

Fingerprint-Based Blood Group Prediction: A Critical Narrative Review of Dermatoglyphic Evidence and Deep Learning Approaches

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Abstract—Fingerprint-based blood-group prediction has evolved from descriptive dermatoglyphic studies to image-classification experiments using modern machine learning. This structured narrative review examines evidence linking fingerprint characteristics with ABO and Rh phenotypes and critically evaluates the transition toward convolutional neural networks, transfer learning, ensemble models, and hybrid approaches. More than thirty directly relevant studies and supporting methodological sources were considered. Classical findings are heterogeneous: several studies report population-level associations between loops, whorls, arches, and blood-group phenotypes, whereas others report null or population-specific relationships. Recent deep-learning studies often report stronger internal classification performance, but comparison is limited by differences in dataset provenance, validation design, participant independence, class balance, and external testing. Particular caution is required when labels are not supported by laboratory-confirmed blood typing. Current evidence supports fingerprint-based blood-group inference as a research hypothesis rather than a clinically validated alternative to serological testing. Future progress depends on verified ground truth, participant-disjoint evaluation, multicentre validation, uncertainty calibration, explainability, and prospective comparison with accepted reference methods.

Index Terms—ABO blood group, convolutional neural networks, deep learning, dermatoglyphics, fingerprint biometrics, Rh factor

I. INTRODUCTION

Determination of ABO and Rh blood groups is a routine but safety-critical procedure in transfusion medicine, transplantation, obstetric care, emergency management and forensic practice. The accepted clinical approach is based on direct demonstration of red-cell antigens and, where appropriate, corresponding antibodies. Any proposed non-invasive surrogate therefore has to be evaluated against an unusually high evidentiary standard: a useful pattern-recognition result is not equivalent to a validated blood-typing assay.

The interest in fingerprints arises from a different biological and technological starting point. Friction-ridge configurations are established during fetal development, are strongly influenced by developmental biology and genetic background, and remain stable enough to support long-term personal identification [1,2]. Classical dermatoglyphic research has consequently examined whether broad ridge-pattern classes – mainly loops, whorls and arches – co-vary with inherited traits, including ABO and Rh blood groups. Reports extending over several decades have produced an uneven picture. Some populations show statistically significant associations, whereas others do not [3-20]. This inconsistency is not a minor detail; it determines how claims of individual-level prediction should be interpreted.

The last five years have introduced a second line of work. Instead of reducing a fingerprint to a single categorical pattern, deep-learning systems ingest the

image itself and learn multi-scale texture, ridge-flow and minutiae-related representations. Patil and Ingle were among the early authors to frame the problem computationally, first through fingerprint map reading and later through an optimized CNN [21,22,24]. Subsequent reports have used ResNet, EfficientNet, CNN ensembles and other architectures [30,34-41,45,47]. Several papers report internal accuracies above 90%. Those figures require unusually careful interpretation. In particular, a popular 6,000-image Kaggle dataset used in this research area states in its own data card that it was derived from SOCOFing and computationally grouped because no suitable real-world fingerprint-and-blood-group dataset was available [49]. The original SOCOFing corpus contains 6,000 fingerprint images from 600 African participants and provides gender, hand and finger labels, but no ABO/Rh phenotype [50]. Thus, high performance on the derivative dataset may reflect reproducibility of its assigned labels rather than a validated biological relationship. Subject identity, acquisition independence and blood-group ground truth must therefore be established separately for every predictive study.

A critical review is therefore timely. The central question is no longer simply whether one fingerprint pattern occurs more frequently in one blood group. It is whether the full chain of evidence – biological plausibility, data provenance, statistical independence, model design, external validation and clinical reference testing – is sufficiently strong to support reliable prediction. This paper reviews that chain rather than treating reported accuracy as the sole criterion of progress.

A. Objectives of the Review

The objectives of this review are to: (i) synthesize population-based evidence on the association between fingerprint patterns and ABO/Rh blood groups; (ii) examine the transition from descriptive dermatoglyphics to automated fingerprint-image classification; (iii) compare recent deep-learning strategies without conflating results obtained under different datasets and validation designs; (iv) identify recurring methodological weaknesses; and (v) propose a research framework capable of producing clinically and scientifically credible evidence.

