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ANALYSIS OF DERMATOGLYPHIC HERITABILITY : A STUDY OF PHENOTYPIC RELATIONSHIPS

by

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Analysis of Dermatoglyphic Heritability: A Study of Phenotypic Relationships

Chair: Randall R. Skelton

The area of dermatoglyphics has been researched for over 100 years. Starting with observations between fingerprint pattern type and its occurrence rate in biologically related individuals by Galton, the quest for answers to genetic questions determined from observing dermatoglyphics has continued into the 21st century. Great strides have been made in the application of statistical formulas to dermatoglyphic data and in the methods used to extract and analyze the data resulting in a better understanding of the mechanics of heritability.

This study continues the course set out by previous research to further investigate the heritable qualities of three main components of fingerprints: pattern type, ridge count and minutiae count. The desire is to provide more insight into the mechanics behind dermatoglyphic heritability by observing the relationships between pattern type and ridge count and to include minutiae count as a contributor to the knowledge base of genetic research. Investigating dermatoglyphic heritability is important in physical anthropology for gaining a better understanding of past population movements and providing insight into evolutionary change. Forensic science and medicine also benefit by dermatoglyphic studies for the information they provide regarding what makes us individuals and why certain genetic diseases attack particular individuals.

To test the hypothesis that minutiae count can be included with pattern type and ridge count as an indicator of inheritance, data for all three attributes were gathered from a total of 13 families consisting of 96 individuals. A method was introduced for establishing a reproducible area of the fingerprint in which to extract the minutiae count quantitatively regardless of fingerprint pattern size. The information was then analyzed by employing Pearsons r to observe correlations between minutiae and ridge counts. The data were also subjected to a second test incorporating a heritability formula to extract the level of heritable significance for all three attributes.

The null hypothesis that the relationships between these dermatoglyphic configurations, including minutiae counts, are purely random events was rejected upon the completion of these tests. The hypothesis that there is a significant connection between the relationships, including minutiae count and heritability was supported.

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Chapter 1: Introduction

Fingerprints occupy a fascinating and ever-evolving niche in the annals of human history. Since the time that *Homo sapiens* first began to physically express himself through the creation of artifacts, fingerprints have been intentionally and unintentionally left behind. Examples of these are seen throughout time and space, from Neolithic bricks of the city of Jericho, around 7,000 B.C., to prehistoric carvings in New Grange dating to 3,000 years B.C. (Lee and Gaensslen, 1991). Recognizable pattern types have been observed in ancient drawings, and the fingerprints of crafted artisans bear silent testimony to their maker's existence, impressed for eternity, on the surface of excavated pottery sherds (Lee and Gaensslen, 1991).

Some of the first indications of an awareness of fingerprints as a means of identification are observed on preserved scrolls from early Chinese dynasties and in clay seals from ancient Babylonia in observance and agreement to long since expired contractual obligations (Ashbaugh, 1999). It is through these kinds of artifacts that the notions of uniqueness and importance of fingerprints in early mankind may be observed.

It was in the late 17th century, that fingerprints first came under formal scientific study. Many early pioneers of fingerprint research, such as plant morphologists Nehemiah Grew and Marcello Malpighi, analyzed the ridged skin that appeared in raised relief on the surface of the fingertips and palms of all humans. This research concentrated primarily on the physiology of ridged skin observed on the hands and fingers (Lee and Gaensslen, 1991). Studies begun soon after recognized that all primates, human and nonhuman, share this dermal expression known commonly as friction ridges. The evolutionary explanation for the presence of friction-ridged skin is linked to the necessity of our forebears to grasp onto objects in their environment. The presence of friction ridges on these areas of the hands and feet, in concert with sweat pores aligned along these ridges in regular intervals, make the entire orchestration of grasping, holding and manipulating objects possible (Holt, 1968; Lee and Gaensslen, 1991). The configurations of these ridges on the fingertip pads of all primates, human and nonhuman, form identifiable pattern types that have been established since the 18th century. These patterns consist of three primary types: arches, loops and whorls (Olsen, 1978). Although all primates share these dermatoglyphic patterns, there is a significant difference in the appearance of pattern types between the species, with nonhuman primates exhibiting primarily the pattern known as the whorl, or more specifically, the more elongated form referred to as the elliptical whorl (Brandon, *et al*, 1997; Lee and Gaensslen, 1991). Humans exhibit all three-pattern types on their fingers with a fairly predictable distribution of 65 percent loops, 5 percent arches and 30 percent whorls (Jones, 2000). Research suggests that the whorl pattern type is likely the most primitive expression of all three (Lee and Gaensslen, 1991).

Over the last two centuries, volumes of research have been produced on the subject of fingerprints. One of the most prolific and important contributors to the research of dermatoglyphics is Sir Francis Galton. Galton, who had studied medicine and mathematics prior to his work in dermatoglyphics, contributed a preliminary study on fingerprint patterns of twins in 1892. This study provided the first evidence that fingerprint pattern types had a hereditary basis (Holt, 1968; Weninger, n.d.).

Another early pioneer in fingerprint inheritance was Harris Wilder, who in 1902 provided research on large amounts of data of biologically related individuals to better understand the mechanics behind dermatoglyphic inheritance. His research again demonstrated that genetics play a significant role in the ridge configurations shared within family groups (Holt, 1968). More studies soon followed by researchers including Cevidalli, Elderton, Bonnievie, Poll and Cummins, which were based on a variety of aspects of the friction ridges of the fingers, hands and feet. This research concluded that in every study, heredity played a key role in the formation of dermatoglyphic ridge arrangement (Moenssens, 1971). Margarete Weninger, in an article entitled "Dermatoglyhics and Heredity", summed up her thoughts on previous work in dermatoglyphics by stating in part that "...it is doubtless that the formation of the dermatoglyphic system, i.e. the course of the lines is caused, for the most part, genetically" (Weninger, n.d.).

Years of research and hundreds of thousands of fingerprints of individuals have been studied to better understand the mechanics of inheritance as is reflected in fingerprint pattern morphology. Through this research, it has been proven that gross pattern type appears to be a strongly inherited feature of friction ridge arrangement (Arietta, *et al* 1992; Bener, 1982; Holt, 1968; Moenssens, 1971). Some studies also indicate a correlation between maternal and paternal contributions of pattern type (Bener, 1982).

A problem that arose early on in dermatoglyphic research was the inherent difficulty of statistically measuring the various attributes of a fingerprint. Early studies concentrated on observing pattern type appearances within family groups and noting the frequency of those appearances. It was soon realized that fingerprint pattern studies alone would not be sufficient for answering the kinds of questions that were increasingly demanding attention. By the mid 1920s, new methods for quantitatively measuring fingerprints were being utilized. These were of two main types; using breadth and height measurements of pattern types per individual, and counting the number of friction ridges that intervened between two fixed points on a fingerprint pattern. Although the idea of the ridge count goes back to Galton, its use in genetic study statistics wasn't fully realized until Bonnevie developed a method to utilize it successfully for all pattern types (Holt, 1968). Since this time, researchers have observed a genetic link to the ridge counts of related individuals. This relatedness has been demonstrated in two ways; by total finger ridge count or TFRC, and finger-to-finger ridge count. TFRC is ascertained by taking the ridge count of each finger within set parameters, and comparing the sum of these numbers against those of offspring or blood related ancestors (Holt, 1968).

Many researchers of dermatoglyphic inheritance have since employed the ridge count in their studies providing more clues to the mechanics of inheritance. One of the major contributors to genetic studies through the analysis of the ridge count is Sarah Holt. She expanded on previous work, and produced volumes of data on familial ridge count studies. Early work from Holt (1952, 1960), showed that "pattern size, as measured by total ridge count, is inherited", and "that the diversity of the ridge-count from finger to finger has a genetic basis." Holt was also one of the first researchers in dermatoglyphic genetics to recognize that environmental influences in utero also have an effect on the development of friction ridges.

In addition to genetic research, ridge counts and pattern types have aided researchers studying the archaeological record and other subdisciplines of anthropology. For example, by analysis of the ridge count and individual ridge breadth measurements, it is possible to reconstruct the roles that children may have served in prehistory. In an article by Kamp, *et al*, measurements were taken from 107 individuals ranging in age from 3 years to adulthood. Through reconstructing the manner in which ancient fingerprints were left in clay, some knowledge was gained as to the types of items children would have created in ancient southwest America. By analyzing the ridge breadths of early artifacts and comparing them to models made in the study, it was concluded that while adults made most of the ceramic vessels, children produced most of the animal figurines (Kamp, *et al* 1999).

