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Fingerprints and paternity testing: a study of genetics and probability in pre-DNA forensic science

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This article is a study of forensic science researchers' attempts to develop paternity tests based on fingerprint patterning, a physical trait that is partially inherited. Pursued in different times and places—ranging from Austria to Japan to China and from the early 20th century to the 1990s—the projects under study represent an ongoing dialogue, carried out through decades of international scientific exchange, about how to extract genetic information from fingerprints and present this data as scientifically-valid evidence in courts of law. Over time, those who engaged in this work increasingly experimented with methods for presenting fingerprint-based evidence of paternity in quantifiable and even probabilistic terms. Fingerprint-based paternity tests remained an obscure area of forensic practice and were eventually overshadowed by advances in serology and DNA profiling. This unfamiliar corner of forensic science, nonetheless, can provide additional perspective on the history of statistical expertise and probabilistic reasoning in modern forensic science, including the application of Bayesian approaches. The larger body of 20th-century 'dermatoglyphics' knowledge out of which these tests emerged also continues to influence the foundation of scientific knowledge on which latent print examination is based today.

Keywords: forensic science; fingerprinting; paternity test; genetics; serology; dermatoglyphics; Bayes Theorem; Essen-Möller formula; history; China.

1. Introduction

Since the start of the 21st century, discussions about the strengths and weaknesses of forensic disciplines and pathways for their reform have been deeply shaped by expectations and standards associated with DNA profiling (Murphy, 2010). As stated in the report of the National Research Council of the National Academies: 'Unlike many forensic techniques that were developed empirically within the forensic community, with little foundation in scientific theory or analysis, DNA analysis is a fortuitous byproduct of cutting-edge science' (National Research Council, 2009, p. 99). Viewed in this way as a 'model forensic discipline' grounded in basic research, academically-validated methods, and probabilistic reasoning, DNA profiling has come to provide a general blueprint for what it might mean to give other forensic disciplines stronger scientific foundations (Murphy, 2010, p. 17; National Research Council, 2009, pp. 128, 133, 139–140; Lynch *et al.*, 2008, pp. 4–5, 306–310). Against this backdrop, the field of latent print evidence has seen a number of new developments. These include, for example, new procedures for formalizing the analysis of fingerprint minutiae, attempts to quantify error and formalize its presentation, and the development of models for using probabilistic reasoning to assess

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the value of latent fingermark evidence (Champod *et al.*, 2016; Edmond *et al.*, 2014; Abraham *et al.*, 2013).

The present moment is not, in fact, the first time that academically-validated methods associated with scientific disciplines such as human genetics or even probabilistic reasoning have influenced forensic applications of fingerprinting. During the 20th century, these same elements coalesced around the interpretation of fingerprint evidence in another area of forensic practice—namely, paternity testing. It is well known that the 20th century saw a revolution in methods of paternity testing that was driven by a series of technical developments in serology, human genetics, and, subsequently, molecular biology (e.g. Patzelt, 2004). The history of fingerprinting intersects with this story via the skein of scientific concerns associated with 'dermatoglyphics', a prolific but obscure discipline concerned with the scientific study of skin ridge patterning on the fingers and palms. Before and after World War II, researchers in this field explored the possibility that fingerprint patterning could yield insights into human heredity, the origins and migrations of racially-defined populations, and even the presence of congenital conditions such as Down syndrome (Cummins and Midlo, 1943; Cole, 2002, pp. 97–118; Miller, 2002, 2003; Asen, 2018).

It was in the context of this multifaceted scientific field that researchers working at various global sites attempted to develop paternity tests that could use fingerprint patterning to investigate the genetic relationship between a known biological parent, putative parent and child. Three such projects are examined in this article: (1) Austrian anthropologist Margarete Weninger's (1896–1987) use of the early 20th-century methodology of 'similarity diagnosis' to incorporate fingerprint evidence into paternity testing; (2) Japanese medico-legal scientist Matsukura Toyoji's (1906–1993) development of a paternity test based on the novel theory of fingerprint pattern genetics that he developed during the 1950s; and (3) Chinese medico-legal researcher Jia Jingtao (1927-) and his colleagues' critical evaluation of Matsukura's approach in 1980s and 1990s China, a context in which DNA profiling was just starting to see adoption. While pursued in very different times and places, these projects represent three points in an ongoing dialogue—carried out through decades of international scientific exchange—about how to extract genetic information from fingerprints and present this data as scientifically-valid evidence in courts of law. Those who engaged in this work increasingly came to experiment with methods for presenting fingerprint-based evidence of paternity in quantifiable and even probabilistic terms.

The research projects that are the focus of this article did not, in any simple or direct sense, lead to the forensic science of today. Over time, the considerable limitations involved in using fingerprint patterning as an object of genetic analysis became apparent. These included the difficulty of identifying the relevant phenotype to be analysed (whether it should be the fingerprint pattern-type, ridge count, or something else) and establishing the relative influence of genes and (prenatal) environment in the formation of these patterns.[1] Those who developed paternity tests necessarily put much time and effort into addressing these questions, if not attempting to resolve them. Over the decades, their work became part of the large body of research in dermatoglyphics that was devoted to investigating the genetics of fingerprint patterning (Mavalwala, 1977; Cole, 2002, pp. 99–103, 109–111, 117–118). These research efforts tended to confirm the partially-inherited nature of fingerprint patterning without conclusively identifying the underlying mechanisms of genetic inheritance. By the end of the 20th century, the epistemic weaknesses of fingerprint-based genetic analysis combined with the greater

[1] As Fiona A. Miller (2002, 2003) has shown, the fact that fingerprint and palm patterning is influenced by both genetics and prenatal environment made dermatoglyphics useful in the diagnosis of congenital conditions such as Down syndrome.

effectiveness of other techniques led to a general diminishing of interest in trying to use fingerprints to establish paternity.

While fingerprint-based paternity testing was at times utilized in judicial practice, it remained an obscure area of forensic practice and was eventually overshadowed by advances in serology and DNA profiling. This largely forgotten subfield of forensic science, nonetheless, can provide additional perspective on the history of statistical expertise and probabilistic reasoning in modern forensics, including the application of Bayesian approaches.[2] Such approaches have become increasingly prominent in various subfields of 21st-century forensic science, including latent print evidence (Cole, 2017). Long before DNA profiling provided an impetus for the use of probabilistic reasoning in today's forensic disciplines, it was serology (and the related discipline of population genetics) that served as an earlier 'model forensic discipline' whose approaches and methods had a tendency to migrate to (and influence standards of evidence in) other areas of forensic practice. This was the context in which Matsukura Toyoji, Jia Jingtao, and their colleagues attempted to work out the mechanisms underlying the genetic inheritance of fingerprint patterning and quantify the significance of this evidence through approaches such as Erik Essen-Möller's formula for calculating Probability of Paternity (e.g. Hummel, 1981).

At a moment today when the scientific validation of latent print evidence is a pressing issue, it is worth considering how the relationship between fingerprinting and scientific knowledge has been understood in the past. Today's discussions about what it means for fingerprinting to be 'scientific' tend to revolve around issues such as validity testing, the determination of error rates, and other ways of improving latent print examination (e.g. Haber and Haber, 2008). By contrast, the 'science' of fingerprints represented by dermatoglyphics was broader than forensic identification in scope, drew on the techniques of other scientific fields such as physical anthropology and population genetics, and, we will see, was defined by epistemic ambiguities from the start. As much as this older science of fingerprints might seem outdated today, there are points of continuity, discussed in the conclusion, that connect this story to the current field of latent print evidence. Examining this unfamiliar history can provide new perspectives on the multilayered nature of today's knowledge about fingerprints and the different ways in which this knowledge has impacted forensic practice in modern times.