II. BIOLOGICAL AND TECHNICAL BACKGROUND

A. ABO and Rh Phenotypes

The ABO system is determined principally by the presence or absence of A and B carbohydrate antigens on red blood cells, while the Rh system is clinically dominated by expression of the D antigen. The eight commonly reported ABO/Rh categories – A+, A-, B+, B-, AB+, AB-, O+ and O- – are therefore biochemical phenotypes. Their reliable determination depends on validated serological or molecular methods. A fingerprint-based classifier does not measure these antigens; at best, it estimates blood-group class from a correlated biometric phenotype. That distinction is fundamental when discussing clinical utility.

B. Fingerprint Development and Dermatoglyphics

Fingerprint ridges arise during prenatal development through interactions among genetic regulation, growth of the volar pads, tissue mechanics and the intrauterine environment. Their final macroscopic forms are conventionally described as loops, whorls and arches, but individual fingerprints contain much richer information: ridge orientation, cores, deltas, ridge counts, local curvature, endings, bifurcations, pores and textural variation [1,2]. Classical studies generally collapse this high-dimensional structure into a small number of categories. Deep-learning methods, in contrast, can represent far more of the image while sacrificing some interpretability.

C. Why an Association Is Biologically Plausible – and Why That Is Not Proof

Both blood-group phenotype and fingerprint development have genetic components, which makes population-level covariation biologically conceivable. However, shared heritability does not imply a direct causal pathway from ABO/Rh genotype to ridge morphology. The strongest historical counterpoint is the linkage analysis by Bener, which found no evidence of linkage between fingertip dermatoglyphic elements and several blood-group systems in a large family and population sample [3]. Modern association studies can still detect correlations produced by ancestry, population structure, sex distribution, sampling or other developmental factors. Consequently, predictive

performance must be demonstrated prospectively and independently rather than inferred from biological plausibility alone.

III. REVIEW METHODOLOGY

This paper was designed as a structured narrative review rather than a formal systematic review or meta-analysis. The distinction is deliberate. The literature is heterogeneous in study design, unit of analysis, fingerprint acquisition, blood-group verification, statistical reporting and machine-learning validation. Pooling effect sizes or accuracies without harmonized definitions would give a false impression of comparability.

A. Search Strategy

The literature search was updated through 16 August 2026. Searches combined terms such as 'fingerprint', 'dermatoglyphics', 'ABO', 'Rh', 'blood group', 'blood type', 'CNN', 'deep learning', 'ResNet', 'EfficientNet', 'transfer learning', 'ensemble', 'non-invasive' and 'biometric prediction'. PubMed/PMC and publisher records from Springer Nature, ScienceDirect, Wiley, Emerald and IEEE proceedings were prioritized, with DOI and bibliographic records used for metadata verification. Backward citation tracking from recent peer-reviewed articles was used to recover older dermatoglyphic studies. When a model depended on a public dataset, the dataset documentation and, where identifiable, the original source dataset were also examined. Methodological papers on fingerprint recognition, deep-learning validation and interpretability were retained when they directly informed critical appraisal of blood-group prediction studies.

B. Eligibility and Synthesis

Studies were retained if they met at least one of the following criteria: (a) empirically examined fingerprint patterns in relation to ABO and/or Rh blood groups; (b) developed a computational model to predict blood group from fingerprint images; or (c) provided methodological evidence directly relevant to fingerprint classification, deep-learning validation or model interpretability. Papers dealing only with reagent-based image interpretation of blood agglutination were not treated as fingerprint-based evidence. Duplicate reports and records with

insufficiently traceable bibliographic information were not used as core evidence. Because the search was intended for critical breadth rather than exhaustive enumeration, no PRISMA claim is made and no formal risk-of-bias score is assigned.