Anthropological population studies have been accomplished by observing trends in pattern type frequencies in genetically isolated groups. Studies of fingerprint patterns and ridge counts of the Karluk village of the Kodiak Island provide insight into ancestral relationships between the Karluk people and Eskimo populations of East Greenland, West Greenland, Southampton Island, East-Central Arctic, Carnation gulf, Point Barrow and St. Lawrence Island (Meier, 1966).

Approximately 10 years after the Karluk village study, Slatis, *et al* researched the fingerprint patterns of 571 individuals of an Israeli community. In this study, a genetic theory was developed based on the appearance of reoccurring pattern attributes in a population isolate. This theory postulated that the basic fingerprint pattern sequence is one of all loop configurations and "that a variety of genes cause deviation from this pattern sequence" (Slatis, *et al* 1976: 288).

A more recent study was undertaken to trace linguistic relationships with the Slovak Roma populations. This study compared the finger ridge counts of three Slovakian Roma populations with 12 world populations to explore relationships among them. The study found a link between the linguistically distinct Roma populations, part of the Indo-

European language family, and the Urali, a South Indian population that is part of the Dravidian language family (Weisensee, *et al* 2003).

Nonhuman primates have also been the subject of study in regards to dermatoglyphic analysis. The potential of cloning primates has opened the door for speculation that duplication of friction ridge configurations may be possible. In a study by Brandon, *et al* (1997), the fingerprints of rhesus monkeys at the Oregon Regional Primate Research Center were examined. These monkeys were not clones in the truest sense of the word as they were created through nuclear transfer. This procedure resulted in monkeys that are not genetically identical, but rather genetically equivalent for monozygotic twins. It was determined that the monkeys in this study exhibited similar fingerprints, but as is the case with human twins, were not identical.

In addition to fingerprint research in forensic identification and anthropology, increasing interest in fingerprint morphology may be observed in the areas of medical science. Over the last 20 years, genetic links have been observed between fingerprint configurations and a host of mental and physical anomalies. In an article by R.M. Godffrey (1994), a relationship between palm size and the presence of a greater than normal ratio of whorl patterns indicated raised blood pressure in adult life, and in another article, the suggestion is made that there is a link between the presence of arch patterns on the left hand and whorl patterns on the right as dermatoglyphic markers for rheumatoid arthritis (Ravindranath *et al* 2003). In an article for *Omni,* psychiatrist Stefan Bracha is quoted stating that "schizophrenia is caused by prenatal insults such as viral infections that injure the brain of the fetus". He found evidence of this theory by studying fingerprints, which are formed during fetal development. His rationale was that fingers form at the same time that the cerebral cortex is undergoing peak development. Because of this co-occurrence of developmental processes, any damaging insult to the fetus at this time would reflect itself also on the fingers. In this study, twins, one with schizophrenia and one without, were observed. As he hypothesized, the affected twin exhibited fewer ridges and smaller than normal finger tips (McAuliffe, 1994).

Although these and many other previous studies indicate a hereditary relationship in pattern type, ridge count and to a lesser degree, minutia count, very little data has been examined simultaneously for all three main considerations observed for genetic heritability in fingerprints. One such study undertaken by Lin, *et al* (1982), researched the similarity of fingerprints between groups of monozygotic and dizygotic twin pairings to observe any possibility of duplication of fingerprints. The results of this study showed that monozygotic twin pairings had the highest degree of similarity in pattern types, ridge counts and minutia counts, indicating a high level of heritability between the twins. While this study made useful observations on the occurrence of similarities between closely related individuals, it did not test the hypothesis that all three phenotypic expressions could be genetically linked using other familial data including the heritable relationships between offspring and parents, grandparents, non-twin siblings, etc., which would provide greater insight into the range of heritable influence on dermataglyphics. In addition, the parameters in which minutiae were extracted from the fingerprint in this study were not well defined or explained. In order to construct a viable database, it would be necessary to construct a specific quantitative and replicable area to extract the minutiae count.

Minutiae, also known as ridge events, refer to “the details of morphology of a single ridge and include branchings, interruptions of the continuity of a ridge, and isolation of short ridge segments. Minutia reflect the formation of new ridges subsequent to the period of initial ridge formation” (Babler, 1991: 98). Minutiae, the most diminutive characteristic in dermatoglyphics, present themselves in three primary configurations: bifurcations, ending ridges and dots (Cowger, 1993). The placement of these ridge events and their association with one another within a pattern type are the essential elements of forensic fingerprint identification, as it has never been observed that these events are ever replicated on any one person or between persons (Moenssens, 1971).

In forensic identification, the contention stands that an identification can be made from any area of the friction ridge skin of the fingers even when only a small portion is available. In keeping with this argument, I devised a sampling region of the fingerprint pattern area for this study that could be replicated quantitatively on all individuals' fingers regardless of the age, sex of the individual or size of the fingerprint in which to extract the minutia count. From examination of this area of extraction, I posed my question: if fingerprint patterns show heritability within a biologically related family group, and it has been proven that ridge counts are also highly heritable, could it be observed through a quantitative method that minutia counts will share some of the same earmarks of inheritance? It is the authors' opinion that a correlation will be found, albeit to a lesser degree than pattern type and ridge count, indicating that minutiae count is also a heritable trait. The null hypothesis would be observed by low correlation and heritability values indicating that something other than genetics is responsible for the manifestations of friction ridge arrangement. This would support previous studies, which make the claim that while pattern type and ridge count show-varying degrees of relative inheritance, minutiae counts are largely a random event (Cummins and Midlo, 1943).

There has not been a significant amount of data produced to observe heritability correlations between pattern type, ridge count and minutia count. This is somewhat due to the difficulty in manipulating mixed variables in a manner conducive to providing the kind of information that is sought. It is also due to a changing trend in research to look more to environmental effects as a probable cause for minutiae arrangement, and to look at this characteristic as an individual isolate and not as a related part of an integrated whole.

Current research by Werthiem and Maceo promotes the argument that in addition to genetic influence, there appears to be a significant connection between the stresses of the intrauterine environment upon the volar pads of the developing fetus and the resulting ridge and pattern configurations ultimately observed (Wertheim and Maceo, 2002). While the case for this argument is strong and agreement is made that environmental stressors do contribute to aspects of friction ridge arrangements, it is my belief that genetics play a significant role in dermatoglyphic expression, including minutiae counts.

Although the search for genetic connection and dermatoglyphic traits is made more difficult simply because of the complexity of the traits themselves and sorting out the interplay of environmental additions is increasingly cumbersome, the area of dermatoglylphic research is still advancing. In the words of Ranajit Charkraborty: "...considerable progress has been made on the genetic basis of affective disorders. Therefore, giving up the study of genetics of dermatoglyphics, because of its inherent complexity alone, is probably not justifiable" (Chakraborty, 1991: 185).

I believe that the data I have gathered and analyzed will show that pattern types, ridge counts and minutia counts will exhibit greater correlation with biologically related groups, and that the degree of genetic association will parallel to some extent, with the degree of genetic relationship. While I believe that a similarity of these attributes will be revealed, I do not believe that duplication or a correlation approaching 100 percent will be observed among any of these attributes.

The study of pattern, ridge and minutia inheritance is important for observing the mechanics involved in the genetics of inheritance and also to determine the validity of the uniqueness of fingerprints as a method of identification. Human genetics is an increasingly important area of study as more and more adverse human conditions are being attributed to the presence or absence of certain elements in an individual's genetic profile. In the area of medicine alone, the connection observed between the appearance of certain dermatoglyphic traits and physical and mental anomalies is already providing insight into potential avenues of treatment. Researching pattern, ridge and minutiae inheritance is equally as important to the field of forensic science, as it is the uniqueness of fingerprints that is at the corner stone of forensic identification. In forensic science, the ability to maintain the uniqueness of the fingerprint as a viable means of personal identification becomes more and more important in courts of law worldwide. By being able to demonstrate similarities between the closest possible genetic relationships while still affirming the law that nothing in nature will ever repeat itself, the canon of human individuality will be sustained.

CHAPTER 2: MATERIALS AND METHODS

The data for this study were collected personally from a population of individuals of no particular ethnic or socially diagnostic population group over a period of 1 year. This population primarily resided or still resides in the city of Missoula, Montana and the immediate area surrounding the city. A few individuals in the study were family members of the test subjects visiting from other areas of the country.

I did not focus on a particular demographic inasmuch as a family unit is concerned. My original intention was to focus on family groups consisting of two or more generations of individuals comprised of two parents, grandparents, children, etc. I noticed early on in the study, however, that the typical family of both parents with children was not often encountered. While my study does include groups that approach the typical family distribution of individuals, I also have groups comprised of siblings only and single parent families. The ages of the individuals in my study range from 3 years to over 90. A total of 13 families comprise my population sample.

