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Can Fingerprint Patterns Predict ABO and Rh Blood Groups? A Critical Review of Dermatoglyphic Evidence and Deep Learning Evaluation

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Abstract: ***Fingerprints can be captured in seconds and without a needle, so the idea of reading someone's ABO and Rh blood group from them is understandably attractive. The harder question is whether it actually works. A pattern that turns up a little more often in one blood group than another, across a whole population, is not the same thing as a reliable prediction for the person sitting in front of a scanner. In this narrative review we look at the observational dermatoglyphic studies, the newer deep learning work, and what the medical machine learning literature says about trustworthy evaluation. Some studies report significant associations; others, of similar size, find nothing useful. We consider why populations might disagree, why testing for an association is a different task from eight-class image classification, and where the usual weak points lie: images from the same person ending up in both training and test sets, demographic confounding, uneven class prevalence, unclear image sources, no independent external testing, poor calibration, and the clinical cost of a wrong label. Our own earlier CNN experiment is treated here as published exploratory evidence and is not re-reported as a new result. We then set out a practical evaluation framework built on verified blood-group labels, subject-disjoint data splits, transparent reporting and prospective validation, all of which should come before any medical use is considered. On the evidence so far, the question deserves more careful, hypothesis-driven work, but fingerprints have not been shown to be a clinically reliable way of determining ABO/Rh status.***

Keywords— Dermatoglyphics, ABO Blood Group, Rh Factor, Fingerprint Biometrics, Convolutional Neural Networks, Evidence Appraisal, Data Leakage, External Validation

I. INTRODUCTION

At first sight, predicting blood group from a fingerprint means linking two measurements that have very little to do with each other. ABO and Rh(D) typing tells us which antigens sit on the surface of red cells, and laboratories have well-established methods for doing it. Dermatoglyphics, on the other hand, is concerned with the shape of the friction ridges that form on the fingertips before birth. Heredity plays a part in both, but that alone does not mean one can be read off the other [1], [2].

Cheap fingerprint sensors and convolutional neural networks (CNNs) have made it easy to collect and classify large numbers of ridge images, and this is a big part of why interest in the idea has grown. Still, a good accuracy figure in a paper does not show that ridge patterns carry enough information to identify a blood group in any clinically meaningful sense.

This paper is a review, not a new experiment. We ask what the published studies really show, where bias may still be creeping in, and what a reasonable reporting standard for future work would look like. Throughout, we keep coming back to one distinction: a statistical association at the group level is not the same as accurate, repeatable prediction for an individual. The difference matters because an ABO or Rh result that is wrong cannot be used to select blood for transfusion [1].

II. REVIEW SCOPE AND ANALYTICAL APPROACH

A. Questions Guiding the Review

Four questions shape the review. First, are the reported links between visible fingerprint pattern types and blood groups reproducible? Second, do image-based learning systems actually beat simple prevalence baselines?

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Third, what methodological safeguards are needed to rule out shortcut learning? And fourth, how should possible applications be described while their clinical validity remains unproven?

B. Source Selection and Boundaries

We chose peer-reviewed observational studies from several regions so that both positive and null results were represented. Where possible we favoured recent work (2017 to 2026) that reported participant numbers and stated its conclusions clearly. Standard references on biometrics, data augmentation and blood-testing practice were used for methodological background [1], [9], [10]. Our previously published eight-class CNN study is cited as related work [8]. The review is a focused, interpretive synthesis. It does not claim systematic database coverage, and we have not pooled effect sizes or carried out a meta-analysis.

C. Evidence Categories

It helps to keep three kinds of evidence apart: observational comparisons of loops, whorls and arches; predictive models trained on images; and clinical validation of an actual decision process. An observational p-value tells us whether two distributions look independent in a given sample. It cannot stand in for a subject-level confusion matrix. In the same way, accuracy on a test set says nothing, by itself, about biological cause, calibration or safety in medical use.

III. OBSERVATIONAL FINDINGS: AGREEMENT AND CONFLICT

A. Studies Reporting Associations

Manikandan et al. reported an association between dermatoglyphic features and blood group in 150 participants [3]. In a larger study of 800 adults from eastern India, the link with ABO was significant ($p = 0.0003$), but the Rh comparison was not ($p = 0.08$) [5]. Joseph et al. also found an ABO association, although their analysis rested on only 50 people and 500 digit impressions [6]. The most recent study, by Bhan et al., reported $p = 0.030$ in a cohort of 1,040 volunteers from Assam. The authors themselves warned against reading the result at the individual level and listed fingerprint-level pseudoreplication among the study's limitations [7].