2. 20th-Century developments in paternity testing

Much is at stake in the ability to determine with certainty that a child is or is not the offspring of particular biological parents. As historian Nara B. Milanich (2019) has shown, modern understandings of paternity in the Americas and Europe emerged at the intersection of varied political, legal, social and cultural concerns, not to mention through the involvement of experts of diverse disciplinary backgrounds who constructed paternity as a biological fact that could be investigated through scientific methods. While the practical applications and legal admissibility of paternity testing practices differ across different legal (and political) systems, the confirmation of biological parentage is, generally speaking, an area of applied scientific knowledge that impinges upon a broad range of legal, administrative and cultural concerns in modern societies.[3]

[2] For more on the use of such approaches in the history of various forensic fields, see Taroni *et al.* (1998).

[3] For example, in 1980s and 1990s China, a context to which we will return below, paternity tests were used to resolve the following kinds of issues: questions of forensic evidence in rape or abduction cases, civil disputes involving divorce and child-support, cases involving the mistaken identification of infants in hospitals, and even the need to confirm biological parentage within the context of China's 'birth planning' policies (commonly referred to as the One-Child Policy), which

A watershed moment in the history of paternity testing occurred in the first half of the 20th century with the discovery of the ABO blood groups as well as advances in knowledge of their heredity and distribution in different populations (Schneider, 1983, 1996). The resulting explosion in blood groups research, which was carried out at a truly international level, gave rise to new fields such as immunology and seroanthropology, and also provided forensic medicine with new methods for identifying individuals on the basis of blood type. The understanding that blood group factors were inherited in predictable ways that followed Mendelian laws also made it possible to establish with certainty which combinations of parents could yield a child of a certain blood type and which could not (Lattes, 1932, pp. 245–250). By the 1920s, parentage tests that relied upon this logic to exclude a putative parent were being used in Germany and Austria. Over the 1920s and 1930s, these methods were adopted in other continental European countries, even though there was still wide variation in the extent to which national legal systems were accepting of such evidence (Lattes, 1932, pp. 250–256; Schwidetzky, 1954, p. 2; Schneider, 1983, pp. 553–555).

Over subsequent decades, the use of blood-based paternity tests saw a number of further developments. Additional blood group systems were discovered—MN in the late 1920s, Rh in 1940, and so on, including additional sub-groups within the existing systems—and these were added to the battery of genetically-determined serological factors upon which parentage tests could be based (Sussman, 1976). Applying knowledge of the highly variable human leukocyte antigen (HLA) system, which only started to develop in the 1950s, provided an additional set of powerful tools for excluding a putative parent (Bryant, 1980, pp. 110–118; Kaye and Ellman, 1979).

Another major innovation was the development of methods for determining probability of paternity when an exclusion could not be made. Early on, paternity tests could only *exclude* a putative parent. They could not confirm parentage on the basis of blood type given that there would always be many individuals in society who shared the same blood types as the biological parents. The Swedish geneticist and psychiatric research scientist Erik Essen-Möller (1901–1992) developed a formula, based on Bayes' Theorem, which would become foundational to how this issue was resolved. In cases involving one putative father, the formula was given as:

$$W = \frac{1}{1+\frac{y}{x}}$$

In this formula, x denoted the chance that the putative father and known biological mother would yield a child embodying the specific genetic makeup (blood types or other serological factors) of the child in question, whereas y denoted the chance of the known biological mother and a random man from the relevant population yielding a child with these genes (Hummel, 1981, 1984; Sussman, 1976, pp. 124–131). The value that resulted, W, was the 'Probability of Paternity', and it represented the likelihood of the putative father being the actual biological father weighed against the likelihood that he was not.

Since mid-century, this formula as well as other ways of expressing the likelihood of paternity such as the 'Paternity Index' (which is presented as a ratio rather than as a percentage) have been used in the legal systems of various countries. By the time that DNA profiling began to transform practices of

penalized couples for having more than a prescribed number of children. See Yang *et al.* (1991, p. 166); Lu (1994, p. 80); Wang and Shen (1994, p. 243); Sun *et al.* (2002, p. 149).

forensic identification in the 1980s, paternity tests relying on the examination of blood and HLA factors were widely used, albeit not without controversy or misunderstandings of application or interpretation (Kaye, 1989). Such tests were used not simply to exclude a putative parent, but also as the basis for a calculation of Probability of Paternity, Paternity Index, or other ways of calculating the likelihood of paternity (Valentin, 1980; Litovsky and Schultz, 1998).

Paternity tests based on analysis of genetically-inherited serological factors were not the only ones that were used. Throughout the 20th century, forensic experts and law courts in various countries have also relied upon examination of a range of other physical and physiological traits—for example, physical resemblance of facial features or the ability to taste phenylthiocarbamide (PTC)—in such tests (Milanich, 2019, Chapter 5; Schwidetzky, 1954; Bryant, 1980, pp. 18–27). An important theoretical foundation for such (non-serological) paternity tests was provided in the work of Hermann Werner Siemens (1891–1969) (Schmuhl, 2008, pp. 60–68; Teo and Ball, 2009). Siemens was a proponent of Nazi racist ideologies and eugenics who is conventionally viewed as a founding figure and systematizer of twin research in human genetics. By studying the relative variability of many different traits across monozygotic (single-egg) and fraternal twins, Siemens was able to identify certain traits that routinely appeared to be similar or identical in monozygotic twins but not in fraternal twins (Siemens, 1927; Newman *et al.*, 1968 [1937], pp. 19–21; Schmuhl, 2008, pp. 60–61). In order to diagnose the unknown zygosity of other pairs of twins, one could examine the similarities or differences in these specific traits—for example, hair and eye colour—which had been shown to appear with great regularity in monozygotes (Newman *et al.*, 1968 [1937], 55–93).[4]

Siemens' 'similarity diagnosis' was influential not only in human genetics research at the time and after, but also in forensic parentage testing. This approach, which relied upon the comparison of multiple heritable traits, provided an opening for fingerprint patterning to become a viable source of evidence in such cases. It is important to remember that prior to the rise of human genetics based on molecular biology, the patterning of friction ridge skin was viewed as a physical trait worthy of genetic study due to its partially inherited nature, imperviousness to environmental influence, and convenience of use (e.g. Rife, 1953, p. 389). This was the context in which researchers turned to fingerprints as one of the traits that could potentially be used in paternity tests.

3. 'What Has One to Observe [in Paternity Testing]?... Properly Speaking Everything!': the anthropological approach of Margarete Weninger

We find one elaboration of this kind of approach in the work of Austrian anthropologist Margarete Weninger, a long-time faculty member of University of Vienna. Early on, Weninger became a member of the Working Group on Genetic Biology founded by her spouse Josef Weninger (1886–1959) at this school in the early 1930s. This group was dedicated to researching the genetic inheritance of various anatomical characteristics and also applying this knowledge in forensic appraisals of questioned parentage, which had been sought from the anthropology faculty since the mid-1920s (Teschler-Nicola, 2007, pp. 58–59; Schaumann and Plato, 1987). Weninger was also a participant in the Marienfeld Project, in which the members of the Working Group applied their various fields of expertise (Weninger's was dermal patterning of the hands) to investigate the anthropological parameters and ethno-racial identity of a local German-speaking community in Romania (Teschler-Nicola,

[4] Anthropology and genetics researchers of the interwar and post-World War II periods also investigated fingerprint patterning as one of the traits that could be used to differentiate monozygotic from dizygotic twins (e.g. MacArthur, 1938; Newman *et al.*, 1968 [1937], pp. 62–64, 83–85, 87, 92–93).

