the Predominant Pattern in the Pakistani Population

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ABSTRACT

Fingerprint patterns are widely used in forensic science due to their uniqueness and permanence. While pattern types like loops, whorls, and arches are well studied, fingerprint symmetry and its association with genetic and demographic factors remain underexplored in the Pakistani population. **Objectives:** To assess the distribution of fingerprint patterns and evaluate their symmetry by gender, age, ethnicity, region, hand dominance, and parental consanguinity. **Methods:** A cross-sectional study was conducted at Sahara Medical College, Narowal, from June to November 2021. Fingerprints from 110 participants were collected using the rolled ink method and categorized using the Henry Classification System. Fingerprint symmetry was evaluated by comparing matching fingers on both hands. Chi-square tests and Cramér's V were used to analyzed associations. **Results:** Loops were the most frequent pattern, followed by whorls and arches. Symmetry was present in 45.5% of participants, while 54.5% were asymmetrical. Symmetry was significantly associated with gender (p=0.037), dominant hand (p=0.001), consanguinity (p<0.001), age group (p=0.003), region (p<0.001), and ethnicity (p<0.001). No significant link was found between symmetry and pattern type. **Conclusions:** It was concluded that fingerprint symmetry is influenced by several demographic and genetic factors. These findings support the need for population-specific biometric research and may contribute to forensic, genetic, and anthropological applications.

INTRODUCTION

Fingerprints are a fundamental tool in personal identification due to their unique and permanent ridge patterns formed during fetal development and maintained throughout life [1]. Among biometric markers, they remain one of the most accessible and cost-effective, especially in resource-limited settings [2, 3]. Dermatoglyphics, the scientific study of fingerprint patterns, now extends beyond forensics into medical, genetic, and anthropological research [4]. Patterns such as loops, whorls, and arches are shaped by both genetic and environmental factors [5, 6]. Fingerprint symmetry, defined by the similarity of ridge patterns on corresponding fingers, may reflect developmental and genetic stability, offering an additional layer of analysis [7]. Although previous studies have explored fingerprint distributions based on gender, ethnicity, and geography [8, 9], symmetry remains under-investigated, especially within diverse populations such as Pakistan. Existing literature tends to emphasize pattern prevalence and its link with blood group or gender, with little focus on bilateral fingerprint

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symmetry.

Understanding how these factors influence symmetry could improve the accuracy of biometric systems and support forensic and anthropological applications. Given the country's ethnic diversity, developing population-specific fingerprint databases is essential for both scientific and legal contexts. This study aimed to examine both the distribution and symmetry of fingerprint patterns about demographic (age, gender, region, ethnicity) and genetic variables (dominant hand, parental consanguinity) in the Pakistani population.