B. Studies Reporting No Useful Relationship

The negative evidence is just as substantial. Chaudhary et al. studied 700 participants in Nepal and found no significant association, and certainly nothing strong enough to support fingerprint-based blood grouping [2]. Thakur et al. reached a similar null result in 300 people from central India [4]. Taken together, these studies make it hard to assume that ridge pattern types give a stable signature of ABO/Rh status that holds from one population to the next.

TABLE I. SELECTED OBSERVATIONAL STUDIES AND THEIR IMPLICATIONS

Study	Participants	Reported finding	Interpretive limit
Chaudhary et al., 2017 [2]	700	No significant ABO/Rh association	Does not support grouping by pattern type.
Manikandan et al., 2019 [3]	150	Association reported	Small sample; prediction never tested.
Thakur et al., 2019 [4]	300	No significant ABO association	Null result; may be population-specific.
Rastogi et al., 2023 [5]	800	ABO $p = 0.0003$; Rh $p = 0.08$	Signal differs between ABO and Rh.
Joseph et al., 2025 [6]	50 (500 prints)	ABO association reported	Ten prints from one person are not ten independent people.
Bhan et al., 2026 [7]	1,040	ABO association $p = 0.030$	Authors warn about pseudoreplication and individual prediction.

C. Why Study Outcomes May Differ

Some of this disagreement probably comes from differences in recruitment, ancestry, age mix, which digits were examined, how patterns were categorised, and the local prevalence of each blood group. Many studies also classify every finger separately. If ten impressions from one person are counted as ten independent observations, the effective sample size is inflated, sometimes considerably. A significant result in one study and a null result in another may therefore say as much about design as about biology. Any future pooled analysis needs to treat people, not fingerprint files, as the independent sampling unit.

ABO and Rh also need to be looked at separately. Several studies suggest a possible ABO association while finding weak or no evidence for Rh [5], [6]. The eight-class problem (A+, A−, B+, B−, AB+, AB−, O+, O−) is not simply a finer-grained version of four-class ABO. It needs supporting evidence for both antigen systems, and enough examples from the rarer Rh-negative classes to say anything useful about them.

IV. BIOLOGICAL PLAUSIBILITY AND INFERENCE

A. Genetic Influence Does Not Imply Deterministic Prediction

Ridge formation is the outcome of complicated growth processes in the fetus, whereas ABO and Rh status depends on specific red-cell antigens and the genes that encode them. Two traits can both be heritable without being strongly correlated. A neat developmental story linking the two is best treated as a hypothesis to be tested, not as a known biochemical mechanism that explains what a network has learned.

B. From Population Correlation to Person-Level Decisions

Imagine that a particular fingerprint pattern is more common in people with blood group B than in other groups. It does not follow that most people with that pattern are group B. Whether an individual can be classified correctly depends on conditional probabilities, on how common each group is in the population, and on how much the pattern distributions overlap. Before any practical claim is made, we need confidence intervals, effect sizes and direct tests of prediction.

C. Alternative Explanations

A model can also tell the image classes apart for reasons that have nothing to do with ridges. Each labelled folder may have been collected in a different setting, there may be near-duplicate images, compression may differ between files, or the scan backgrounds may not match. These possibilities have to be ruled out before learned features are credited to dermatoglyphic biology. High accuracy after a random file-level split is particularly suspect when the same person has images on both sides of the split.

V. DEEP LEARNING APPROACHES AND THE STATE OF EVIDENCE

A. What Convolutional Models Can Learn

CNNs build up a picture of an image from local structure, layer by layer, and can pick up ridge orientation, texture and contrast without anyone designing a descriptor for them. That flexibility is useful when looking for a subtle signal, but it also gives the network plenty of room to latch onto shortcuts that have nothing to do with blood type. So the real question is not whether a CNN can fit a labelled dataset; it usually can. The question is whether it still discriminates once the imaging hardware, the subjects and the collection sites change. Augmentation and regularization help with some kinds of overfitting, but they cannot remove confounding that is built into the data [9], [10].