The review framework emphasized five points: transparent source selection, distinction between association and individual-level prediction, explicit attention to dataset provenance, scrutiny of validation design, and separate interpretation of internal and external performance. Studies were synthesized qualitatively because their populations, fingerprint acquisition methods, blood-group verification procedures, units of analysis, and computational protocols were too heterogeneous for defensible statistical pooling.

IV. EVIDENCE FROM CLASSICAL DERMATOGLYPHIC STUDIES

A. Recurrent Observation: Loops Predominate, but Associations Vary

Across many regional studies, loops are the most frequent primary fingerprint pattern. Fayrouz et al. reported a relationship between fingerprint distributions and blood groups in a Libyan population [6]. Verma et al. [10], Manikandan et al. [16], Aamir et al. [23], Rastogi et al. [25] and several other investigations also reported loop predominance with some degree of ABO association. Eboh's 490-participant study likewise found loops to be most frequent, but it did not find a significant association with ABO group; significant associations were reported for Rh status and the combined ABO-Rh classification [7]. The Omani study by Al Habsi et al. found loops in 49.4% of fingerprints and reported a statistically significant association between fingerprint pattern and blood-group classification in 200 participants [28].

The apparent consistency of loop predominance should not be confused with predictive specificity. Loops are common in the general population, so a high proportion within a blood group may reflect the marginal distribution of fingerprint patterns rather than a strong conditional relationship. For individual prediction, what matters is how much the fingerprint changes the probability of a blood-group class beyond baseline prevalence, not whether the dominant pattern is the same in both variables.

B. Null and Mixed Findings Are Equally Important

Several studies challenge a simple fingerprint–blood-group mapping. Bener's linkage analysis found no evidence of linkage between fingertip pattern elements and ABO, MN, Rh, Kell or Xg systems [3]. The Nepalese study by Kc et al. concluded that primary fingerprint distribution was not related to blood group overall, although some digit-level differences were observed [14]. Thakur et al. reported whorls as the dominant pattern in a central Indian sample but did not find a significant association with ABO group [18]. Varlekar et al. similarly reported no statistically significant relationship [29]. Paudel et al. found no significant association with ABO groups in a Kathmandu cohort, although an association with Rh factor was reported [32]. These results argue against treating any single pattern category as a universal surrogate for blood type.

C. Population Structure, Digit Effects and the Unit of Analysis

The literature is strongly population-specific. Studies have been conducted in India, Nepal, Nigeria, Libya, Oman and other regional cohorts, often with modest sample sizes and narrow age ranges. The relative frequencies of fingerprint patterns and blood groups both vary across populations, so an association observed in one setting may not transfer to another. Moreover, each participant contributes up to ten fingers. If every finger is entered into a chi-square analysis as if it came from a different person, the effective sample size is inflated because fingerprints within an individual are not statistically independent. The 2026 Scientific Reports study from Assam is notable for explicitly acknowledging this pseudoreplication concern despite its relatively large sample of 1,040 volunteers [37]. Participant-level models, mixed-effects approaches or cluster-robust inference are therefore preferable.

D. ABO and Rh Should Not Be Collapsed Without Care

ABO and Rh are biologically distinct systems. Some studies report an ABO association but no Rh association, while others report the reverse or a combined ABO-Rh effect [14,25,32,33]. Rare Rh-negative combinations also create sparse cells in conventional contingency tables and severe class imbalance in machine-learning datasets. Reporting

only eight-class accuracy can conceal these differences. At minimum, studies should provide class-wise sensitivity, specificity, precision, recall and confidence intervals, together with class prevalence.

V. FROM STATISTICAL ASSOCIATION TO AUTOMATED PREDICTION

A. Fingerprint Map Reading and Early Machine-Learning Formulations

The computational phase of the field initially retained the assumption that engineered fingerprint descriptors contain information useful for blood-group inference. Patil and Ingle proposed fingerprint map reading and machine-learning-based prediction before moving to a CNN formulation [22,24]. This was an important conceptual shift: rather than asking whether loops are more common in one blood group, the prediction task becomes a multivariate mapping from image-derived features to a categorical phenotype.