2007; Weninger, 1965a, p. 47). Following the end of the Nazi regime, which barred the Weningers from continuing their work due in part to the fact that Margarete Weninger was Jewish (Teschler-Nicola, 2007, pp. 70–71), Weninger went on to explore other subfields of dermatoglyphics research, including the inheritance of dermal patterning on palms and fingers within families and paternity testing (Weninger, 1965a).

Weninger's favoured approach to paternity testing drew on the one that had been used by the Working Group on Genetic Biology in the 1930s—that is, the comparative examination of multiple anthropological traits across known parent, putative parent, and child (Teschler-Nicola, 2007, pp. 59, 63, 70). Weninger provided an overview of this approach at the XI International Congress of Genetics (The Hague, September 1963) in a symposium that was also attended by Norma Ford Walker (1893–1968) and Lionel Penrose (1898–1972), both of whom were important figures in the field of post-World War II dermatoglyphics (Geerts, 1965, pp. 973–1003; Weninger, 1965b; Miller, 2002). Weninger began by distinguishing between traits such as fingerprint patterning that are genetically-influenced yet whose mechanism of inheritance is obscure, on the one hand, and blood groups, the only trait with 'definitive mode of inheritance with discrete phenotypes', on the other. While, as Weninger would note later on, '[it] is obvious that [paternity] exclusions on the basis of traits with known mode of inheritance are decisive', one could in no way discount the value of other characteristics such as fingerprint patterning. Rather, such traits could provide useful evidence if one carried out 'a *detailed comparison* of the similarities of the three probands that ought to include as many characteristics as possible (*polysymptomatic similarity diagnosis*) [italics in original]' (Weninger, 1965b, p. 992). Thus, in response to the rhetorical question 'What has one to observe [in paternity testing]?', Weninger's response was 'Properly speaking everything!' (p. 995).

This was the most productive approach to the use of fingerprint patterning in paternity testing, Weninger suggested, because so many questions remained about its mode of genetic inheritance. As Weninger's own survey of the existing literature showed, investigators had studied the genetic inheritance of various aspects of fingerprint patterning—ridge-counts, pattern-types, size of the fingerprint pattern, and so on—and these had yielded inconclusive results as well as limited value when it came to paternity testing. As should be clear by now, Weninger's approach was not based on principles or methods associated with serology, which had become essential for paternity testing by mid-century. Weninger (1965b, p. 992) did acknowledge the exclusionary value of blood evidence, the rare human trait with 'known mode of inheritance'. It was only when one had to rely upon traits of unknown genetic mechanism such as fingerprint patterning that 'similarity diagnosis' was called for. In such cases, it went without saying, blood-based parentage tests did not – indeed could not – provide a model for the very different kind of genetic material represented by fingerprints.

Weninger was not the only researcher with an interest in using fingerprint patterning as evidence of paternity. By the end of World War II, a number of others in continental Europe and elsewhere had also pursued this area of research (Milanich, 2019, Chapter 5; Lauer and Poll, 1930; Cummins and Midlo, 1943, pp. 246–250).[5] This work proceeded alongside a large quantity of basic research that investigated various aspects of the genetic inheritance of fingerprint patterning. For example, an influential demonstration of the partial heritability of fingerprint patterning came from the work of geneticist Sarah B. Holt (d. 1986) of the Galton Laboratory (University College London) during the 1950s and 1960s. Holt (1968) investigated correlations between the Total Finger Ridge Count values (the total number of ridges observed on all ten fingerprints) of parents and children, monozygotic and dizygotic

[5] Also see the entries of published articles on this topic listed in Mavalwala (1977).

twins, other siblings, and unrelated persons. Holt found that the observed correlations matched the values that would be expected for a physical trait that was governed by the additive effect of multiple genes.

Such work tended to generate more questions than answers not only about the specific mechanisms that were involved in the genetic inheritance of these characteristics but even about the most productive ways in which to classify fingerprint patterns to facilitate genetic study (e.g. Cole, 2002, pp. 109–111). Questions remained, for example, about whether the focus of such work should be inheritance of the pattern-type itself (arch, loop, whorl, and so on) or that of a quantitative value such as ridge counts (Fig. 1). Even among the strongest proponents of dermatoglyphics, it was not unusual to find frank statements about how little was actually known. As Harold Cummins (1894–1976) and Charles Midlo, Tulane University anatomists who were early proponents of this field of study, concluded in the early 1940s: 'Even in the present state of knowledge, dermatoglyphics can claim a place only as a minor accessory in cases of questioned paternity; there are as yet no laws of inheritance so firmly substantiated that they qualify for rule-of-thumb practice' (Cummins and Midlo, 1943, p. 247).

4. Matsukura Toyoji and the 'Biological Value' of fingerprints

An important site for research on the genetics of fingerprint patterning had always been Japan. Since the early 20th century, Japanese researchers had pursued various areas of dermatoglyphics research, including prolific studies of racial variation and genetic inheritance (Asen, 2018, pp. 64–69). As much as European and American figures—Francis Galton (1822–1911) or Harold Cummins, for example—are traditionally viewed as the founding figures of the field of scientific fingerprint research, early 20th-century Japanese research in this field was just as considerable in quantity, coherence and international impact, so much so that it is difficult to imagine that the field of Anglophone dermatoglyphics knowledge could have developed in the way that it did without the data-sets or approaches provided by this research community (pp. 68-69, 70). Some of this research on fingerprints was carried out by academics working within Japan's considerable early 20th-century infrastructure of medico-legal institutes, which emerged under the modernization of Japan's legal and educational systems following the Meiji Restoration of 1868 (Jia, 2000, pp. 290–302). These institutions provided fertile ground for pursuing basic scientific research on various aspects of fingerprint patterning in addition to other problems in forensic science.

All of this provides the context in which Matsukura Toyoji, a prolific researcher and synthesizer of medico-legal knowledge (and professor of legal medicine at Tokushima University and subsequently Osaka University),[6] developed a new theory in the 1950s that was meant to explain the genetic inheritance of fingerprint patterning and provide the basis for a workable paternity test.

4.1 *Defining the genetic mechanism of fingerprint pattern inheritance*

Matsukura's primary assumption was that the most important object of research when studying the genetic inheritance of fingerprint patterning was not the pattern-type of the fingerprint itself—for example, whorl, loop, or arch (Matsukura, 1967; Jia, 1993a, pp. 573–578). Rather, it was the quantifiable degree to which the orientation of the pattern could be said to rotate around a central point—in

[6] Matsukura's authored and edited works included a book of tables of anatomical and physiological statistics of relevance to legal medicine, books on the medico-legal dimensions of medical malpractice, and overviews of legal medicine and its role in criminal investigation.