B. Interpretation of a Published Eight-Class Experiment

In an earlier IJARSCT paper, Rewatkar and Chandankhede (the present authors) trained a CNN on 6,000 labelled fingerprint images and reported roughly 76% accuracy on a validation set of 1,197 images [8]. That result is a reason to investigate further. We do not recompute it here, and it should not be read as a new experiment. A validation score depends heavily on how the data were put together and divided, so the figure cannot be taken as evidence of a fingerprint–blood-type relationship that carries over to other settings until it has been replicated independently, with participant identity, acquisition conditions and label sources properly documented.

The 6,000 figure is also a good example of why the number of images should not be mistaken for the number of independent donors. Several fingers, or repeat captures, from the same person can shrink the effective sample size a great deal. Without participant-level identifiers there is a hard limit on how far any claim of clinical generalization can go, however good the classification metrics look.

C. Performance Metrics in Context

Overall accuracy can hide poor performance on the less common groups. For each of the eight classes, studies should report sensitivity (recall), precision, specificity, F1-score and the number of samples, together with the full confusion matrix. Balanced accuracy, macro-averaged F1 and uncertainty intervals make comparisons less sensitive to class proportions.

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If medical use is ever contemplated, the calibration of the model's confidence and the option to reject or abstain on uncertain cases also need to be examined. No retrospective metric, however, replaces validation against standard laboratory blood grouping.

VI. THREATS TO VALIDITY AND QUALITY CONTROLS

One of the main aims of this review is to separate genuine biological uncertainty from modelling errors that could have been avoided. If a dataset lets the labels be predicted for reasons unrelated to fingerprint morphology, no change of architecture will save the scientific conclusion. The controls below should be specified before training begins, applied without access to the final test set, and reported in the paper.

TABLE II. RECOMMENDED CONTROLS FOR TRUSTWORTHY EVALUATION

Threat	Consequence	Minimum control
Participant overlap	Repeat fingers or scans leak identity cues.	Group every image by person before splitting.
Label uncertainty	Self-reported blood groups may be wrong.	Use documented serological ABO/RhD results.
Capture-site confounding	Device or background stands in for phenotype.	Stratify by device and site; run leave-one-site-out tests.
Class imbalance	High accuracy can hide failure on rare classes.	Macro-averaged scores, per-class counts, confidence intervals.
Preprocessing leakage	Augmented copies cross partition boundaries.	Split first; augment training images only.
Uncalibrated confidence	Wrong answers can look confident.	Calibration curves and abstention analysis.

A. Splitting and Leakage Prevention

Training, tuning and final testing must be done on different participants. If each volunteer gives ten fingerprints, all ten belong in the same partition. Similarity checks run before splitting can catch exact and near-duplicate images. Cropping, data-driven normalization, feature selection and synthetic image generation should, where they apply, be fitted on the training set only. Ideally, someone outside the modelling team should audit these steps.

B. External and Prospective Tests

The external test cohort should come from a different location, scanner, operator and recruitment process than the development data. Performance must be compared against a majority-class baseline and a demographics-only baseline; otherwise the classifier may simply be exploiting how common each blood group is in its source population. A prospective study would enrol consecutive participants, keep the analysts blind to the laboratory results while predictions are made, and report performance with uncertainty bounds.

C. Explainability as an Audit, Not Proof

Saliency maps and class-activation methods show which parts of an image a classifier is paying attention to. A highlighted ridge, though, is not proof of a genetically meaningful feature. Attribution maps should be checked against image borders, compression regions, scanning artefacts and background areas. Showing that performance holds across devices, and survives removal of irrelevant background, is far more convincing than an attractive heatmap.

VII. PROPOSED EVALUATION AND REPORTING FRAMEWORK

A. A Three-Stage Evidence Pathway

Stage 1 (association): estimate the relationship between person-level fingerprint characteristics and independently verified ABO/Rh labels, adjusting for relevant demographic variables. Stage 2 (prediction): train a pre-registered model, test it on participant-disjoint images without further tuning, compare it with calibrated baselines and report errors class by class. Stage 3 (transferability): evaluate the model on a new, independently recruited cohort using a different scanner and clinical setting. A finding that does not hold up at Stage 3 should still be called exploratory.

B. Minimum Information to Publish

A credible paper should report, separately, the number of people and the number of images; how many fingers were taken from each person; the scanner specifications; whether blood groups were confirmed in a laboratory; the distribution of ABO and Rh labels; preprocessing settings; the exact rules used to split the data; how hyperparameters were chosen; the full set of evaluation metrics; and whether code and audit-ready data documentation are available. Access permissions for the dataset and any consent restrictions should also be explained.