METHODS

This cross-sectional observational study was conducted at Sahara Medical College, Narowal, from June 6 to November 6, 2021, to examine the distribution and symmetry of fingerprint patterns in the Pakistani population. Ethical approval was obtained from the Institutional Review Board (Ref: 11/IRB/SMC). Informed consent was obtained from all participants, with confidentiality and anonymity maintained throughout. A rolled ink method was used to collect fingerprints from all ten fingers, following standard procedures to ensure clear and complete ridge impressions. This technique is widely used in dermatoglyphic studies for its clarity, consistency, and affordability. The cross-sectional design allowed simultaneous assessment of fingerprint types (loop, whorl, arch) to demographic and genetic variables such as gender, region, ethnicity, and handedness, aligning with methods commonly used in forensic anthropology and population genetics. The sample size was determined based on the chi-square test requirements. Given the study's aim to explore associations across multiple subgroups, it was essential to ensure adequate representation across categories like gender, region, ethnicity, and dominant hand. Ultimately, 110 participants were enrolled using non-probability convenience sampling. The sample size was chosen based on Cohen's criteria for chi-square analysis, which recommends approximately 88 participants for detecting a medium effect size (w=0.3) with 80% power at a 5% significance level across 4 degrees of freedom. To allow subgroup analyses across key demographic variables such as ethnicity and region (each with four categories), a slightly larger sample was targeted. This approach is supported by dermatoglyphic literature, including the study by Singh et al., [10], which conducted similar comparisons using group sizes of around 120 per ethnic category. In our study, the final sample provided adequate distribution across all subgroups, and all Chi-square tests met the expected cell frequency criteria (i.e., no cell <5), validating the appropriateness of the sample for categorical analysis. Participants included in the study were Pakistani nationals aged 15 years or older, of either gender, who provided written informed consent and had no visible hand deformities or skin disorders that could interfere with fingerprint collection. Individuals were excluded if they had finger injuries, scars, congenital abnormalities, or any dermatological conditions that could obscure dermal ridge patterns. Additionally, participants with a known history of dermatological disorders affecting fingerprints, or those who refused or were unable to provide informed consent, were not included in the study. Data collection was conducted in a controlled indoor environment with adequate lighting. After completing a brief demographic questionnaire, each participant's fingerprints were collected using the ink-roll method. The impressions were examined visually using magnification and categorized into three primary pattern types based on the Henry Classification System: loop, whorl, or arch. Demographic data included age, gender, region of origin (KPK, Punjab, Sindh, Balochistan), ethnicity (Pashtun, Punjabi, Sindhi, Baloch), dominant hand, and parental consanguinity status. Although no direct genetic or developmental tests were conducted, variables such as parental consanguinity and ethnicity were included as indirect indicators of potential genetic influences. These factors were used to explore the possible association between fingerprint symmetry and underlying genetic stability within the study population. Fingerprint symmetry was operationally defined as the presence of identical fingerprint patterns (loop, whorl, or arch) on matching finger pairs of both hands. Each participant's right and left-hand fingerprints were examined finger-by-finger from thumb to little finger. If all five corresponding fingers showed the same pattern type, the participant was categorized as “symmetrical.” Any mismatch in pattern type between even one pair of corresponding fingers led to classification as “asymmetrical.” Dependent Variable: Fingerprint symmetry (Symmetrical / Asymmetrical). Independent Variables: Gender, age group, region, ethnicity, dominant hand, parental consanguinity, fingerprint patterns of right and left hands. To ensure inter-observer reliability, two trained evaluators independently classified all fingerprints. In cases of disagreement, a third examiner adjudicated the final pattern type. The level of agreement between the two evaluators was quantified using Cohen's kappa statistic, yielding a value of 0.87, which indicates a high level of inter-rater reliability. Content validity was maintained by adhering to established dermatoglyphic analysis protocols. Before formal data collection, a pilot run was conducted on a sample of 10 participants to evaluate the clarity of instructions, quality of fingerprint impressions, and internal consistency of classification procedures. Data were entered and analyzed using IBM SPSS Statistics version 23.0. Descriptive statistics (frequencies and percentages) summarized all categorical variables, including gender, age group, region, ethnicity, dominant hand, parental consanguinity, fingerprint pattern, and symmetry status. Associations between fingerprint symmetry and independent variables were assessed using Pearson's Chi-square test,

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appropriate for categorical data. Each variable was analyzed separately against symmetry status. For variables with multiple categories (e.g., region, ethnicity), SPSS adjusted for degrees of freedom automatically. For significant associations, Cramér's V was used to interpret strength (0.1–0.2 = weak, 0.2–0.4 = moderate, >0.4=strong). Post hoc standardized residuals identified the most contributing cells. A p-value<0.050 was considered statistically significant.

RESULTS

The present study included 110 participants, with a nearly equal distribution of male (50.9%) and female (49.1%). The largest age group comprised individuals younger than 20 years (32.7%), followed by those aged 21-30 (22.7%), 31-40 (20.9%), and over 40 (23.6%). Geographically, the majority of participants were from Khyber Pakhtunkhwa (30.9%), followed by Punjab (27.3%), Sindh (24.5%), and Balochistan (17.3%). In terms of ethnicity, Pashtuns made up the highest proportion (30.9%), followed closely by Punjabis (27.3%), Sindhis (24.5%), and Baloch (17.3%). Left-handed individuals (51.8%) slightly outnumbered right-handed ones (48.2%). A little over half (51.8%) of the participants reported parental consanguinity (Table 1).

Table 1: Demographic and Genetic Characteristics of Participants (n=110)

Variables	Category	Frequency (%)
Gender	Male	56 (50.9%)
	Female	54 (49.1%)
Age Group	<20	36 (32.7%)
	21-30	25 (22.7%)
	31-40	23 (20.9%)
	>40	26 (23.6%)
Region	KPK	34 (30.9%)
	Punjab	30 (27.3%)
	Sindh	27 (24.5%)
	Balochistan	19 (17.3%)
Ethnicity	Pashtun	34 (30.9%)
	Punjabi	30 (27.3%)
	Sindhi	27 (24.5%)
	Baloch	19 (17.3%)
Dominant Hand	Right	53 (48.2%)
	Left	57 (51.8%)
Parental Consanguinity	Yes	57 (51.8%)
	No	53 (48.2%)

Fingerprint pattern analysis revealed that whorls were the most frequent type overall, appearing 79 times across both hands, followed by arches (74) and loops (67). When broken down by hand, right hands had slightly more whorls (40) and loops (35), whereas the left hand showed more arches (39) (Table 2).