B. CNN-Based Classification

CNNs are well suited to fingerprint-image representation because local filters can learn ridge endings, bifurcation-like textures, orientation changes and progressively larger spatial configurations; this capability is well established in general fingerprint classification research [42,48]. The optimized CNN reported by Patil and Ingle was compared with LeNet-5, ZFNet and AlexNet and achieved a reported accuracy of 95.27% for its stated blood-group classification task [24]. More recent work has used ResNet-50, EfficientNet-family models and customized CNN pipelines [30,34–40,45,47]. These architectures reduce dependence on manual pattern labeling, but architectural sophistication does not compensate for uncertain phenotype labels or non-independent evaluation data.

C. Transfer Learning, Ensembles and Modern Architectures

Recent studies increasingly adopt pretrained architectures and model ensembles. Sivamurugan et al. explored deep learning on fingerprint images [30]; Revathi et al. applied ResNet-50 [35]; Chavan et al. combined ResNet50, VGG16 and EfficientNetB0 in a stacking framework and reported 93% accuracy [39]. Sachan et al. compared LeNet-5, AlexNet, VGG16,

ResNet50 and InceptionV3 on a public 6,000-image dataset, with ResNet50 performing best [38]. Banavathu et al. compared ConvNeXt-Tiny, ConvNeXt-Small, EfficientNetV2-S, RepVGG-B3g4 and MobileViT-V2 and reported 98.84% internal accuracy for EfficientNetV2-S [40]. ResNet and EfficientNet are established vision architectures [45,47], but their use does not by itself validate the blood-group labels presented to them. Across this literature, dataset provenance, participant-disjoint evaluation and external replication are more consequential than small architectural differences.

D. External Validation: The Most Important Recent Development

The strongest methodological direction in the recent literature is the move toward independent external testing. Mahmood reported development on 6,000 public images followed by external validation on 300 real-world samples in an integrated hybrid framework [41]. That design is stronger than repeated random splitting of one image directory. It nevertheless raises an important provenance question: if the development corpus is the widely reused 6,000-image derivative described above, its assigned blood-group labels require independent justification [49,50]. External results should therefore be assessed together with transparent recruitment, laboratory-confirmed phenotype, scanner characteristics, subject-disjoint sampling and a reproducible mapping between development and external labels. Independent external validation should become a minimum expectation for claims of real-world applicability.

Across the core studies, classical dermatoglyphic investigations most often evaluated loops, whorls, and arches using cross-sectional association tests, whereas recent computational studies used engineered descriptors, convolutional networks, transfer learning, or ensembles. Reported findings range from null or population-specific associations to high internal image-classification accuracy. These results are not directly comparable because sample composition, ground-truth quality, participant independence, augmentation strategy, and external validation differ substantially between studies. The individual papers and their bibliographic details are provided in the reference list.

VI. COMPARATIVE SYNTHESIS: WHAT THE LITERATURE ACTUALLY SUPPORTS

A. Evidence for Association Is Heterogeneous, Not Absent

A defensible reading of the classical literature is neither that fingerprints determine blood group nor that no relationship exists. Rather, population-level associations are repeatedly observed but are not stable enough in direction or magnitude to support a universal rule. The same dominant fingerprint pattern can occur across several blood groups, and significant results depend on region, sample composition, digit, Rh prevalence and analytical choices. This is precisely the setting in which a multivariate model may detect weak combinations of features, but it is also a setting prone to learning confounding structure.

B. Reported Deep-Learning Accuracy Is Not a Common Currency

Accuracy values from different machine-learning papers should not be ranked as though they came from a controlled benchmark. A model evaluated after random augmentation of images from a single source is solving a different problem from a model tested on new participants, a new institution and a different scanner. Preprocessing, class balancing, optimizer choice [43], augmentation [44], split proportions, duplicate handling and seed selection can all change an internal estimate. More fundamentally, the meaning of the target label must be valid. The Kaggle data card for a widely reused 6,000-image 'blood-group' collection states that the images were taken from SOCOFing and computationally grouped because a suitable real-world dataset was not available [49]. The original SOCOFing dataset contains fingerprints from 600 African subjects but does not provide ABO/Rh labels [50]. Therefore, accuracy obtained solely on this derivative collection – whether 76%, 93% or 99% – cannot by itself establish prediction of actual blood group. It demonstrates classification of the labels assigned within that dataset. Clinical or biological inference requires independently measured ABO/Rh ground truth and subject-disjoint external testing.