C. Predefined Success Criteria

Success should be judged against error limits that make sense clinically, not against an arbitrarily low baseline. Transfusion decisions carry serious consequences, and an exploratory fingerprint estimator should never be used to decide donor–recipient compatibility. WHO guidance calls for validated ABO/Rh determination and proper compatibility testing [1]. At most, labels derived from fingerprints could be studied as research signals, under clear restrictions stating that they are not diagnostic.

D. Separate Tests for ABO and RhD

Four-class ABO accuracy and two-class RhD accuracy should each be reported on their own before they are combined into one eight-class figure. Breaking the result down in this way shows whether a classifier is mostly learning local class prevalence or seems to carry real information about each blood-group system. A model might, for instance, do reasonably well on the common ABO classes and yet perform no better than a prevalence-only baseline on the Rh-negative cases. A single combined score would hide that imbalance. Separate analyses also let researchers compare the predictions with the laboratory definition of each target, rather than treating two different antigen systems as if they were interchangeable.

E. Negative Controls and Falsification Tests

A good study design should actively try to prove the fingerprint hypothesis wrong. Useful negative controls include training a model on a cropped patch of blank background; training on images with the ridge detail removed; checking whether file metadata alone predicts the label; and shuffling the blood-group labels within each recruitment centre. If the background-only model does surprisingly well, or if performance falls apart once device effects are removed, confounding needs to be investigated before anyone claims a dermatoglyphic signal. It is also worth comparing a model that sees single, randomly chosen fingers with one that pools all of a participant's fingers. Agreement between the two would be easier to interpret than results from an ever-deeper network.

F. Statistical Precision and Sample Requirements

Every key metric should come with a 95% confidence interval computed at the participant level. Estimates for rare classes can be very uncertain even when the image collection as a whole looks large. Sample-size planning therefore has to be based on the expected number of independent donors in each ABO/Rh category and on the highest error rate that would be acceptable. When several models or preprocessing variants are tried, the authors should explain how they dealt with multiple comparisons and hyperparameter selection. The final test set should stay locked until one pre-specified model and decision rule are ready to be evaluated.

G. Reproducibility and Transparent Limitations

For this line of research to move forward, groups should record how labels were obtained, whether images were screened for duplicates, and what information was missing. Releasing patients' fingerprints publicly is not needed for reproducibility, provided that privacy-preserving audit materials, aggregate distributions, data dictionaries, model configuration files and a controlled route for independent validation are made available. Papers should say plainly when individual identifiers, demographic breakdowns or external cohorts are not available. Being open about these gaps is better science than presenting a promising exploratory score as if it were a validated diagnostic tool.

VIII. ETHICAL AND PRACTICAL CONSIDERATIONS

Fingerprints are highly sensitive identifiers, and once they are linked to medical labels the privacy and consent obligations go well beyond those of an ordinary computer vision dataset. De-identification should keep participant codes apart from identifying details, and study protocols should set out controlled access, how long data will be kept, and what happens when a participant withdraws. Reusable biometric images should not be released without a lawful and ethically sound reason.

The wording used to describe these systems should also match the evidence. A phrase like "blood group detection" suggests that the system measures antigens, when in fact fingerprint image analysis only estimates a label statistically. Until a system has been externally validated and approved for use, "experimental fingerprint-based blood-group prediction" is the more honest description. Any demonstration interface should state that its output must not be used for transfusion, transplantation, emergency matching or diagnosis.

IX. OPEN PROBLEMS AND FUTURE RESEARCH

Several problems remain open. First, multi-centre datasets are needed that link scanned fingerprints to laboratory-confirmed blood groups through non-identifying participant IDs. Second, evaluations should check whether any signal survives across ancestry, sex, device type, individual fingers and geography. Third, it has to be shown that ridge-pattern features do better than demographic and prevalence baselines on their own. Fourth, models should be calibrated and tested on their ability to hold back uncertain predictions instead of being forced to pick one of eight labels.

Fifth, the uncertainty about the underlying biology should be tackled with pre-registered hypotheses and independent replication, not just bigger networks. An ablation study could compare hand-crafted loop/whorl/arch features, ridge texture descriptors, CNNs on raw images, and models trained with the background removed. Negative and inconclusive results deserve to be published in full. Together, these steps would help tell a genuine, transferable association apart from correlations that belong to one particular dataset.