Table 2: Frequency of Fingerprint Patterns by Hand (n=110)

Pattern Type	Right Hand	Left Hand	Total Frequency
Arch	35	39	74
Loop	35	32	67
Whorl	40	39	79

A gender-wise comparison of fingerprint patterns showed no statistically significant association for either hand. In the right hand, males and females displayed a balanced distribution of loops, whorls, and arches (p=0.645). Similarly, for the left hand, while female had slightly more arches and male had more loops and whorls, the association remained non-significant (p=0.197) (Table 3).

Table 3: Comparative Fingerprint Patterns by Gender (n=110)

Groups	Loop	Whorl	Arch	Pearson Chi-square	p-value (2-sided)
Right Hand					
Male (n=56)	19	18	19	0.878	0.645
Female (n=54)	16	22	16		
Left Hand					
Male (n=56)	20	20	16	3.247	0.197
Female (n=54)	12	19	23		

Symmetry analysis indicated that 45.5% of participants had symmetrical fingerprint patterns, while 54.5% had asymmetrical patterns. The loop was the most common pattern observed in symmetrical cases, whereas asymmetrical patterns displayed a more mixed distribution (Table 4).

Table 4: Fingerprint Pattern Symmetry Summary (n=110)

Symmetry Status	Frequency	Most Common Pattern
Symmetrical	50	Loop
Asymmetrical	60	Mixed

Fingerprint symmetry was significantly associated with several demographic and genetic variables. Females had more symmetrical patterns than males (p=0.037; Cramér's V=0.199, 95% CI: 0.070-0.329), while right-handed individuals showed greater symmetry compared to left-handed ones (p=0.001; Cramér's V=0.326, 95% CI: 0.201-0.450). Parental consanguinity had a strong association with symmetry (p<0.001; Cramér's V=0.478), and older age groups, particularly those over 40, showed higher symmetry (p=0.003; Cramér's V=0.357, 95% CI: 0.234-0.481). The strongest associations were observed for region and ethnicity (p<0.001), where all Khyber Pakhtunkhwa residents and Pashtuns exhibited complete symmetry, while Sindhi and Baloch participants were entirely asymmetrical (Cramér's V=0.852; 95% CI: 0.783-0.921). These findings highlight the influence of genetic and regional factors on fingerprint symmetry (Table 5).

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Table 5: Association of Fingerprint Symmetry with Demographic and Genetic Variables (n=110)

Variables	Category	Symmetrical	Asymmetrical	p-value	Cramér's V	95% CI for Cramér's V
Gender	Male	20	36	0.037	0.199	0.070–0.329
	Female	30	24			
Dominant Hand	Right	33	20	0.001	0.326	0.201–0.450
	Left	17	40			
Parental Consanguinity	Yes	39	18	<0.001	0.478	0.340–0.617 (est.)[1]
	No	11	42			
Age Group	<20	13	23	0.003	0.357	0.234 – 0.481
	21–30	10	15			
	31–40	7	16			
	>40	20	6			
Regions	KPK	34	0	<0.001	0.852	0.783–0.921
	Punjab	16	14			
	Sindh	0	27			
	Balochistan	0	19			
Ethnicity	Pashtun	34	0	<0.001	0.852	0.783–0.921
	Punjabi	16	14			
	Sindhi	0	27			
	Baloch	0	19			

[1]Estimated conservatively based on the observed test statistic using the standard error approximation