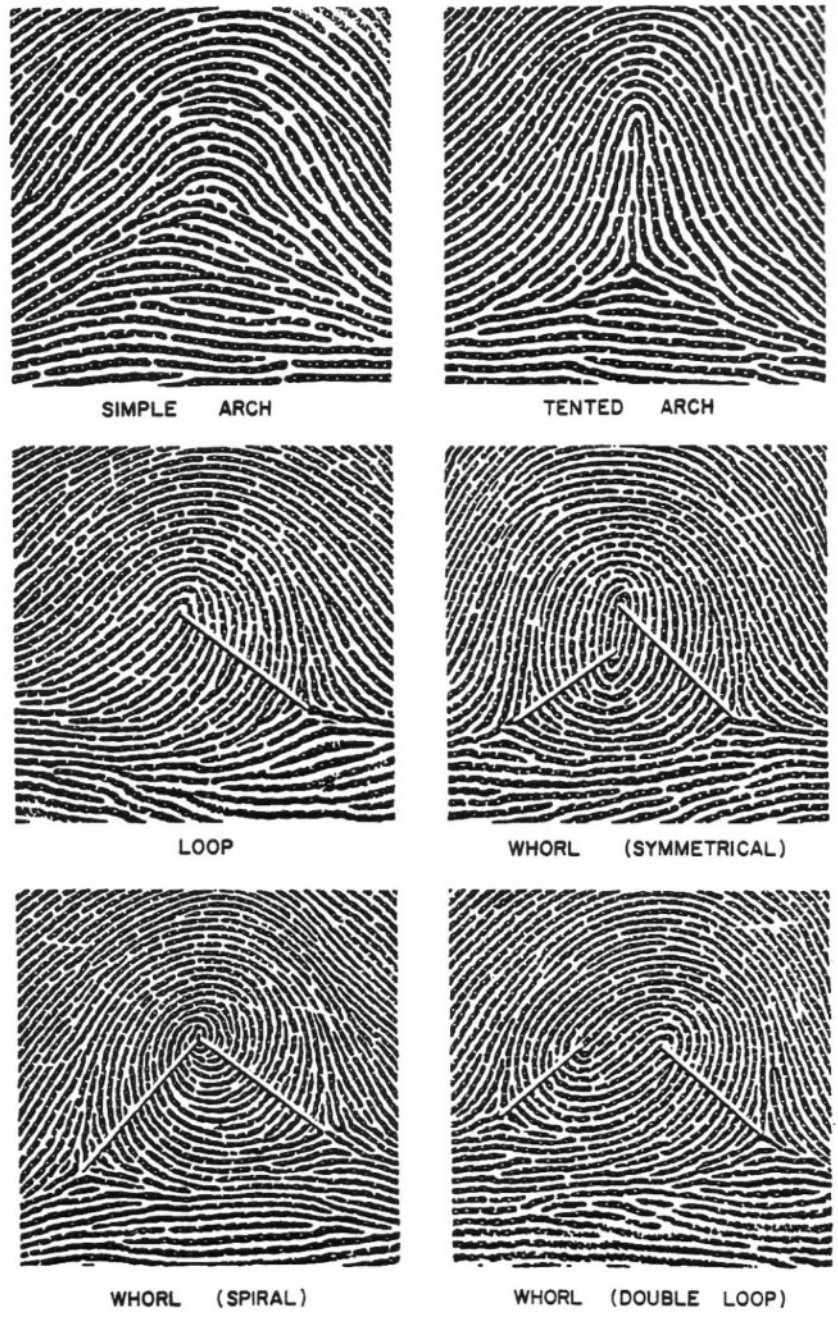

FIG. 1. Main types of fingerprint patterns with lines indicating method for counting ridges.
Source: S.B. Holt (1968). *The Genetics of Dermal Ridges*. Charles C Thomas · Publisher, Springfield, p. 20. Courtesy of Charles C Thomas Publisher, Ltd.

TABLE 1 *Ranges of biological value and associated genotypes*

Biological value	Genotype
6–96	0 (aabbccdd)
102–162	1 (Aabbccdd)
168–180	2 (AaBbccdd)
186–204	3 (AaBbCcdd)
210–240	4 (AaBbCcDd)
246–270	5 (AABbCcDd)
276–294	6 (AABBCcDd)
300	7 (AABBCCDd)
0	8 (AABBCCDD)

Note: Dominant factors indicated by capital letters. Based on Yonemura (1981, p. 129).

other words, its degree of 'winding'. Arches could be said to represent the least amount of winding, loops a moderate amount, and whorls the most, with three additional types (looping arch, whirling loop and whirling arch) reflecting intermediate degrees of winding between these pattern-types (Matsukura, 1967, pp. 228–233).[7] The degree of winding of each one of a person's fingerprints could be expressed in a numerical value: arches were assigned a value of 6, loops 18, whorls 30, and so on. Matsukura designated the sum of these values for all 10 fingers as the 'Biological Value' (BV) of a person's fingerprints (Matsukura, 1967, p. 233). A person's BV could range from 0 to 300 depending on the configuration of pattern-types across all of the fingers.[8]

Matsukura went even further, however, suggesting that the degree of winding, represented in quantitative terms as the BV, could be analysed as a physical character (phenotype) governed by alleles at four genetic loci (Matsukura, 1967, pp. 235–236). An individual who inherited a greater number of dominant factors at these loci could be expected to express more winding in their fingerprints, thus having more whorls. Individuals who inherited fewer dominant factors would have less winding, expressed in more arches. The entire observed range of human fingerprint pattern variation could thus be mapped onto nine distinct genotypes, each associated with a different number of dominant factors, ranging from zero (aabbccdd) to eight (AABBCCDD) across these four genetic loci (Table 1).

While all of this was, in Matsukura's admission, 'of course merely of a hypothetic nature', the distribution of BV values that Matsukura observed in a sample of 1365 persons from the 'general public' matched the distribution that was theoretically expected under this four-loci genetic model, as did his survey of the distribution of BV genotypes among the parent–child groupings of 329 families

[7] In conceptualizing fingerprint patterning in this way, Matsukura was building upon the work of medico-legal expert Hōjō Harumitsu (1898–1971), who had posited that the fingerprints of children might be expected to differ from those of their biological parents in certain predictable ways—namely, a given pattern-type (for example, an arch or loop) in the parent might transmute into a slightly different, albeit recognizably transitional pattern-type in the child. Under this theory, the focus of investigation shifted from the individual pattern-types themselves to the mutual relations between them, now conceptualized as part of an organic whole of genetically-influenced interactions. For an explanation of Hōjō's theory, see Jia (1993a, pp. 570–572).

[8] As Matsukura (1967, p. 234) showed, each BV value tended to have certain characteristic configurations of fingerprint patterning that were associated with it. In 81.2% of cases, for example, those who had a BV of 282 could be expected to have one loop, one whirling loop, and eight whorls. The rest of the time (in 18.8% of cases), they could be expected to have three whirling loops and seven whorls.

TABLE 2 *Possible and impossible parent–child genotype groupings*

Parents' genotypes	Child's genotype	
	Possible	Impossible
1 x 1	0–2	3–8
1 x 2	0–3	4–8
1 x 3	0–4	5–8
1 x 4	0–5	6–8
1 x 5	1–5	0, 6–8
1 x 6	2–5	0, 1, 6–8
1 x 7	3–5	0–2, 6–8
1 x 8	4–5	0–3, 6–8

Note: This table only indicates parental combinations in which one parent is of genotype 1. A complete listing would include all possible combinations of parents (genotypes 0–8). Based on Matsukura (1967, p. 242).

(Matsukura, 1967, pp. 236–240). On this basis, Matsukura claimed to have discovered a new law describing the genetic inheritance of fingerprint patterning.