X. CONCLUSION

The published evidence on fingerprint morphology and ABO/Rh status is mixed. Some observational studies report significant relationships, while others, just as carefully documented, find none. Deep learning makes the hypothesis easier to test with richer image representations, but apparent predictive success may come from subject overlap, site-specific artefacts or population structure rather than from blood-group information. We therefore recommend person-level inference, external replication, transparent baselines and a clear line between experimental prediction and clinical testing. For now, fingerprints are not an established substitute for laboratory blood grouping, and whether they relate to ABO/Rh phenotypes at all remains a question for well-controlled research.

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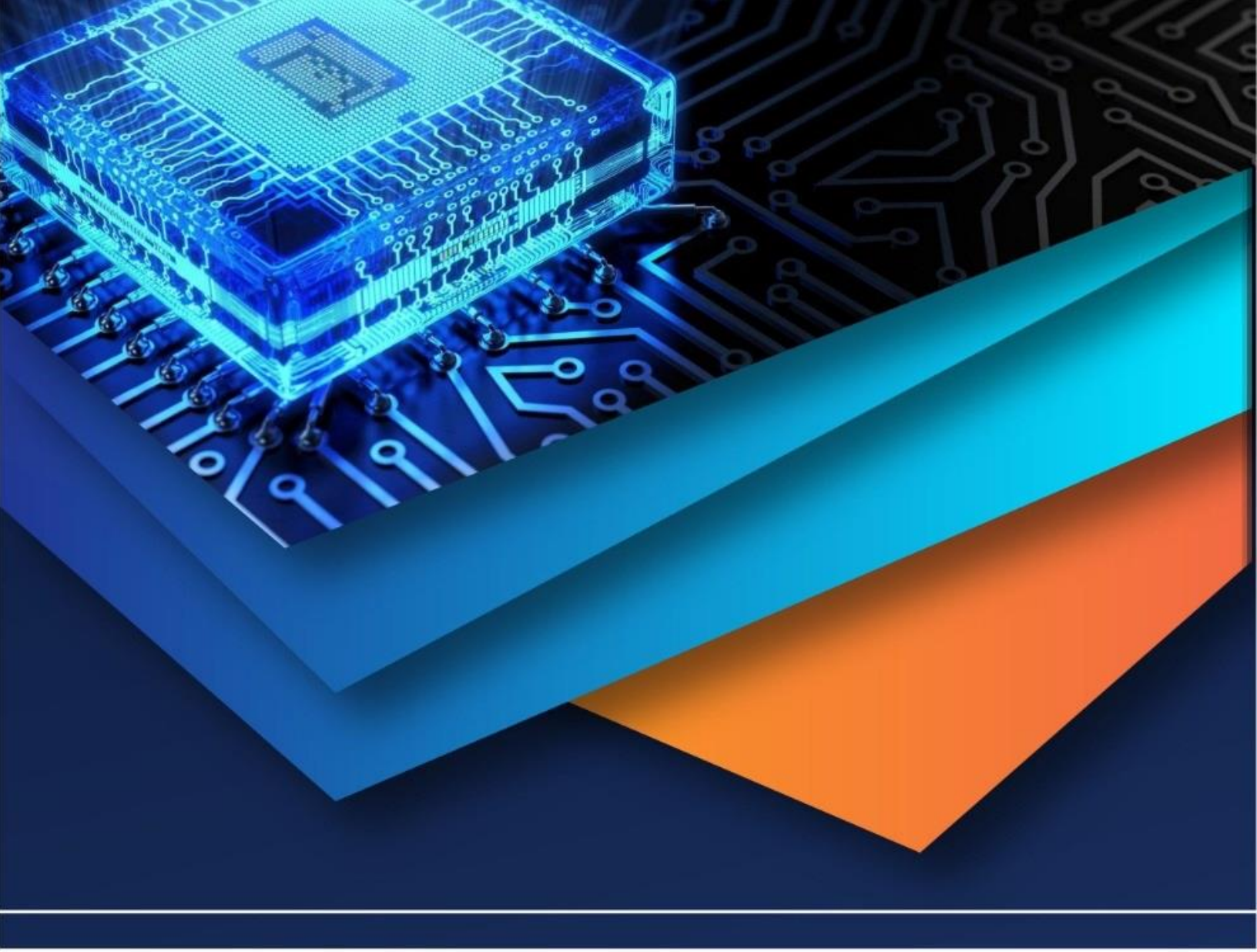
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