Originally, 100 individuals were in my study, however, I was ultimately able to use only 96 of them. Of the 4 excluded from the study, 3 were individuals who were very young and could not be printed successfully. The one other individual was elderly with friction ridge skin so worn on the fingers as to no longer be visible.

In a few instances, I encountered fingerprint cards where incomplete impressions had been recorded of several fingerprints. In these cases where the loss of information due to incomplete printing interfered with the ridge count, minutia count or pattern type analysis of a particular finger, a value of zero was applied for that finger in the analysis.

The individuals for this study were obtained through word of mouth only. No posted advertisements were used to gain subjects for this study in accordance with standards put forth by the Institutional Review Board at the University of Montana.

Fingerprinting of the individuals included in this study was performed at the location of their individual preference. Approximately ½ of the individuals chose to be printed at their homes while the remaining number was printed at the Impression Evidence Section of the Montana State Crime Lab in Missoula, Montana.

Fingerprints were taken primarily utilizing the rolled ink method. This method is historically the oldest method used for the gathering of fingerprint records, and is still in wide use today.

A fingerprint card was designed from a standard 8.5 x 11 sheet of copy paper. A grid system including a space for each of the 10 fingers was incorporated along the free edge on all 4 sides of the card. The center of the card provided information lines for noting the subject's family standing, i.e. Father, Mother, Sister, etc., and a space for the entry of their assigned family number. No names of individuals were affixed to the cards in accordance with the Institutional Review Boards regulations governing the handling of human subject information. Ink was then applied to each finger in succession starting with the right thumb, each of which was rolled in its corresponding space on the card. Enough space was allowed so that each finger could be rolled twice to obtain as much information as possible. In the center left and right of each card, space was also allowed for the recording of plain fingerprint impressions. Again, this was done to provide as much fingerprint information as possible. A secondary method was used in the case of individuals with poor friction ridge structure or young children. This method is referred to as the powder and tape method. To employ this method, black fingerprint powder is lightly dusted onto the surface of each finger and clear tape is applied over the powdered finger. The tape is then carefully lifted off the finger, and placed onto a plastic transparent sheet protector. By viewing from the opposite side through the sheet protector, the correct orientation of the fingerprint can be observed. This method proved to be extremely useful in printing individuals with poor ridge structure and resulted in excellent reproduction of even the most miniscule details.

Three characteristics of a fingerprint were explored in this study. The first characteristic examined was pattern type. Each of the pattern types was assigned a corresponding numeric code and entered into an Excel database. Appendix 1 depicts the legend used for each of the pattern types analyzed in this study. The next characteristic was the ridge count for each finger. This was assessed through the standard method used by fingerprint examiners, which consists of counting the intervening ridges as they cross a line drawn between the delta and the apex of the core of each fingerprint. In the case of loop patterns, the count was done from either the left or the right depending on the slope or slant of the loop pattern. In a loop pattern, there is only one delta as can be seen in Appendix 1.2. In the whorl pattern, the left delta was chosen as the default delta in all cases except for when a formation approaching the double loop whorl appears in the core. In this case, the delta on the side of the upthrusting loop in the core was used. This can be observed in Appendix 1.3. Arches, plain or tented, were not considered in this study for ridge count or minutia count since a strong, quantifiable area for measurement could not be established. They were, however, considered in the pattern aspect of the study. The next analysis performed was taking the total number of minutia events from a selected area of each fingerprint. I defined this area by taking the line drawn from the delta to the core, and marking a 70-degree angle from the delta to form a triangle, as depicted in Appendix 1.3. All minutiae within the 70-degree triangle were counted for each finger. No distinction was made between the three main types of minutia in the count or where they appeared in the extraction area. To offset calculation error, a +/- 1 was applied to all ridge counts and minutia counts.

After each fingerprint card had been completed for all 3 definable attributes of the fingerprint, the data were entered into an Excel spreadsheet for each finger and for each attribute. After all 96 people had been entered, the information was transferred into the statistical software SPSS11 to calculate the Pearson correlation coefficient and to provide a correlation matrix to observe any significant relationships found within the data.

A separate calculation for heritability was performed on the data by pairing each individual against every other individual in the study and calculating the occurrence of similarity for each finger and each phenotypic attribute. The results were then sorted according to degree of relationship: .5 percent for parent to child and sibling to sibling, .25 for aunt/uncle to niece/nephew and grandparent to grandchild, .125 for 1st cousins, grandparent to great grandchild and uncle/aunt to great-grand niece/nephew, and 0 for unrelated individuals. Three pairs of individuals had a relatedness of .0625, but were excluded due to the small sample size in this category. Total counts of matches in each attribute were then gathered for each category of inheritance and a concordance value was calculated for all. A regression formula for predicted concordance from relatedness was calculated using Excel, and an estimate of the concordance for genetically identical individuals was calculated. These estimates were then plugged into a formula for heritability (1998), defined by Dr. Randall Skelton and modified from a traditional formula for estimating heritability from concordance of monozygotic twins presented by Ljichi and Ljichi. This formula states that heritability can be calculated by dividing the concordance for genetically identical individuals minus the concordance between unrelated pairs, by 1 minus the concordance between unrelated pairs (Skelton, 2004).

$$H = \frac{C_0 - \hat{C}_1}{1 - C_0}$$

Where H = estimate of heritability,

C_0 = concordance among unrelated pairs (relatedness = 0)

$\hat{C}_1$ = estimated concordance among genetically identical pairs (from regression equation)

This formula was applied to pattern type, ridge count and minutia count, in order to estimate the heritability for each fingerprint attribute. The results were then placed in descending order of significance sorted by the 3 variables.

Finally, totals for the occurrence of every pattern type per finger were calculated for the entire population. These totals were entered by finger and by total number of occurrence. A range was then determined for each finger, illustrating the types of patterns observed for each.

The results from all of the statistical analyses were then compiled onto the tables listed in Chapter 3 in order to observe any similarities and dissimilarities between the 3 areas studied.

CHAPTER 3: RESULTS

The results of the statistical analyses suggest a strong relationship between certain elements of the data. The resulting findings are presented in tables 1-4. Table 1 illustrates the results of the Pearson correlation coefficient test on ridge and minutia count data only. The majority of fingers were represented at a minimum of 50 percent correlation with at least one pair of matching variables. Due to the large number of variables, only those pairings with a correlation of 60 percent or greater are listed. One of the first observations made was that more significant correlations occurred in the minutiae column than in the ridge count column. This would indicate that there is a tendency for a greater relationship among minutia counts between fingers than among ridge counts between fingers.

Table 1: Results of correlation matrix based on ridge and minutia data

***RC with RC**	**r 60%**		****MC with MC**	**r 60%**		**RC with MC (same finger)**	**r %**
Finger position			Finger position			Finger position	
R Thumb	LT		R Thumb	LT		R Thumb	60%
R Index	LI		R Index	RM,LI		R Index	60%
R Middle	0		R Middle	RI, RR, RL		R Middle	60%
R Ring	LM,LR		R Ring	R.M, !RL,LT,LI,LR,LL		R Ring	69%
R Little	!LL		R Little	RM,RR,LR,!LL		R Little	64%
L Thumb	RT		L Thumb	RT,RR, LI		L Thumb	65%
L Index	RI		L Index	RI, RR,LI,LL		L Index	64%
L Middle	RR, LI		L Middle	0		L Middle	70%
L Ring	RR		L Ring	RR,RL,!LL		L Ring	55%
L Little	!RL		L Little	!RR,!RL,LI,LR		L Little	50%

Legend: *RC=Ridge Count
**MC=Minutia Count
! = 70%

Shorthand used: RL=Right Little. …

Also, in the ridge count column and the minutiae count column, 70 percent correlation occurs in combinations where either the right or left little finger is involved. This only occurs when the pairing is comprised of both little fingers or one little finger and either the left or right ring finger. This phenomenon is not observed in any other similar variable pairings.

Another similar observation occurs in the right and left thumbs for minutiae count and ridge count where only when one occurs does the other occur. This observation is made at the 60 percent correlation level.

The far right column of Table 1 illustrates the results of a search for correlations between ridge and minutia counts. It is significant to mention that the author did not expect to find correlations based on the same finger, but that the results themselves dictated these findings. In each incidence that a strong correlation for a minutia count with a ridge count was calculated, the result was a same finger correlation. The smallest correlation was observed at 50 percent on the left little finger, while the greatest correlation was observed at 70 percent on the left middle finger.