4.2 *Applying the biological value in paternity tests*

As a researcher in legal medicine, Matsukura was interested in using this theory to develop practical testing procedures for evaluating paternity claims in the legal context. In the 1950s and early 1960s, Matsukura (1964; 1965) himself handled at least 23 cases in which serological tests were supplemented with analysis of the BV values of the known parent, putative parent and child, as well as with examination of facial resemblance and in some cases other characteristics of fingerprint patterning. Other Japanese medico-legal experts also analysed fingerprint patterning in cases of questioned paternity during this period, sometimes using Matsukura's method and at other times analysing the genetics of fingerprint patterning in other ways (e.g. Ueno, 1964; Shikata, 1964; Nanikawa *et al.*, 1990).

One of the ways in which Matsukura's theory could be used in paternity tests was to exclude a putative father, especially for cases in which an exclusion could not be made on the basis of serological testing. The logic was as follows: given that a child's BV was determined by the *number* of dominant genetic factors inherited from the parents at the four loci hypothesized by Matsukura, one could easily tell whether the genotypes of known biological mother and putative father contained the necessary genetic material to produce the BV observed in the child in question. To put it another way, there were limits to which combinations of parental BV genotypes could produce a child of a certain genotype, and an examiner could use this knowledge of the possible and impossible parent–child groupings to exclude a putative parent (Table 2).

In one case that Matsukura (1967, p. 261) handled, for example, a putative father could not be ruled out by serological testing, yet was excluded by fingerprint examination: according to Matsukura's theory, the parental combination of genotypes 1 and 5 (BV values of 150 and 264, respectively) could not have yielded a child of genotype 6 (BV 288). In another case, this time involving two possible fathers, analysis of both MN blood factors and BV values established that one of the men could not

possibly have been the true biological father (Matsukura, 1967, p. 262). This was because the first putative father (of genotype 5) could have yielded the child in question with the known biological mother (given that the parental combination of genotypes 5 and 3 could yield a child of genotype 6) whereas the second putative father (genotype 2) could not have.

When a putative father could not be ruled out in this way, Matsukura instead characterized the fingerprint evidence with a frequency-percentage (labelled 'rate of appearance') that was listed in the same table as the results of serological testing and other examinations that were carried out. In one case involving a known biological mother and putative father of genotypes 4 (BV 216) and 3 (BV 198) and child of genotype 7 (BV 300, equivalent of 10 whorls), Matsukura (1965, p. 54) calculated that the frequency with which this particular child-genotype (7) would appear among this parental combination (genotypes 4 and 3) was the low value of 0.1%. In another case, this time involving a parental combination of genotypes 5 and 6 (BV values of 264 and 294) and child of genotype 6 (BV 276), the frequency was calculated as 38%.[9] These percentage values represented not a Probability of Paternity (in the way that this concept was used in serological testing), but rather simply the frequency with which one might expect to find a child of a certain BV genotype among parents of particular combinations of genotypes, according to Matsukura's four-loci theory. Thus, the frequency (38%) obtained in the latter case simply indicated a grouping of parental and child genotypes that was much more likely to occur than the grouping encountered in the former case (0.1% frequency).

4.3 *Probability of paternity*

Over subsequent decades, other Japanese researchers went beyond Matsukura's presentation of frequencies to develop more sophisticated methods for calculating the probability that a putative father was the biological father on the basis of an analysis of BV values. In doing so, they directly drew on methods that were being used at the time in serological paternity tests. Furuya Yoshito and Shintaku Kikue (1976) of Tokyo Medical and Dental University, for example, calculated all possible Probability of Paternity values for different groupings of BV genotypes of known mother, putative father, and child. These values were presented in an easy-to-use table that other examiners could use to find the relevant figure without having to carry out the calculations themselves. According to Furuya and Shintaku, these calculations were made 'on the basis of Bayes's theorem [*sic*]'. Undoubtedly, this referred to Essen-Möller's formula.[10] A similar approach was followed by Yonemura Isamu (1981), a medico-legal expert at the medical school of Shinshu University, who also used Essen-Möller's formula to calculate the Probability of Paternity for BV values. Just like Furuya and Shintaku, Yonemura also presented this information in tables that could be consulted by examiners to find the relevant figure without carrying out the calculations.

We can see how this Bayesian approach to determining probabilities associated with Matsukura's BV analysis might have been used through an elaboration that appeared in a Chinese textbook of forensic anthropology in the early 1990s, a context discussed further below. In explaining Matsukura's method to Chinese readers, medico-legal expert Lin Ziqing used Furuya and Shintaku's table of

[9] Tables listing the frequencies with which each child-genotype was expected to occur for each combination of parents were included in Matsukura's (e.g. 1967, p. 239) published work. The frequencies that Matsukura presented in his cases at times coincide with and at times slightly differ from those provided in the published tables, suggesting that Matsukura was working with other tables of frequencies (or multiple such tables) over the 10+ year period in which the cases were handled.

[10] For other examples from contemporary Japanese medico-legal literature in which the formula for calculating Probability of Paternity was presented as being derived from Bayes' Theorem without mention of Essen-Möller, see Matsukura (1974, p. 355); Yonemura (1981, p. 128).

TABLE 3 *Finding probability of paternity: a hypothetical case*

Mother	Thumb	Index	Middle	Ring	Little
Right hand	Arch	Arch	Arch	Arch	Looping Arch
Left hand	Loop	Arch	Looping Arch	Arch	Loop
Putative father	Thumb	Index	Middle	Ring	Little
Right hand	Loop	Loop	Loop	Loop	Loop
Left hand	Loop	Loop	Loop	Loop	Loop
Child	Thumb	Index	Middle	Ring	Little
Right hand	Arch	Loop	Loop	Loop	Loop
Left hand	Arch	Arch	Arch	Loop	Loop

Note: Based on Jia (1993a, p. 581).

probabilities to resolve a hypothetical case involving a known mother, putative father, and child with the configuration of fingerprints indicated in Table 3 (Jia, 1993a, pp. 581–582). Following Matsukura's method, each of these pattern-types was assigned a value indicating its degree of winding (arches = 6, loops = 18, and so on). BV values were then calculated for each person (in this case, 96, 180 and 132 for mother, putative father and child), and this in turn formed the basis for determining each person's genotype (0, 2 and 1). As Lin noted, it was not impossible for parents of genotypes 0 and 2 to yield a child of genotype 1, thus one could not exclude the putative father on this basis. Rather, inserting these values into the table of probabilities provided by Furuya and Shintaku would yield a Probability of Paternity of 66.168%, which did not allow for paternity to be confirmed or ruled out either way.

As Lin Ziqing noted, the highest Probability of Paternity that could be obtained on the basis of Matsukura's method was 91.637%, which was the greatest value that appeared in Furuya and Shintaku's table (Jia, 1993a, pp. 580–581; Furuya and Shintaku, 1976, p. 21). The significance of this percentage could be further elucidated, Lin noted, by translating it into language following the style of Konrad Hummel's well-known 'verbal predicates' for Probability of Paternity values, which circulated widely (albeit in modified form) in the Japanese and Chinese forensic science literature of this period (e.g. Matsukura, 1974, p. 375; Zheng, 1982, p. 296; Jia, 1984, p. 17). Thus, the highest level of certainty that one could obtain from Matsukura's test might be characterized by the verbal predicate 'likely the father', a judgment associated with values falling within the range of 90–95%. Much like the procedures for calculating Probability of Paternity on which the work of Furuya and Shintaku and Yonemura were based, this method for translating numerical probabilities into language had also originated within the context of serological testing, only subsequently migrating into dermatoglyphics.