C. Statistical Association and Image Classification Answer Different Questions

A chi-square study asks whether pattern frequencies differ more than expected under independence. A CNN asks whether an image can be assigned to a label at useful predictive accuracy. A statistically significant association can have negligible predictive utility, while a high predictive score can arise from non-biological shortcuts. The two evidence streams should therefore be triangulated rather than treated as interchangeable. If a CNN truly captures a blood-group-related dermatoglyphic signal, its salient regions and features should be anatomically plausible, reproducible across devices and populations, and remain predictive after controlling for confounders.

VII. CRITICAL METHODOLOGICAL ISSUES

A. Dataset Provenance and Ground-Truth Verification

The most consequential weakness in the current deep-learning literature is dataset provenance. For every image, a credible study should be able to state who provided the fingerprint, how the corresponding blood group was established, whether multiple fingers or repeated impressions belong to the same individual, and which scanner or acquisition protocol was used. This is not a theoretical concern. The data card for a widely used 6,000-image Kaggle 'Finger Print Based Blood group dataset' states that it was created from the SOCOFing dataset and that fingerprint features were computationally grouped because there was no suitable real-world dataset for the intended task [49]. The original SOCOFing publication describes 6,000 images from 600 African participants with metadata for gender, hand and finger name; it does not describe ABO or Rh measurement [50]. Accordingly, those derived labels should not be treated as clinical ground truth unless an independent source demonstrates how verified blood types were linked to the images. Studies using such a corpus can validly evaluate image-classification reproducibility, but they cannot establish non-invasive blood typing from that evidence alone. Future datasets should use laboratory-verified ABO/Rh results or authenticated clinical records and preserve participant identifiers for subject-disjoint evaluation.

B. Participant-Level Independence and Data Leakage

Participant-level independence is non-negotiable. If one participant contributes multiple fingers or repeated captures, all images from that participant must remain within one partition. Otherwise, the model may learn person-specific ridge characteristics and encounter the same person in both training and testing. This can produce an optimistic estimate even when no direct blood-group signal is present. The same principle applies to augmentation: transformations should be generated only within the training partition after subject-level splitting, consistent with established augmentation practice [44].

C. Pseudoreplication in Conventional Studies

The statistical analogue of image leakage is pseudoreplication. Ten fingerprints from one participant are correlated observations. Counting 2,000 fingerprints from 200 individuals as if there were 2,000 independent participants can make standard errors too small and p-values too optimistic. Modern analyses should model participant as a cluster or random effect, or reduce the data to participant-level features before testing group differences. Bhan et al. explicitly identify this issue, which should encourage re-analysis of earlier literature where feasible [37].

D. Class Imbalance and Rare Rh-Negative Groups

Eight-class ABO/Rh prediction is intrinsically imbalanced in many populations because Rh-negative classes and AB groups are less common. Overall accuracy can therefore mask clinically important failures. Macro-averaged F1, per-class recall, balanced accuracy and one-vs-rest sensitivity/specificity should accompany accuracy. If oversampling or SMOTE is used, it must be confined to the training data; synthetic or replicated samples must never enter validation or test sets. Confidence intervals should be reported, especially for rare classes.

E. Domain Shift and Device Dependence

Fingerprint images are affected by sensor optics, resolution, compression, finger pressure, moisture, skin condition, age and acquisition technique. A network may therefore become a classifier of the

acquisition pipeline rather than blood group. External validation must intentionally change these conditions. Multicenter datasets should record device metadata so that performance can be stratified by scanner and site. Robustness testing should include low-quality and partial prints rather than only curated images.