Table 1.2: Same finger correlations and associated pattern type

RC with MC (same finger)		**r**		***Pattern Type Observed**
R Thumb		60%		Right slope loop, Plain Whorl, Double Loop Whorl
R Index		60%		Right slope loop, plain whorl, left slope loop
R Middle		60%		Right slope loop, plain whorl
R Ring		69%		Right slope loop, plain whorl
R Little		64%		Right slope loop, plain whorl
L Thumb		65%		Left slope loop, double loop whorl, plain whorl
L Index		64%		Left slope loop, plain whorl
L Middle		70%		Left slope loop
L Ring		55%		Left slope loop
L Little		50%		Left slope loop

*Only those occurring >10 times per finger

In addition to the results of the correlation matrix, the results of the heritability pairings were found to be significant. These results are listed in Table 2, listed in descending order by heritability. It is obvious that the greatest degree of heritability appears on the right ring finger for pattern type, followed closely by the pattern type for the right thumb and the minutiae count for the right little finger. The next level drops down to the 42-47 percent range where only pattern type is represented as exhibiting a significant degree of heritability. At the 29-35 percent level, the results are mixed between the left index and left ring fingers for pattern type, and right index and left index for ridge count. This is the first instance where there is a correlation between two variables and a particular finger. The only other significant correlation between two variables can be seen at the 17-19 percent level with the ridge and minutiae counts for the left little finger.

Table 2: Heritability chart including all three fingerprint components

Heritability results in descending order:	**Pattern type:**	**Ridge count:**	**Minutiae count:**
60%	R Ring		
50-53%	R Thumb		R Little
42-47%	L Middle, L Thumb, R Little		
29-35%	L Index, L Ring	R Index, L Index	
22-26%	L Little		R Middle, L Middle, L Ring
17-19%	R Index	R Ring, L Little	L Little
6-13%		L Ring, R Little, R Middle	R Index, R Ring, R Thumb
1-5%		L Middle, R Thumb, L Thumb	L Thumb
*-.9- -7%	R Middle		L Index

*An error rate of 10% was assumed in the above calculations

Table 3: Pattern type totals per finger for entire population

	TA	AA	AW	DLW	CPW	PW	RSL	LSL
R Thumb		1		12	1	24	57	
R Index	9	8	1	5		23	33	17
R Middle	1	9		2	2	11	71	
R Ring	1	3		1	9	34	48	
R Little	2				2	12	78	2
L Thumb		3		13		12	2	66
L Index	8	13	1	7	4	13	17	33
L Middle	3	10		1	5	8	3	66
L Ring		4		3	5	18	4	62
L Little	1				2	10	2	81

*Pattern type short hand: TA=Tented Arch, AA=Plain Arch, AW=Accidental Whorl, DLW= Double loop Whorl, CPW= Central Pocket Loop Whorl, PW = Plain whorl, RSL=Right Slope Loop, LSL=Left Slope Loop.

Table 3 reflects the distribution of pattern type per finger and the total number of occurrences for each pattern type. One of the observations immediately apparent is the rare occurrence of the accidental whorl, which appears only twice in the entire sample. An interesting note is that it appears only on the index fingers, once on the right index finger, and once on the left index finger. These two individuals were not biologically related.

Other findings include the observation that the left index finger appears to be the one with the greatest degree of diversity of pattern type as all 8 pattern types are represented on that finger. The most commonly occurring pattern types, which appear on all fingers, are the right slope loop with a total of 315 occurrences and the plain whorl with 165 occurrences. The overall largest number of pattern type represented on any finger is the left slope loop with 327 total occurrences.

One last observation concerning pattern type is a similarity seen with the little fingers of both hands. The right and left little fingers only exhibit 5 of the 8 patterns: the tented arch, the central pocket loop whorl, the plain whorl, the right slope loop and the left slope loop.

From the various tests applied, it is evident that certain aspects of the data are more relevant than others when attempting to extricate the elements involved with genetic inheritance. Performing the long-hand pairings of individuals by relatedness is an excellent mechanism for extracting significant measurements of heritability, while running a correlation matrix of those quantifiable measurements of the fingerprint provides a reliable tool for observing the strength of relationships between these two variables. Analyses of these results together indicate definite and significant heritability relationships observed through the phenotypic expressions of the fingerprints.

CHAPTER 4: DISCUSSION

The results of this study suggest that there are indeed varying degrees of heritability which can be observed through the correlations between ridge counts and minutia counts. An unexpected outcome was the significant differences in correlations between pattern type, ridge count and minutia count. The expectations harbored prior to the outcome of these statistical tests were based on results from previous studies that indicated much stronger correlations with pattern type and ridge counts on all fingers. Minutiae count represented itself in this study as a much stronger indicator of heritability than what was originally anticipated.

Regarding the findings of the correlation coefficient matrix, the significant relationship observed between the ridge count and minutiae count of the same finger should be given proper attention. This correlation is the strongest on the left middle finger of all individuals represented in the sample, and weakest on the left little finger.

An argument could be made that the correlation is based on the size of the fingerprint pattern with an accompanying large ridge count, which would likely correspond with a large minutiae count. In my personal opinion, I do not believe this to be true. In my day-to-day work as a fingerprint examiner, I analyze fingerprints with varying degrees of concordance between ridge count and minutiae count. However, to overcome any bias that I may entertain, I extracted a small random sample of 25 fingerprints of the pattern types listed in Table 1.2 to observe empirically the relationship between ridge and minutia counts on a same finger basis. While this sample is small, I do believe that it provides satisfactory representation of an unrelated group of individuals. The fingerprints were selected from all 13 families in no particular order except that no more than one person in a family was represented in the sample. My results were much as I had expected.

The range of correspondence between ridge count and minutia count for the listed pattern types provided an average of 32 percent for all fingers tested. If it was true that minutiae count always correspond in like number to ridge count, a much higher number should be observed. At 32 percent, this number does not approach the high degree of correlation seen in the ridge count/minutiae count matrix where significant correlations of all possible combinations are presented. My interpretation of these findings is that there is a strong correlation between ridge count and minutiae count on a per finger basis and that something other than chance plays a role. The argument has been addressed previously in this study that environment has a greater impact on minutiae count then genetics. However, the fact that all 10 fingers show a 50 percent or greater correlation on a same finger basis between ridge count and minutiae count indicate that environment alone has a far less impacting role on minutiae count then what has typically been observed.

Another surprising result from this study was the strength of relationship observed between the little fingers of both hands. From all of the statistical tests, it can be seen that a significant relationship exists between these fingers in all three areas. Of the 8 different pattern types examined in this study, the little fingers exhibited the same 5: the tented arch, central pocket loop whorl, plain whorl, left slope loop and right slope loop. In no instance were any of the other pattern types exhibited. For ridge count, the right and left little fingers had a 70 percent correlation. The minutia count for these two fingers also exhibited a 70 percent correlation. In addition, these fingers shared pairings with the right ring and left ring fingers both at the 60 percent correlation level. These findings suggest that further research is required to explore the ramifications of the possible genetic links observed between these particular fingers.

Other observations in this area of the study included the strong correlation between pattern types and their appearances on certain fingers. The right ring finger stood alone at 60 percent heritability for pattern type, while the right thumb followed close behind at 53 percent. While the observation of the right thumb is significant, it would provide greater insight into the mechanics of heritability to explore the relationships between the right ring finger and both little fingers, as these appear to be the most significant indicators of inheritance in this study.

Heritability can be observed in notable degrees after the right ring finger and right thumb. In fact, for pattern type, all fingers of the left hand exhibit 22-47 percent heritability. The right hand is in close approximation of the left at 17-60 percent heritability, except for the right middle finger, which exhibits 0 percent. It is obvious that inheritance does play a role in pattern type as they appear on several fingers on a finger-to-finger basis, albeit not to the same degree for all fingers.

It is also true that ridge count has a genetic connection, but to a much lesser degree than pattern type. And surprisingly by numbers alone, minutiae count shows greater overall heritability than ridge count when observing the right little, right middle, left middle and left ring fingers.

It is important to note that this study makes no correlations between location and type of minutiae being observed within a fingerprint. All observations are made based on total numbers of minutiae only on a finger by finger basis.

A final comment in this section is regarding the occurrence of the accidental whorl, which appeared on opposite index fingers of two unrelated individuals. While the rarity of encountering the accidental whorl is observed in the area of forensic science, its appearance in this manner is nonetheless striking. No interpretation of this result is made at this time. However, its appearance in this particular manner lends itself to the possibility of a latent physiological anomaly expressing itself dermatoglyphically. A personal interview in connection with the gathering of fingerprint data may have elucidated this observation.