On this point, it is worth noting just how much Matsukura's fingerprint-based approach to paternity testing was influenced by the more widely-used and authoritative field of serology. Much as in forensic uses of serology, Matsukura's approach was based on an analysis of both the inheritance of genes within putative biological family groupings and the distribution of the same genes within the larger population. In the cases that Matsukura handled, the examination of fingerprints was used to supplement the testing of blood groups and other serological factors, which influenced how the fingerprint evidence was presented. In the work of Furuya and Shintaku as well as that of Yonemura, the influence

was even more direct, resulting in the calculation of an actual Probability of Paternity on the basis of Essen-Möller's formula. Even Furuya and Shintaku's presentation of all possible Probability of Paternity values in an easily-consulted table utilized the exact same format that was used to provide such information in serological testing (Hummel *et al*., 1971; Lee, 1980). In all of these ways, serology provided a model for the use of fingerprint evidence in paternity tests.

5. Fingerprint-based paternity tests on the eve of DNA profiling: the case of 1980s and 1990s China

One way to evaluate the legacy of Matsukura's four-loci theory of fingerprint pattern inheritance is by examining its reception in 1980s and 1990s China. Following the end of the Maoist period and the initiation of the economic reforms of the late 1970s, China's police and judicial organs saw rapid development, and this in turn facilitated an expansion of medico-legal practice, academic research in forensic science, and training programmes ranging from short-term courses to advanced graduate education (Huang, 1997). These developments were buttressed by Chinese researchers' new connections with other countries' forensic experts, institutions, and knowledge, including those of Japan. This was the context in which Matsukura's theory was introduced into China and critically evaluated by Chinese medico-legal researchers.

5.1 *Paternity testing in post-Mao China*

Paternity testing was one area of forensic practice that saw a resurgence during this period. By the late 1980s, Chinese medico-legal experts were assisting police and judicial officials in questioned paternity cases by testing various blood group systems (ABO, MN, P, Rh), serum protein systems, red cell enzyme systems, and HLA, not simply for exclusions but also to calculate the likelihood of paternity (commonly in the form of a Paternity Index value or Relative Chance of Paternity percentage) (Zhao *et al.*, 1984; Zhang *et al.*, 1991; Yang *et al*., 1991; Wang and Shen, 1994). By the early 1990s, Chinese medico-legal experts were starting to offer DNA profiling in cases involving questioned paternity, even though it was still not widely used at this point (Lu, 1994, p. 83; Sun et al., 2002, p. 154).

As much as the testing of blood groups and HLA rapidly gained authority in post-Mao China, the examination of other physical and physiological traits also remained part of the repertoire of paternity testing. In describing the different traits that could be tested in such cases, early reform-era textbooks of legal medicine generally mentioned the examination of physical appearance, dermal ridge patterning, earwax type (wet or dry), ability to taste PTC, and other physical characteristics as yielding genetic evidence that could be used to supplement serological testing. One of these textbooks, edited by Li Baozhen (1986, p. 261), noted that the ridged skin patterning of fingers, palms, and soles 'has definite reference value' in paternity tests because family members demonstrate 'a definite resemblance' that is determined by genetics. Another textbook, edited by Zheng Zhongxuan (1982, p. 296), noted that examining characteristics such as fingerprint and palm patterning and facial resemblance in addition to serological testing could yield a 'suitably reasonable judgment – that is to say, the accuracy provided by a combined probability obtained from different kinds of tests can improve the reliability of parentage appraisals'.

Beyond the discussions that appeared in textbooks, such methods were used in cases as a supplement to serological testing. In a case involving a dispute over child support handled by judicial authorities in Beijing in late 1986, for example, a range of methods were employed to attempt to

establish paternity.[11] The plaintiff in the case, a Li Yinzhu, accused Qi Chuntian of avoiding his responsibility to provide child support for their son, Qi Ran, who had been born out of wedlock in late 1985. Qi denied being the father. Paternity testing in the case was handled by the medico-legal office of the Higher People's Court of Beijing. The examiners began by investigating each person's ability to have sexual intercourse and conceive a child, as well as the timeline of the pregnancy. Next they examined the fingerprints, palm patterning, ability to taste PTC, earwax, and physical appearance of mother, putative father, and child, thereby establishing that Qi Ran had 'many characteristics that were similar to those of Qi Chuntian'. The examiners then conducted serological tests across 15 systems (including blood groups, serum proteins, red cell enzymes, and HLA), none of which ruled out Qi as the biological father.

In the end, the decisive metric was the 98.35% cumulative Probability of Exclusion of Non-Fathers, which indicated a very high likelihood that a man who was not the biological father would already have been excluded by the tests. On the basis of these tests, the court affirmed that Qi Chuntian was the biological father and ordered him to pay child support.

5.2 *Jia Jingtao's research on fingerprint genetics*

Within a legal and academic-research context in which fingerprints had some degree of salience as evidence in questioned paternity cases, it is not surprising that Chinese researchers engaged with Matsukura's theory of the genetic inheritance of fingerprint patterning. This evaluation of Matsukura's work took place through the work of Jia Jingtao and his colleagues in the legal medicine department of China Medical University, one of the earliest schools to re-establish an educational program in legal medicine after the end of the Maoist period. Jia himself had joined the faculty of the medical school in the 1950s, having studied under Chen Dongqi (1912–2006), an expert in legal medicine who had completed his own medical education at the Japanese-administered Manzhou Medical College during the 1930s (this institution was subsequently absorbed by China Medical University). In the post-Mao period, this department became one of the first to offer doctoral training in legal medicine and Jia Jingtao oversaw the training and completion of at least eight doctorates from the late 1980s to mid-1990s (Huang, 1997, pp. 162–163).

During this period, Jia developed the department's capabilities in both forensic serology and forensic anthropology, the latter being the sub-discipline within legal medicine under which his fingerprint-related research was carried out (Jia, 1993b, p. 452). In forensic serology, Jia worked out procedures for calculating Probability of Paternity and Probability of Exclusion of Non-Fathers values (also known as 'Exclusion Probability of Parentage') on the basis of Chinese gene frequency data (Jia, 1984; Jia and Song, 1986). Jia and his colleagues' work on the genetics of fingerprint patterning followed its own progression.

In the mid-late 1980s, Jia and his colleagues Lin Ziqing and Song Hongwei (at the time a PhD student under Jia) carried out a survey of existing research on the inheritance of fingerprint patterning (Lin *et al.*, 1987). Organizing their article around previous work on the inheritance of form, pattern-type, ridge count, and pattern direction (ulnar, radial or symmetrical) of fingerprints, they described the theories of Matsukura and others, with a heavy reliance on Japanese dermatoglyphics research. They concluded their review by questioning the validity of existing attempts to establish a 'biological

[11] An account of the case was included in a collection of medico-legal appraisal cases compiled by China's highest judicial authority, the Supreme People's Court. See Fayi anli bianxuan zu (1988, pp. 60–61).

classification' of fingerprint patterning, and suggested that these were without basis in biology and heavily influenced by 'subjective factors'. Jia and his colleagues further acknowledged that the 'mechanism of inheritance of fingerprints has still not been made clear'.