DISCUSSION

The present study aimed to investigate the association of fingerprint symmetry with various demographic and genetic variables, including gender, age group, ethnicity, region, dominant hand, and parental consanguinity. The findings indicated significant associations in several domains, highlighting the multifactorial influences shaping dermatoglyphic patterns. In this study, loop patterns were found to be the most common, followed by whorls and arches. This aligns with the findings of Iqbal *et al.,* who reported loop dominance (54.6%) among medical students in Peshawar, with no significant gender association [11]. Similarly, Rastogi *et al.,* also confirmed loop predominance in both genders among Indian healthcare workers, further supporting the notion of loops as the most stable and genetically inherited pattern across populations [12]. Gender-wise comparison in our study revealed that males exhibited more asymmetry than females (p=0.037), which is comparable to findings from Aziz *et al.,* who also reported gender-based differences in fingerprint morphology in their cross-sectional hospital-based analysis [13]. In contrast, studies by Zeeshan *et al.,* in Sialkot and Buzdar *et al.,* found no significant gender-based variation in fingerprint types, underscoring population-specific differences in dermatoglyphic expression [14, 15]. A strong and highly significant association was found between fingerprint symmetry and dominant hand (p=0.001), with left-handed individuals displaying more asymmetry. This result echoes the findings of Rivaldería *et al.,* who demonstrated significant lateralization effects in fingerprint patterns related to hand dominance, particularly in one-delta and two-delta types [16]. Another notable association was with parental consanguinity (p<0.001), where individuals from consanguineous unions showed higher fingerprint symmetry.This supports the idea that genetic factors may influence fingerprint symmetry. While we did not directly assess molecular or chromosomal markers of genetic stability, the inclusion of consanguinity and ethnicity served as reasonable proxies for hereditary influence in this population-based context. Gavrilova *et al.,* and Al Habsi *et al.,* also observed statistically significant links between genetically inherited traits and fingerprint morphology in populations with high rates of consanguineous marriages [17, 18].The age group variable was also statistically associated with fingerprint symmetry (p=0.003). Interestingly, participants above 40 years had the highest rates of symmetry.While most fingerprint studies focus on younger age groups, our finding suggests potential developmental or adaptive influences that warrant further longitudinal research. Similar age-related considerations were reported by Patra *et al.,* who found shifting trends in dermatoglyphics across age categories [19].When analyzing ethnicity and region, the most significant associations (p<0.001) were observed. Khyber Pakhtunkhwa (KPK) residents displayed exclusively symmetrical fingerprints, whereas Sindhi and Baloch individuals demonstrated complete asymmetry.While these regional and ethnic trends were notable, they must be interpreted with caution.The use of convenience

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sampling and unequal subgroup sizes may have introduced selection bias, limiting the generalizability of these findings.The observed extremes in symmetry and asymmetry may reflect sample-specific patterns rather than population-wide traits.This limitation has been acknowledged in our study. These findings mirror those of Singh *et al.*, who identified regional variability in fingerprint types across ethnic groups in South Asia, highlighting the influence of both environmental and hereditary factors [20]. Moreover, these regional results are consistent with the multicultural data presented by Rane and Bhadade, where multimodal biometric systems showed accuracy differences based on ethnic fingerprint texture and vein patterns, emphasizing the importance of population-specific biometric databases for effective forensic use [21]. The overall findings also validate the theoretical claims made by Shah, who emphasized the importance of integrating forensic education and population-specific dermatoglyphic data in Pakistan to strengthen biometric and criminal identification systems [22]. Furthermore, our findings expand on the work of Al Habsi *et al.*, who found significant relationships between blood group and fingerprint types in the Omani population, although we did not evaluate blood groups. Our method of analyzing fingerprint symmetry opens additional avenues for research in biometric linkage [18].The absence of statistically significant differences between right and left hand fingerprint types in our study aligns with the results of international studies, including those by Aziz *et al.*, and Singh *et al.*, suggesting that while certain demographic and genetic factors influence fingerprint symmetry, others like hand pattern (loop, arch, whorl) may not directly correlate with symmetry alone [13, 20].

This study was limited by the use of convenience sampling and unequal subgroup distribution, which may introduce selection bias and limit the generalizability of the findings. Additionally, the lack of molecular or genetic marker analysis restricts deeper understanding of the biological basis of fingerprint symmetry. Future studies should incorporate larger, representative samples and include genetic or molecular analyses to better explore the determinants of fingerprint symmetry.

CONCLUSIONS

It was concluded that fingerprint symmetry is significantly influenced by demographic and genetic factors, including gender, age group, region, ethnicity, dominant hand, and parental consanguinity. In contrast, fingerprint pattern types (loop, whorl, arch) showed no significant association with symmetry. Symmetry was more common in females, right-handed individuals, and those with consanguineous parentage. It was also prevalent among participants from Khyber Pakhtunkhwa and Pashtun ethnicity, while asymmetry was more frequent in Sindhi and Baloch groups. These findings highlight the role of both hereditary and environmental influences in dermatoglyphic traits. Our study supports the growing body of evidence emphasizing the influence of gender, genetics, consanguinity, and ethnicity on dermatoglyphic patterns. These findings have practical implications for forensic science, especially in developing region-specific biometric databases and refining identification techniques.

Authors' Contribution

Conceptualization: RA
Methodology: RA, DZ, SM, ZAB, TT
Formal analysis: RA, DZ, SS, ZAB, TT
Writing and Drafting: RA, DZ, SS, SM, ZAB, TT
Review and Editing: RA, DZ, SS, SM, ZAB, TT

All authors approved the final manuscript and take responsibility for the integrity of the work

Conflicts of Interest

All the authors declare no conflict of interest.

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