CHAPTER 5: CONCLUSION

The outcome of the data analysis of this project supports the existing body of data which suggests at least some dermatoglyphic attributes such as pattern type and ridge count are heritable phenotypic expressions. The statistical tests applied confirm what has already been presented previously, although somewhat different exact heritabilty estimates and correlations were obtained. Although many arguments have been made that minutiae counts are attributable primarily to environmental factors alone, the data support the hypothesis set out in the introduction of this study that minutiae do tend to follow similar genetic dictates to those which ridge count and pattern type respond. This conclusion is based on each test that was applied to the minutiae count. The application of a correlation matrix to the data teased out relationships between ridge count and minutiae count that significantly implies that the two are connected on a finger-by finger basis. The hypothesis that this is due to a corresponding relationship between large/small ridge count and large/small minutiae count was tested and rejected by selecting and observing the counts of 25 random fingerprints and calculating the relationship between them. The results did not provide the kind of relationship observed in the correlation matrix, suggesting that something other than correlating ridge count/minutiae count is responsible.

The heritability formula applied to the data gathered from the person to person pairings also provided confirmation of the argument that pattern type and ridge count are, to varying degrees, heritable traits. In addition, this test supported the hypothesis that minutiae count is at least partially inherited and allowed the null hypothesis, which states that minutiae occurrence is a random event, to be rejected. On several fingers, the heritability of minutiae surpassed that of ridge count.

The results of this study suggest that further research should be explored in all areas of dermatoglyphics. Future research problems to be addressed include the separating out of the myriad of contributing forces that influence the formation of friction ridge skin. Recent research has concentrated on the impact of intrauterine stressors on the developing fetus and the possible resulting dermatoglyphic effects as a result of these stressors. Continued research in this area as well as ongoing population studies will help provide the necessary information required to separate out the causal factors associated with dermatoglyphic expression.

Better understanding of the genetic processes behind the manifestation of dermatoglyphic arrangements continues to be an important undertaking across a variety of scientific disciplines. Persevering in this area will assist in providing genetic clues into close and distant human relationships of the present, provide insight into our evolutionary past and give us a glimpse to the kinds of changes we as a species, might expect to encounter in the future. In forensic identification, the science of being able to observe similarity in phenotypic expressions while at the same time recognizing the stamp of individuality will endure and stand only to be strengthened by continued research. Additionally, continued research in the connection of genetic disease and the appearance of dermatoglyphic abnormalities shows great promise for early detection and the impetus for the development of potential treatment options.

By presenting a method in which to quantifiably define an area for minutia count, I hope to encourage future studies in the area of minutiae type, orientation and structure to observe if any correlations between them and inheritance can be made.

Lastly, it is my hope that the results of this research provide some additional insight into the mechanics of inheritance and provide another avenue of thought to explore in future investigations.

"I made inquiries, and was surprised to find, both how much had been done, and how much there remained to do". Francis Galton (Chakraborty, 1991:151)

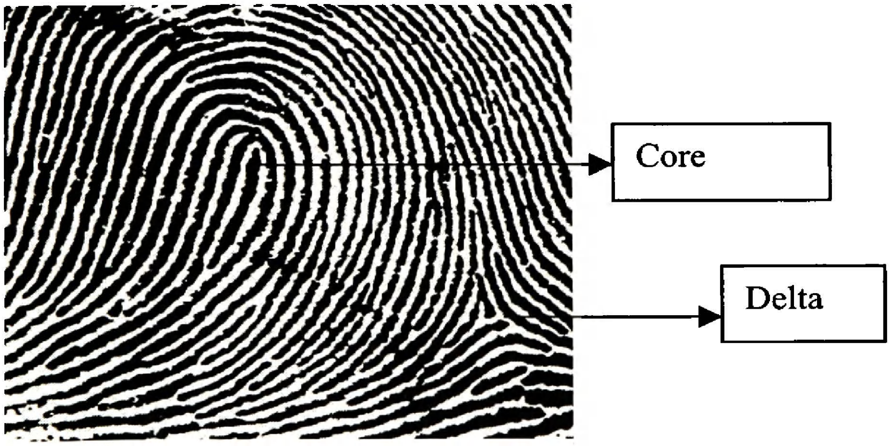
APPENDIX I: DEFINITIONS

APPENDIX I: DEFINITIONS

PATTERN TYPE LEGEND

Left Slope Loop	1
Right Slope Loop	2
Plain Whorl	3
Central Pocket Loop Whorl	4
Double Loop Whorl	5
Accidental Whorl	6
Plain Arch	7
Tented Arch	8

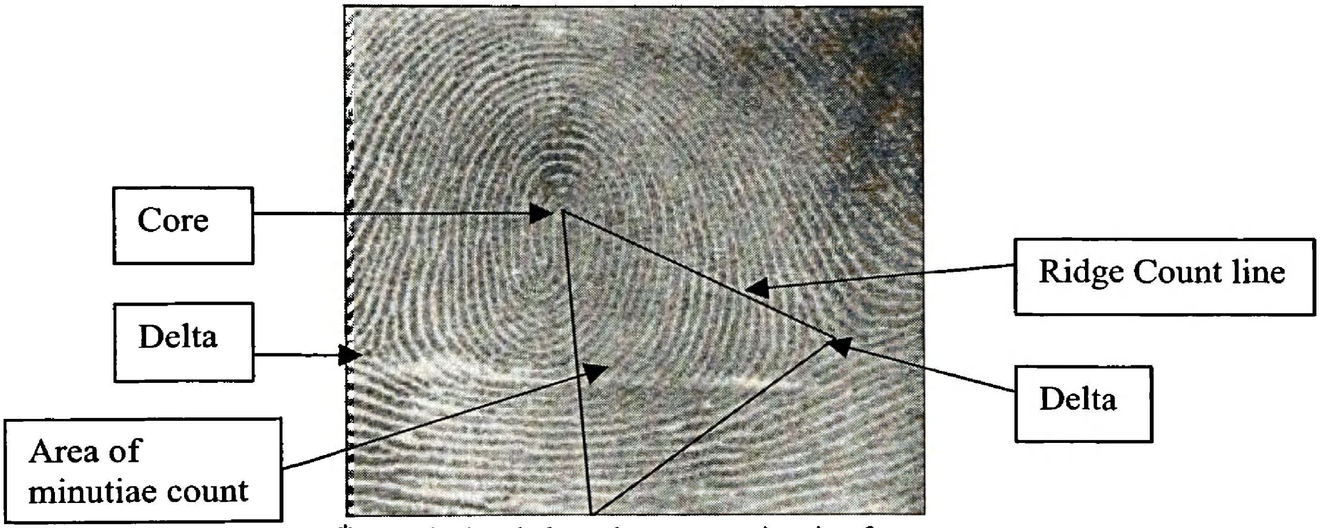
APPENDIX 1.2: LOOP PATTERN



APPENDIX 1.3: RIDGE COUNT AND MINUTIAE COUNT AREAS DEFINED

Minutiae extraction area is comprised of the ridge-count line from delta to core, and the triangle formed by the 70-degree enclosure from point of delta.

WHORL PATTERN



*Area depicted above is an approximation for illustration purposes only.

APPENDIX 2: RAW DATA

RAW DATA BY PATTERN TYPE

Person	Family	FP 1P	FP 2P	FP 3P	FP 4P	FP 5P	FP 6P	FP 7P	FP 8P	FP 9P	FP 10P
Mother 1	1	2	1	2	2	2	5	1	1	1	1
Father 1	1	2	1	2	4	2	1	3	1	3	1
Son 1.1	1	2	3	2	4	2	1	1	1	1	1
Son 1.3	1	3	3	2	2	2	3	1	1	1	1
Son 1.4	1	2	5	4	4	2	1	3	1	1	1
Daugh.1.5	1	2	2	2	2	2	1	1	1	1	1
Son 1.6	1	2	3	2	2	2	1	1	1	1	1
Son 1.6, child 1	1	2	2	2	2	2	1	1	1	1	1
Son 1.6, child 2	1	3	3	2	3	2	1	3	1	1	1
Mother 2	2	5	6	2	2	2	5	2	2	2	3
Father 2	2	5	2	2	3	2	1	1	1	5	1
Daughter 2.1	2	2	3	2	2	2	1	2	1	4	1
Daughter 2.2	2	2	2	2	2	2	1	3	1	1	1
Daughter 2.1, child 1	2	2	1	2	2	2	1	2	1	1	1
Mother 3	3	3	5	2	3	2	3	3	1	3	3
Father 3	3	3	5	3	3	2	5	2	3	1	1
Son 3.1	3	5	3	2	3	3	3	3	3	3	4
Son 3.1 Spouse	3	3	7	7	8	1	3	7	7	7	1
Son 3.1, Child 1	3	2	2	2	3	2	1	4	1	3	1
Son 3.2	3	3	3	5	5	2	5	5	3	5	1
Son 3.3	3	3	3	3	3	2	3	3	3	3	1
Mother 4	4	0	8	8	2	2	1	8	1	1	1
Father 4	4	2	8	2	2	2	1	1	1	1	1
Son 4.1	4	2	8	2	2	2	1	8	7	1	1
Son 4.1, Spouse	4	4	2	2	4	2	1	1	1	1	1
Son 4.1, Child 1	4	2	2	2	2	2	1	1	1	1	1
Daughter 4.2	4	2	1	2	2	2	1	1	1	1	1