Jia and his colleagues also collected population data on the distribution of fingerprint ridge counts and pattern-types among Han Chinese living in Jilin province (Lin and Jia, 1989a,c). By this point, a considerable body of research on population-level fingerprint variation among China's other ethnic groups had been conducted, and Jia and his colleagues drew on this literature in their own work. They viewed this work as foundational research that was relevant not only to methods of individual identification in policing and forensics (implicitly, for example, latent print examination), but also to anthropological study of the 'origins and migrations of nationalities, the relations between different nationalities, and *medico-legal parentage appraisals* [italics added]' (Lin and Jia, 1989a, p. 366). In questioned paternity cases, possessing baseline data on dermatoglyphic variation within the general population would help an examiner to better evaluate the significance of any similarities and differences observed across the fingerprints of known mother, putative father and child. Population-level gene frequency data would also be necessary if one wanted to calculate Probability of Paternity, a concept that was clearly of interest to Jia and his colleagues in the fields of both serology and dermatoglyphics.

5.3 *Evaluating the applicability of Matsukura's theory for a Chinese population*

Possessing data on the population-level distribution of fingerprint characteristics within China was also useful because it allowed Jia and his colleagues to test the applicability of Matsukura's four-loci theory for a population that could, potentially, have a distribution of pattern-types (and thus genotypes) that was different from the one that Matsukura had studied when developing his theory in Japan. In response to this question, Lin Ziqing and Jia Jingtao (1989b) published an article in the *Journal of Forensic Medicine*, a publication associated with the Chinese Ministry of Justice's Academy of Forensic Science, detailing the results of their testing of Matsukura's theory. As described in the article, Lin and Jia had surveyed the fingerprint pattern-types of 412 families (1662 people in total) in Jilin province, the same local population that had been the focus of their other work on the distribution of fingerprint characteristics. Each set of fingerprints in the sample was classified by pattern-type, BV, and genotype (0–8), according to Matsukura's system.

Lin and Jia found that the observed distribution of pattern-types and genotypes only partially matched Matsukura's data. For example, the Han Chinese population that they surveyed had more looping arches and whorls and fewer loops than had been found in most studies that used Japanese population samples, including Matsukura's own work (Lin and Jia, 1989b, p. 34). Expectedly, the distribution of BV genotypes (which was related to the distribution of pattern-types) also differed from that which Matsukura had observed in Japan. Lin and Jia also found that in 4.13% of families examined in their study, there were parent–child genotype groupings that should have been impossible according to Matsukura's theory (pp. 33-34). As discussed above, the ranges of possible and impossible parent–child genotype groupings were crucial information that had allowed Matsukura to exclude putative fathers in the cases that he handled. This discrepancy thus had serious implications for the applicability of Matsukura's four-loci theory for questioned paternity cases involving individuals identified as Han Chinese. It suggested that Matsukura's paternity testing method was less suitable for China.

In the end, Jia and his colleagues managed to strike a not unoptimistic tone, despite the persistent uncertainties surrounding the genetics of fingerprint patterning. While the fact that this physical trait

was influenced by genetics was beyond question, the mechanisms of this influence were simply still unclear. After providing a summary of various theories about the inheritance of fingerprint patterning in his textbook of forensic anthropology, Jia (1993a, pp. 521–522) concluded:

> However, due to the complexity of the inheritance of fingerprints, a number of [research] achievements that have already been made have mostly remained at the stage of being hypotheses. Not only is it that the genetic loci determining the inheritance of fingerprints are still unclear, but that the genotypes along with their expression – that is, phenotypes – are still unable to be clearly established in the same way as are blood groups. Thus, we believe that the inheritance of dermal ridge features and their application in parentage appraisals still represent an important field with a pressing need for continuing diligent investigation.

Jia and his colleagues' engagement with these issues did not end with their critique of Matsukura's approach. Jia along with Lin Ziqing and Song Hongwei developed their own method for using fingerprint patterning in paternity tests, introducing their approach in an article published in an English-language supplement to the *Journal of China Medical University* as well as in a long section of Jia's textbook of forensic anthropology (Lin *et al.*, 1988; Jia, 1993a, pp. 582–597). Their approach involved calculating various values that described what they called the 'Intimate Degree' of fingerprints—that is, the degree to which a particular grouping of known biological mother, putative father and child demonstrates similarity across all individuals' fingerprints going beyond that which would be expected among a grouping of random people. The results of such tests, as the authors explained, could be presented as a percentage value, either in the form of a Probability of Paternity or Probability of Exclusion of Non-Fathers. These were, of course, the very same concepts that were used to quantify the weight of evidence in questioned paternity cases involving serological testing.

6. General discussion and conclusion

By the time that Jia Jingtao and his colleagues put forward this last innovation in fingerprint-based paternity testing, the testing of blood groups and HLA had already become the norm in such cases, to be followed soon after by the ascent of DNA profiling. Subsequently, the idea that fingerprint patterning could serve as valid and useful evidence in paternity testing would lose whatever legitimacy it had enjoyed earlier in the 20th-century. It goes without saying that fingerprint-based paternity testing is not part of today's discussions of forensic uses of fingerprinting, which focus on fingermark detection and source attribution. This section briefly discusses the decline of dermatoglyphics and then describes some points of continuity between this older field of knowledge and current uses of fingerprinting in forensic identification.

6.1 *The decline of dermatoglyphics*

As Simon A. Cole (2002, pp. 111–117) has described, the scientific study of fingerprint patterning—out of which the discipline of dermatoglyphics emerged—began to decline in status early in the 20th century despite 'small pockets of research' that persisted for decades afterward. One of the reasons that this happened, Cole argues, is that police examiners distanced themselves from dermatoglyphics in order to construct fingerprints as 'solely an individual identifier' without any connection to a subject's race, heredity, or other identifying personal characteristics. Doing so was meant to make

their identification practices 'seem less value-laden, more factual' (pp. 100–101, 112–113) and, ostensibly, to separate police identification work from a body of research that was contradictory and inconclusive. By implication, not only was dermatoglyphics knowledge divorced from identification work, but over time it lost status and authority.

The subfield of dermatoglyphics concerned with paternity testing was peripheral, to be sure, but also persistent. The examples described in this article confirm the genuinely international scope of this field as well as its long lifespan: the paternity tests discussed above developed in disparate locations, ranging from continental Europe to East Asia, and over a period that spanned much of the 20th century, even continuing into the 1980s and 1990s.[12] The researchers who developed these techniques were not, as a rule, uninfluential or marginal figures (e.g. Cole, 2002, p. 113). The fingerprint-related research that they carried out was developed in connection with other established academic fields. We have seen, for example, that Jia Jingtao applied his knowledge, experience and interest in forensic applications of serology to his research on fingerprints. Whatever the outcome of these efforts, in a certain sense they exemplify the kind of academically-grounded, experimentally-rigorous research process that is being called upon today as the basis for the production and validation of new forensic knowledge (Cole, 2010).

This example, as well as the others discussed in this article, suggests a field of knowledge that was generally receptive to developments that were occurring in other scientific fields. Even as the collective enterprise of scientific fingerprint research was declining in importance, it was still evolving. At the same time, of course, the examples discussed above show that there were limits to this field's potential for development and even effectiveness. Basic questions about the mode of inheritance of fingerprint patterning were never resolved satisfactorily despite the attention of generations of researchers. In the end, the deep changes that have occurred in genetics since the mid-late 20th century have not made fingerprints a *more* productive or valuable object of inquiry for studying human heredity. Rather, answers for the anthropological, genetic and medical questions posed by generations of dermatoglyphics researchers are now sought in molecular biology or elsewhere.