F. Explainability and Biological Plausibility

Explainability is particularly important because the proposed predictor is not based on a known direct biochemical mechanism. Grad-CAM and related attribution methods can indicate whether the model relies on ridge structures, cores, deltas or image borders and acquisition artifacts [46]. Attribution alone does not prove biological validity, but repeated localization to plausible ridge regions across independent datasets would provide more confidence than accuracy alone. Feature-attribution analyses should be pre-specified and complemented by ablation studies.

G. Calibration, Uncertainty and the Cost of Error

Clinical classification requires more than a hard label. Predicted probabilities should be calibrated so that a nominal 90% confidence corresponds approximately to a 90% empirical success rate. Uncertain predictions should be rejected rather than forced into one of eight classes. In any future point-of-care implementation, the system should be framed as a screening or triage aid that triggers confirmatory testing, not as an autonomous transfusion decision system.

Future studies should meet minimum methodological standards: laboratory-confirmed ABO/Rh ground truth; participant-level train, validation, and test separation; documentation of scanner and acquisition protocol; reporting of class counts and imbalance handling; sensitivity, specificity, precision, recall, F1-score, calibration, and confusion matrices; external testing on an independent population or device; artifact and leakage audits; explainability analysis; and clear reporting of code, split logic, and model-selection procedures.

VIII. RESEARCH GAPS

The review identifies six gaps that should define the next phase of work.

- 1) A validated multi-institutional fingerprint–blood-group dataset does not yet exist at a scale comparable with mature biometric benchmarks. Public datasets should include participant IDs, finger identity, repeated captures, scanner metadata, demographic variables and laboratory-verified labels.
- 2) The biological basis of any predictive signal is insufficiently characterized. Studies should examine whether ridge density, orientation-field statistics, minutiae topology or other interpretable features vary reproducibly with blood-group phenotype after accounting for ancestry, sex and age.
- 3) External validation remains uncommon. Models should be frozen before testing on new institutions and devices, and results should be reported without post-hoc tuning on the external set.
- 4) The field lacks prospective studies. A clinically credible design would enroll consecutive participants, acquire fingerprints under a predefined protocol, obtain standard ABO/Rh typing independently, and evaluate the locked model prospectively.
- 5) Uncertainty and calibration receive little attention. Rejection options, probability calibration and decision-curve analysis are needed before any screening application can be discussed responsibly.
- 6) Most papers report algorithmic performance but not reproducibility artifacts. Public code, participant-disjoint split files and model checkpoints would greatly improve scientific comparability.

IX. RECOMMENDED FRAMEWORK FOR FUTURE RESEARCH

A. Stage I: Evidence-Grade Dataset Construction

Recruitment should occur across several centers with prespecified demographic strata. Blood group should be established by an accepted laboratory method. Each participant should contribute a defined set of fingers and, ideally, repeated captures under controlled and mildly perturbed conditions. Data governance must preserve participant identity internally while releasing de-identified subject codes for research splitting.

B. Stage II: Transparent Baselines Before Deep Networks

Before deploying complex architectures, researchers should establish transparent baselines: blood-group prevalence, primary fingerprint pattern, ridge density, orientation histograms and conventional classifiers. A deep network should be considered useful only if it improves on these baselines under the same participant-disjoint external test. Crucially, no baseline or deep model is meaningful for blood-group inference unless the target labels themselves are independently verified.

C. Stage III: Deep Learning With Nested Validation

Model selection should occur within the development cohort using nested or carefully separated validation. ResNet, EfficientNet and lightweight mobile architectures are reasonable candidates because they have demonstrated strong fingerprint-image representation capacity [35,38-40,47,48]. Hyperparameter search must not use the final external test set. If multiple models are compared, the comparison should include uncertainty intervals rather than a single best accuracy.

D. Stage IV: Explainability, Calibration and Failure Analysis

Before external deployment, the model should undergo attribution analysis, artifact audits, calibration testing and failure stratification. Errors should be examined by blood group, Rh status, scanner, sex, age, image-quality score and fingerprint pattern. A robust model should fail gracefully, with low confidence on ambiguous or out-of-domain images.