Daughter 4.2 Spouse	4	5	2	7	2	2	5	7	7	7	1
Daughter 4.2, Child 1	4	2	3	5	2	2	1	2	1	1	1
Daughter 4.2, Child 1, Spouse	4	3	1	2	3	3	1	2	1	3	1
Daughter 4.2, Child 1, Child 1	4	2	3	2	2	2	1	2	1	1	1
Daughter 4.2, Child 1, Child 2	4	3	1	7	2	2	2	7	8	1	1
Daughter 4.2, Child 2	4	2	7	2	7	2	1	7	1	1	1
Son 4.3	4	2	7	7	7	2	1	7	7	1	1
Mother 5	5	3	2	2	2	2	1	1	1	1	1
Daughter 5.1	5	2	3	2	2	2	1	3	3	1	1
Daughter 5.1, Spouse	5	2	2	2	2	2	1	1	1	3	1
Daughter 5.1, Child 1	5	2	3	2	2	2	2	2	1	2	1
Son 5.2, Spouse	5	2	2	2	3	2	1	1	1	1	1
Son 5.2, Child 1	5	3	2	3	2	2	5	1	1	1	1
Son 5.2, Child 2	5	5	2	2	2	2	5	2	1	1	1
P. Grandmother 6	6	2	2	7	3	2	1	7	7	1	1
P. Grandfather 6	6	2	1	2	2	2	1	8	1	1	1
M. Grandmother 6	6	3	3	2	3	2	3	3	1	3	1
M. Grandfather 6	6	5	5	3	3	3	5	1	1	3	3
Son 6.1	6	2	1	7	2	2	1	7	1	1	1
Son 6.1, Spouse	6	3	3	4	3	3	1	1	4	3	4
Son 6.1, Child 1	6	2	8	2	3	4	1	2	1	1	1
Son 6.1, Child 2	6	5	1	2	3	2	1	3	1	4	1
Son 6.2	6	2	8	2	2	2	1	2	1	1	1
Son 6.2, Spouse	6	3	1	3	3	1	1	4	1	3	1
Son 6.2, Child 1	6	2	2	2	2	2	1	2	8	1	1
Son 6.2, Child 2	6	2	1	2	2	2	7	7	1	2	1
Mother 7	7	2	2	2	2	2	1	1	7	1	1
Father 7	7	2	3	2	3	2	1	3	1	1	1

Son 7.1	7	2	3	2	3	2	1	5	1	5	1
Son 7.1, Spouse	7	2	1	2	2	2	1	2	1	1	1
Son 7.1, Child 1	7	2	2	2	2	2	1	2	1	1	1
Son 7.1, Child 2	7	2	8	2	2	8	1	1	1	1	2
Mother 7, Sister	7	2	2	2	4	2	1	7	7	7	1
Mother 8	8	7	7	2	7	8	7	7	1	7	8
Father 8, Brother	8	3	2	2	3	3	3	2	8	1	1
Daughter 8.1	8	2	7	2	4	2	1	7	2	2	2
Daughter 8.1, Child 1	8	3	7	2	3	2	5	7	1	1	1
Son 8.2	8	5	8	2	2	2	5	1	7	1	1
Son 8.3	8	5	1	2	2	2	5	2	4	1	1
Son 8.4	8	3	3	2	3	2	1	1	1	4	1
Son 8.4, Spouse	8	2	2	2	3	2	1	5	3	3	1
Son 8.4, Child 1	8	3	3	3	3	3	1	5	3	3	3
Son 8.4, Child 2	8	2	1	2	3	2	1	1	1	3	1
Son 8.4, Spouse, Mother	8	2	2	2	3	3	1	1	1	3	1
Son 8.4, Spouse, Father	8	5	1	3	3	3	1	6	5	1	3
Daughter 8.5	8	2	7	7	2	2	1	2	7	1	1
Daughter 8.5, Spouse	8	5	2	2	2	2	1	1	1	1	1
Daughter 8.5, Spouse, Niece	8	2	2	2	2	2	5	8	1	4	3
Daughter 8.5, Spouse, Mother	8	2	2	2	2	2	1	1	1	1	1
Mother 9	9	3	3	3	3	3	3	3	1	3	3
Son 9.1	9	3	2	2	3	3	3	5	1	4	3
Daughter 9.2	9	3	2	2	3	2	1	1	1	3	3
Father 10	10	2	3	3	3	3	1	1	1	1	1
Fathers Brother 10.1	10	2	8	2	3	2	1	1	1	1	1
Fathers Brother 10.2	10	2	2	2	2	2	1	8	1	1	1

Fathers Sister 10.3	10	2	8	2	2	2	1	7	1	1	1
Son 10.1	10	2	3	3	3	3	1	3	3	1	3
Mother 11	11	3	2	2	2	2	3	8	1	1	1
Daughter 11.1	11	5	3	2	4	2	1	5	1	1	1
Daughter 11.2	11	3	3	2	4	4	3	4	4	1	1
Mother 12	12	2	2	7	2	2	1	1	1	1	1
Father 12	12	2	2	2	3	2	1	1	4	1	1
Mothers Sister	12	2	1	2	2	2	1	4	1	1	1
Daughter 12.1	12	2	2	2	4	2	1	1	4	3	1
Daughter 12.2	12	2	2	2	2	2	1	1	1	1	1
Son 12.4	12	2	7	7	2	2	7	8	7	1	1
Mother13	13	2	2	2	2	2	3	8	2	1	1
Father13	13	3	5	3	2	2	5	5	1	1	1
Son 13.1	13	2	1	2	3	2	1	1	1	1	1

RAW DATA BY RIDGE COUNT

Person	Family	FP 1R	FP 2R	FP 3R	FP 4R	FP 5R	FP 6R	FP 7R	FP 8R	FP 9R	FP 10R
Mother 1	1	7	3	3	0	0	2	0	0	1	0
Father 1	1	6	2	3	6	3	5	4	7	5	0
Son 1.1	1	9	6	3	5	2	7	4	0	5	2
Son 1.3	1	8	5	2	10	6	9	5	6	6	2
Son 1.4	1	13	6	4	7	5	5	5	4	1	1
Daugh.1.5	1	0	3	4	2	0	3	0	0	0	0
Son 1.6	1	6	1	1	2	4	4	2	2	0	0
Son 1.6, Child 1	1	14	10	7	6	3	6	10	5	3	2
Son 1.6, Child 2	1	22	11	10	10	8	14	13	3	4	5
Mother 2	2	11	10	4	1	0	5	3	1	0	0
Father 2	2	9	2	6	13	10	2	2	6	3	4
Daughter 2.1	2	13	7	8	7	4	6	0	4	12	4
Daughter 2.2	2	7	1	11	5	7	5	4	3	2	2
Daughter 2.1, Child 1	2	7	2	5	4	2	2	3	2	0	0
Mother 3	3	2	3	6	5	5	6	0	6	0	0
Father 3	3	18	7	12	12	9	13	0	10	9	6
Son 3.1	3	16	9	12	21	10	14	11	10	9	7
Son 3.1 Spouse	3	15	0	0	0	0	4	0	0	0	2
Son 3.1, Child 1	3	0	2	0	0	2	1	2	0	2	2
Son 3.2	3	15	10	14	12	10	10	13	8	8	9
Son 3.3	3	15	5	7	14	12	11	9	9	10	8
Mother 4	4	0	0	0	2	0	0	0	0	0	0
Father 4	4	2	0		5	2	4	0	3	0	1
Son 4.1	4	0	0	0	0	0	2	0	0	2	2
Son 4.1, Spouse	4	8	0	3	4	0	4	3	2	3	0
Son 4.1, Child 1	4	11	2	1	3	3	5	1	2	10	4
Daughter 4.2	4	0	0	2	0	0	0	0	2	0	0