6.2 *Afterlives of dermatoglyphics knowledge*

Despite these shifts in the status of dermatoglyphics, today's forensic science researchers continue to find value in certain parts of this older body of knowledge. It is not unusual, for example, to find discussions of the anatomy and physiology, embryology and even genetics of dermal ridge patterning in today's literature on latent print evidence (e.g. National Institute of Justice, 2011, Chapter 3). The authors of such works tend to present these topics as a way of explaining or validating the 'uniqueness and persistence' of finger ridge patterning. These principles are still viewed as foundational to latent print examination despite the fact, expounded by Cole (e.g. 2009) and others, that the claim of fingerprint uniqueness cannot in itself guarantee the accuracy or reliability of fingerprint examination methods or evidence. The report of the National Research Council (2009, pp. 143–144), for example, included the following sentence: 'Some scientific evidence supports the presumption that friction ridge patterns are unique to each person and persist unchanged throughout a lifetime.' The footnote supporting this statement cited key authors of the 20th-century dermatoglyphics literature such as Harold Cummins and Charles Midlo as well as Sarah B. Holt.

[12] For more on the considerable amount of dermatoglyphics research that has been carried out in East Asia throughout the 20th century, see Asen (2018).

A more sophisticated discussion is found in *Fingerprints and Other Ridge Skin Impressions*, by Champod *et al.* (2016, pp. 1–31). This work covers similarly fundamental topics (for example, anatomy, morphogenesis, and genetics of friction ridge skin), but does so in order to illuminate the principles of 'permanence', 'variability', and 'selectivity' of fingerprint patterning, which are emphasized in lieu of 'uniqueness' (p. 27). These concepts support the authors' use of a Bayesian approach to formalizing the forensic decision-making process and weighing the significance of latent print evidence through the use of likelihood ratios (pp. 33-126). Here too foundational authors of dermatoglyphics are cited, including Cummins and Midlo, Holt and others, and there is substantial use of the work of Michio Okajima, whose contributions to the earlier dermatoglyphics literature included studies on comparative dermatoglyphics and the embryology of dermal ridge patterning (Biographical Sketch, 1994).

As a field concerned with a wide range of scientific concerns, the scope of dermatoglyphics was significantly broader than the forensic examination of latent fingermarks. Today, by contrast, it is the latter that has become the most important site for the application of scientific knowledge about fingerprints. Another manifestation of this shift in focus is the emphasis that is placed today on fingerprint minutiae, features that are relevant to latent print examination but that were not the focus of most of the 20th-century work on dermatoglyphics. As we have seen, earlier generations of researchers tended to view pattern-types, ridge counts, and other characteristics—not fingerprint minutiae—as being most relevant to the anthropological, genetic and forensic questions about which they were most concerned.

6.3 *The problem of population-level fingerprint pattern variation*

In paternity testing, the most salient question is the relationship between the members of a putative biological family unit. In such tests, fingerprint patterning was not used as evidence of individual identity, but rather of the genetic relationship pertaining to a specific group of individuals. We might say that in paternity testing the emphasis was placed on using fingerprints to investigate 'collective identity', to use Cole's (2013, p. 77) phrasing, rather than individual identification.[13] The focus was not on identifying one individual to the exclusion of others, but rather on establishing an individual's association with a biological family unit and, in a certain sense, defining the parameters of that person's genetic makeup. There were also instances in which the use or development of paternity testing procedures involved making claims about the distribution of fingerprint patterning at the level of *populations*. Matsukura (1967, p. 237), for example, tested his theory of fingerprint pattern inheritance by surveying 1365 members of the 'general public'. Jia and his colleagues tested the applicability of Matsukura's theory by surveying individuals who were identified as members of China's Han majority, a designation that followed the official system for classifying the country's ethnic groups (Lin and Jia, 1989b).

Today researchers are also concerned with understanding fingerprint pattern variation at the level of populations rather than simply that of individuals. This issue has emerged, for example, in the development of methods for presenting latent fingermark evidence in probabilistic form. As part of this work, researchers are exploring ways of presenting such evidence as a likelihood ratio 'comparing (a) the likelihood of observing a given fingermark considering that it originates from a particular person and (b) the likelihood of observing that fingermark considering that it originates from a random

[13] This issue is also addressed in Cole (2018), as well as Cole (2007), which explores the connections and tensions between 'individualization' and 'racial categorization' in the history of American fingerprinting.

individual in a relevant population', the latter requiring a 'reference database' of population-level data (Neumann *et al.*, 2015, p. 168; Neumann *et al.*, 2012). The issue of population-level variation in fingerprint patterning is also relevant for attempts to formalize the procedures for selecting fingerprint features (especially minutiae) for analysis, which also involves determining their relative value for making an identification (Expert Working Group on Human Factors in Latent Print Analysis, 2012, pp. 55–62). Evaluating the evidentiary value of fingerprint characteristics in this way involves determining the relative 'rarity' of different features in the larger population.

In support of this and other applications, researchers have already turned to the question of how frequently particular classes of fingerprint minutiae appear across the different fingers of individuals and in different human populations (Fournier and Ross, 2016; Gutiérrez *et al.*, 2007; Gutiérrez-Redomero *et al.*, 2011, 2012; Dankmeijer *et al.*, 1980).[14] It seems likely that more research will be done in this area in the future. Both the 2009 report of the National Research Council and a 2012 report sponsored by the National Institute of Justice and National Institute of Standards and Technology have identified producing data on 'the frequency of [fingerprint] features in different populations' as an area of productive research (National Research Council, 2009, pp. 139–140; Expert Working Group on Human Factors in Latent Print Analysis, 2012, p. 75). This work is meant to improve the evidentiary value of fingermarks discovered at crime scenes. Once again, the goal of current research is narrower in scope than that of the older field of dermatoglyphics, which was concerned with producing general anthropological knowledge about different human populations.

6.4 *Conclusion*

Looking back from the start of the 21st century, it is apparent that there are aspects of both continuity and change in the foundation of scientific knowledge that supports fingerprint identification. Researchers continue to study fingerprint patterning at the level of individuals and populations, in the process negotiating its meanings as both a signifier of individual identity and an indicator of broader socially-relevant categories (Cole, 2007, 2013, 2018). New concepts of proof and statistical techniques (and, of course, technologies) continue to transform the base of knowledge underlying forensic uses of fingerprint patterning, much as they did throughout the 20th century. From this perspective, today's attempts to apply scientific validation, population data, and Bayesian approaches to the field of latent print evidence should not be viewed as wholly unprecedented. Rather, they represent one more iteration of negotiations between fingerprinting, scientific disciplines, and probabilistic reasoning that have been evolving over decades.

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[14] For discussion of some of the pitfalls of using 'race' as a category for classifying populations in such research, see Cole's (2018, pp. 5–10) critique of Fournier and Ross' (2016) study of fingerprint minutiae variation. Cole refutes the claim advanced by Fournier and Ross that one might be able to 'predict the [racial] ancestry of an individual' from an examination of fingerprint minutiae. By implication, Cole claims, '[the] limited practical significance of corroborating a fingerprint association with an ancestry analysis [a possibility raised by Fournier and Ross] suggests that dermatoglyphics may be a hammer in search of a nail' (p. 8). Cole's point is well-taken in regard to this particular way of using dermatoglyphics knowledge. At the same time, it is important to note that the kind of 'predictive' approach outlined by Fournier and Ross is one that has been unusual even among 20th-century dermatoglyphics researchers, who were much more interested in surveying fingerprint-pattern variation across racially-defined groups than they were in attempting to determine racially-defined identities in individuals (e.g. Asen, 2018).

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