E. Stage V: Prospective External Evaluation

The decisive experiment is prospective external evaluation against laboratory-confirmed blood group. No participant or acquisition session from model development should appear in the test cohort. The primary endpoint should be prespecified, and clinically relevant false-negative and false-positive patterns should be reported. Until such studies demonstrate reproducible performance, fingerprint prediction should remain a research or preliminary-screening technique.

X. CLINICAL, FORENSIC AND ETHICAL IMPLICATIONS

A. Clinical Use

The most important clinical conclusion is conservative: a fingerprint classifier should not currently determine transfusion compatibility, donor selection or any other high-stakes decision. Validated immunohematologic testing – and molecular methods where clinically indicated – remains necessary for blood-group determination. A future fingerprint model could be investigated as a research or pre-screening aid, but only after prospective validation with laboratory-confirmed ground truth and an interface that communicates uncertainty and mandates confirmatory testing.

B. Forensic Use

Forensic applications have a different evidentiary threshold. A probabilistic blood-group estimate could, in principle, narrow a search or support investigative triage when combined with other evidence. Yet the result should never be represented as individual identification. The 2026 Assam study appropriately describes such associations as supplementary rather than deterministic [37]. Any forensic deployment would also require population-specific calibration and clear reporting of likelihoods rather than categorical assertions.

C. Privacy and Biometric Governance

A system that infers medical attributes from biometric data raises privacy concerns beyond ordinary fingerprint matching. Fingerprints are difficult to revoke once compromised, while blood-group information is health-related data. Dataset consent should therefore state that medical-attribute inference is being studied, and deployed systems should minimize storage, encrypt templates, separate biometric and health records, and restrict secondary use.

XI. LIMITATIONS OF THIS REVIEW

This review has several limitations. It is a structured narrative review rather than a registered systematic review, so it does not claim exhaustive capture of every publication. The underlying literature is unusually heterogeneous, and several older studies

are accessible primarily through journal archives or citation chains rather than standardized databases. No formal risk-of-bias instrument was applied because the corpus spans cross-sectional association studies, conference papers, image-classification experiments and methodological reviews. Reported machine-learning accuracies were therefore synthesized qualitatively rather than pooled. Dataset documentation was used to audit provenance where available; such documentation is not itself a peer-reviewed clinical validation source, but it is directly relevant to determining what labels a public corpus actually contains [49,50]. Finally, rapid publication activity during 2025-2026 means that the technical literature may continue to change after the search date.

XII. CONCLUSION

Research on fingerprint-based blood group prediction has progressed from descriptive dermatoglyphics to sophisticated deep-learning systems, but the maturity of the evidence has not advanced uniformly. Classical studies show that fingerprint pattern distributions can differ across ABO/Rh groups in some populations, yet null and contradictory findings are common. These results support the existence of population-level structure but do not establish a universal fingerprint signature for blood type. Deep learning broadens the search space by using the entire fingerprint image and has produced impressive internal classification results. The central methodological question, however, is whether those models learn a reproducible biological signal or merely reproduce participant identity, acquisition characteristics, dataset-specific artifacts or constructed labels. The provenance audit of the widely reused 6,000-image derivative dataset is particularly important because its source documentation does not establish laboratory-confirmed ABO/Rh labels [49,50]. Participant-level leakage, pseudoreplication, class imbalance, uncertain ground truth and limited external validation therefore remain substantial threats to validity. The field should therefore shift its emphasis from maximizing accuracy on a single public dataset to establishing whether a genuine blood-group-related signal exists under verified conditions. Laboratory-confirmed ground truth, subject-disjoint splitting,

external validation across scanners and populations, uncertainty calibration and explainable feature analysis should be treated as core design requirements. If such studies demonstrate reproducible discrimination beyond prevalence and demographic baselines, fingerprint-based inference may merit further evaluation as a supplementary screening technology. On present evidence, however, it should not be represented as a validated method of blood typing or as a replacement for established laboratory testing.

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