Daughter 4.2 Spouse	4	4	5	0	0	0	3	0	0	0	1
Daughter 4.2, Child 1	4	5	3	3	4	2	3	2	3	2	0
Daughter 4.2, Child 1, Spouse	4	6	2	4	7	6	4	1	3	4	4
Daughter 4.2, Child 1, Child 1	4	3	1	0	0	0	3	0	5	4	0
Daughter 4.2, Child 1, Child 2	4	8	3	0	1	0	5	0	0	0	4
Daughter 4.2, Child 2	4	8	0	1	0	2	6	0	0	1	0
Son 4.3	4	3	0	0	0	0	0	0	0	0	0
Mother 5	5	6	4	0	0	0	0	0	0	0	0
Daughter 5.1	5	5	9	5	5	1	4	3	6	5	4
Daughter 5.1, Spouse	5	10	7	9	5	2	7	4	6	4	0
Daughter 5.1, Child 1	5	7	16	8	6	6	10	14	15	6	10
Son 5.2, Spouse	5	5	2	4	6	3	3	1	2	1	1
Son 5.2, Child 1	5	16	2	10	19	11	13	11	6	15	11
Son 5.2, Child 2	5	16	4	3	12	1	7	0	5	5	0
P. Grandmother 6	6	2	1	0	0	0	0	0	0	0	0
P. Grandfather 6	6	2	3	2	3	1	1	0	3	3	1
M. Grandmother 6	6	6	7	4	9	2	4	2	8	0	3
M. Grandfather 6	6	15	5	0	3	3	11	8	7	7	7
Son 6.1	6	6	4	0	6	0	3	0	1	1	0
Son 6.1, Spouse	6	13	10	14	12	7	7	5	9	9	6
Son 6.1, Child 1	6	2	0	1	6	4	1	0	3	3	0
Son 6.1, Child 2	6	11	4	1	9	4	4	2	4	2	4
Son 6.2	6	7	0	0	0	1	5	0	3	1	3
Son 6.2, Spouse	6	4	4	0	3	1	3	1	1	1	2
Son 6.2, Child 1	6	1	1	0	0	2	0	0	0	0	0
Son 6.2, Child 2	6	1	0	1	0	0	0	0	0	1	0
Mother 7	7	4	3	2	1	0	1	1	0	0	0
Father 7	7	8	0	3	0	5	2	4	2	4	2

Son 7.1	7	5	7	4	7	3	4	8	9	3	2
Son 7.1, Spouse	7	12	0	3	1	0	0	0	5	2	1
Son 7.1, Child 1	7	6	13	11	5	5	7	2	5	5	0
Son 7.1, Child 2	7	6	0	0	2	0	3	0	3	0	2
Mother 7, Sister	7	5	1	1	0	0	0	0	0	0	0
Mother 8	8	0	0	1	0	0	0	0	2	0	0
Father 8, Brother	8	5	0	3	8	3	9	0	0	6	1
Daughter 8.1	8	1	0	0	0	0	0	0	0	1	0
Daughter 8.1, Child 1	8	8	0	5	0	2	2	0	0	0	0
Son 8.2	8	2	0	0	0	0	5	0	0	0	1
Son 8.3	8	3	0	2	4	2	7	2	5	4	2
Son 8.4	8	4	12	6	3	1	6	3	6	2	2
Son 8.4, Spouse	8	7	8	4	2	0	4	5	7	2	0
Son 8.4, Child 1	8	11	10	12	14	7	3	7	8	11	7
Son 8.4, Child 2	8	3	0	7	5	4	5	7	4	8	3
Son 8.4, Spouse, Mother	8	6	4	4	2	2	6	3	8	1	0
Son 8.4, Spouse, Father	8	3	2	1	6	5	3	0	1	7	3
Daughter 8.5	8	3	0	0	0	4	2	1	0	4	5
Daughter 8.5, Spouse	8	8	0	0	3	3	0	0	2	1	2
Daughter 8.5, Spouse, Niece	8	3	1	1	8	2	1	0	3	1	3
Daughter 8.5, Spouse, Mother	8	5	1	1	4	2	3	1	2	4	0
Mother 9	9	6	3	4	6	0	9	6	6	0	0
Son 9.1	9	9	5	4	8	4	10	6	4	3	3
Daughter 9.2	9	7	2	7	13	7	6	4	0	5	3
Father 10	10	5	12	3	10	4	2	0	2	3	0
Fathers Brother 10.1	10	4	0	0	11	12	8	4	4	3	6
Fathers Brother 10.2	10	12	1	8	3	3	2	0	5	7	4

Fathers Sister 10.3	10	1	0	3	0	0	4	0	0	0	0
Son 10.1	10	8	12	6	13	5	6	11	5	8	8
Mother 11	11	6	0	3	0	0	4	0	1	0	2
Daughter 11.1	11	12	2	2	7	1	8	5	1	1	4
Daughter 11.2	11	6	4	3	9	0	8	2	1	2	0
Mother 12	12	2	1	0	2	0	1	1	2	1	0
Father 12	12	8	6	0	8	4	5	4	15	6	1
Mothers Sister	12	5	0	1	5	0	5	4	1	0	0
Daughter 12.1	12	7	3	3	3	2	1	2	1	2	1
Daughter 12.2	12	3	3	4	3	0	0	3	3	1	1
Son 12.4	12	4	0	0	1	4	0	0	0	4	0
Mother 13	13	5	1	1	0	1	1	0	0	0	0
Father 13	13	12	6	6	10	6	4	5	4	9	4
Son 13.1	13	5	0	1	3	1	4	0	0	8	4

RAW DATA BY MINUTIAE COUNT

Person	Family	FP 1M	FP 2M	FP 3M	FP 4M	FP 5M	FP 6M	FP 7M	FP 8M	FP 9M	FP 10M
Mother 1	1	7	3	3	0	0	2	0	0	1	0
Father 1	1	6	2	3	6	3	5	4	7	5	0
Son 1.1	1	9	6	3	5	2	7	4	0	5	2
Son 1.3	1	8	5	2	10	6	9	5	6	6	2
Son 1.4	1	13	6	4	7	5	5	5	4	1	1
Daugh.1.5	1	0	3	4	2	0	3	0	0	0	0
Son 1.6	1	6	1	1	2	4	4	2	2	0	0
Son 1.6, Child 1	1	14	10	7	6	3	6	10	5	3	2
Son 1.6, Child 2	1	22	11	10	10	8	14	13	3	4	5
Mother 2	2	11	10	4	1	0	5	3	1	0	0
Father 2	2	9	2	6	13	10	2	2	6	3	4
Daughter 2.1	2	13	7	8	7	4	6	0	4	12	4
Daughter 2.2	2	7	1	11	5	7	5	4	3	2	2
Daughter 2.1, Child 1	2	7	2	5	4	2	2	3	2	0	0
Mother 3	3	2	3	6	5	5	6	0	6	0	0
Father 3	3	18	7	12	12	9	13	0	10	9	6
Son 3.1	3	16	9	12	21	10	14	11	10	9	7
Son 3.1 Spouse	3	15	0	0	0	0	4	0	0	0	2
Son 3.1, Child 1	3	0	2	0	0	2	1	2	0	2	2
Son 3.2	3	15	10	14	12	10	10	13	8	8	9
Son 3.3	3	15	5	7	14	12	11	9	9	10	8
Mother 4	4	0	0	0	2	0	0	0	0	0	0
Father 4	4	2	0		5	2	4	0	3	0	1
Son 4.1	4	0	0	0	0	0	2	0	0	2	2
Son 4.1, Spouse	4	8	0	3	4	0	4	3	2	3	0
Son 4.1, Child 1	4	11	2	1	3	3	5	1	2	10	4
Daughter 4.2	4	0	0	2	0	0	0	0	2	0	0
Daughter 4.2 Spouse	4	4	5	0	0	0	3	0	0	0	1

Daughter 4.2, Child 1	4	5	3	3	4	2	3	2	3	2	0
Daughter 4.2, Child 1, Spouse	4	6	2	4	7	6	4	1	3	4	4
Daughter 4.2, Child 1, Child 1	4	3	1	0	0	0	3	0	5	4	0
Daughter 4.2, Child 1, Child 2	4	8	3	0	1	0	5	0	0	0	4
Daughter 4.2, Child 2	4	8	0	1	0	2	6	0	0	1	0
Son 4.3	4	3	0	0	0	0	0	0	0	0	0
Mother 5	5	6	4	0	0	0	0	0	0	0	0
Daughter 5.1	5	5	9	5	5	1	4	3	6	5	4
Daughter 5.1, Spouse	5	10	7	9	5	2	7	4	6	4	0
Daughter 5.1, Child 1	5	7	16	8	6	6	10	14	15	6	10
Son 5.2, Spouse	5	5	2	4	6	3	3	1	2	1	1
Son 5.2, Child 1	5	16	2	10	19	11	13	11	6	15	11
Son 5.2, Child 2	5	16	4	3	12	1	7	0	5	5	0
P. Grandmother 6	6	2	1	0	0	0	0	0	0	0	0
P. Grandfather 6	6	2	3	2	3	1	1	0	3	3	1
M. Grandmother 6	6	6	7	4	9	2	4	2	8	0	3
M. Grandfather 6	6	15	5	0	3	3	11	8	7	7	7
Son 6.1	6	6	4	0	6	0	3	0	1	1	0
Son 6.1, Spouse	6	13	10	14	12	7	7	5	9	9	6
Son 6.1, Child 1	6	2	0	1	6	4	1	0	3	3	0
Son 6.1, Child 2	6	11	4	1	9	4	4	2	4	2	4
Son 6.2	6	7	0	0	0	1	5	0	3	1	3
Son 6.2, Spouse	6	4	4	0	3	1	3	1	1	1	2
Son 6.2, Child 1	6	1	1	0	0	2	0	0	0	0	0
Son 6.2, Child 2	6	1	0	1	0	0	0	0	0	1	0
Mother 7	7	4	3	2	1	0	1	1	0	0	0
Father 7	7	8	0	3	0	5	2	4	2	4	2
Son 7.1	7	5	7	4	7	3	4	8	9	3	2

Son 7.1, Spouse	7	12	0	3	1	0	0	0	5	2	1
Son 7.1, Child 1	7	6	13	11	5	5	7	2	5	5	0
Son 7.1, Child 2	7	6	0	0	2	0	3	0	3	0	2
Mother 7, Sister	7	5	1	1	0	0	0	0	0	0	0
Mother 8	8	0	0	1	0	0	0	0	2	0	0
Father 8, Brother	8	5	0	3	8	3	9	0	0	6	1
Daughter 8.1	8	1	0	0	0	0	0	0	0	1	0
Daughter 8.1, Child 1	8	8	0	5	0	2	2	0	0	0	0
Son 8.2	8	2	0	0	0	0	5	0	0	0	1
Son 8.3	8	3	0	2	4	2	7	2	5	4	2
Son 8.4	8	4	12	6	3	1	6	3	6	2	2
Son 8.4, Spouse	8	7	8	4	2	0	4	5	7	2	0
Son 8.4, Child 1	8	11	10	12	14	7	3	7	8	11	7
Son 8.4, Child 2	8	3	0	7	5	4	5	7	4	8	3
Son 8.4, Spouse, Mother	8	6	4	4	2	2	6	3	8	1	0
Son 8.4, Spouse, Father	8	3	2	1	6	5	3	0	1	7	3
Daughter 8.5	8	3	0	0	0	4	2	1	0	4	5
Daughter 8.5, Spouse	8	8	0	0	3	3	0	0	2	1	2
Daughter 8.5, Spouse, Niece	8	3	1	1	8	2	1	0	3	1	3
Daughter 8.5, Spouse, Mother	8	5	1	1	4	2	3	1	2	4	0
Mother 9	9	6	3	4	6	0	9	6	6	0	0
Son 9.1	9	9	5	4	8	4	10	6	4	3	3
Daughter 9.2	9	7	2	7	13	7	6	4	0	5	3
Father 10	10	5	12	3	10	4	2	0	2	3	0
Fathers Brother 10.1	10	4	0	0	11	12	8	4	4	3	6
Fathers Brother 10.2	10	12	1	8	3	3	2	0	5	7	4
Fathers Sister 10.3	10	1	0	3	0	0	4	0	0	0	0
Son 10.1	10	8	12	6	13	5	6	11	5	8	8

Mother 11	11	6	0	3	0	0	4	0	1	0	2
Daughter 11.1	11	12	2	2	7	1	8	5	1	1	4
Daughter 11.2	11	6	4	3	9	0	8	2	1	2	0
Mother 12	12	2	1	0	2	0	1	1	2	1	0
Father 12	12	8	6	0	8	4	5	4	15	6	1
Mothers Sister	12	5	0	1	5	0	5	4	1	0	0
Daughter 12.1	12	7	3	3	3	2	1	2	1	2	1
Daughter 12.2	12	3	3	4	3	0	0	3	3	1	1
Son 12.4	12	4	0	0	1	4	0	0	0	4	0
Mother 13	13	5	1	1	0	1	1	0	0	0	0
Father 13	13	12	6	6	10	6	4	5	4	9	4
Son 13.1	13	5	0	1	3	1	4	0	0	8	4

APPENDIX 3: STATISTICAL ANALYSIS

Correlations

		FP_1R	FP_2R	FP_3R	FP_4R	FP_5R	FP_6R
FP_1R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_2R	Pearson Correlation	.487**					
	Sig. (2-tailed)	.000					
	N	96					
FP_3R	Pearson Correlation	.492**	.504**				
	Sig. (2-tailed)	.000	.000				
	N	96	96				
FP_4R	Pearson Correlation	.458**	.513**	.533**			
	Sig. (2-tailed)	.000	.000	.000			
	N	96	96	96			
FP_5R	Pearson Correlation	.327**	.435**	.508**	.588**		
	Sig. (2-tailed)	.001	.000	.000	.000		
	N	96	96	96	96		
FP_6R	Pearson Correlation	.675**	.465**	.477**	.506**	.379**	
	Sig. (2-tailed)	.000	.000	.000	.000	.000	
	N	96	96	96	96	96	
FP_7R	Pearson Correlation	.512**	.631**	.660**	.569**	.503**	.559*
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_8R	Pearson Correlation	.382**	.496**	.720**	.625**	.420**	.450**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_9R	Pearson Correlation	.238*	.439**	.425**	.698**	.557**	.404**
	Sig. (2-tailed)	.019	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_10R	Pearson Correlation	.270**	.344**	.462**	.468**	.778**	.427**
	Sig. (2-tailed)	.008	.001	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_1M	Pearson Correlation	.605**	.391**	.396**	.388**	.321**	.560**
	Sig. (2-tailed)	.000	.000	.000	.000	.001	.000
	N	96	96	96	96	96	96
FP_2M	Pearson Correlation	.397**	.596**	.419**	.395**	.380**	.356**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_3M	Pearson Correlation	.451**	.461**	.591**	.513**	.429**	.439**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	95	95	95	95	95	95
FP_4M	Pearson Correlation	.366**	.429**	.430**	.692**	.526**	.491**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_5M	Pearson Correlation	.332**	.360**	.403**	.550**	.639**	.411**
	Sig. (2-tailed)	.001	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_6M	Pearson Correlation	.505**	.349**	.354**	.482**	.371**	.653**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_7M	Pearson Correlation	.408**	.481**	.455**	.452**	.385**	.480**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96

Correlations

		FP_1R	FP_2R	FP_3R	FP_4R	FP_5R	FP_6R
FP_8M	Pearson Correlation	.406**	.483**	.615**	.510**	.371**	.511*
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_9M	Pearson Correlation	.228*	.311**	.397**	.511**	.408**	.348*
	Sig. (2-tailed)	.026	.002	.000	.000	.000	.001
	N	96	96	96	96	96	96
FP_10M	Pearson Correlation	.338**	.305**	.327**	.444**	.476**	.442*
	Sig. (2-tailed)	.001	.003	.001	.000	.000	.000
	N	96	96	96	96	96	96

Correlations

		FP_7R	FP_8R	FP_9R	FP_10R	FP_1M	FP_2M
FP_1R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_2R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_3R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_4R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_5R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_6R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_7R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_8R	Pearson Correlation	.637**					
	Sig. (2-tailed)	.000					
	N	96					
FP_9R	Pearson Correlation	.499**	.536**				
	Sig. (2-tailed)	.000	.000				
	N	96	96				
FP_10R	Pearson Correlation	.420**	.392**	.541**			
	Sig. (2-tailed)	.000	.000	.000			
	N	96	96	96			
FP_1M	Pearson Correlation	.420**	.316**	.303**	.300**		
	Sig. (2-tailed)	.000	.002	.003	.003		
	N	96	96	96	96		
FP_2M	Pearson Correlation	.568**	.448**	.303**	.371**	.445**	
	Sig. (2-tailed)	.000	.000	.003	.000	.000	
	N	96	96	96	96	96	
FP_3M	Pearson Correlation	.529**	.463**	.402**	.393**	.564**	.606**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	95	95	95	95	95	95
FP_4M	Pearson Correlation	.526**	.472**	.524**	.444**	.563**	.471**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_5M	Pearson Correlation	.465**	.418**	.493**	.527**	.513**	.339**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.001
	N	96	96	96	96	96	96
FP_6M	Pearson Correlation	.525**	.380**	.417**	.326**	.653**	.471**
	Sig. (2-tailed)	.000	.000	.000	.001	.000	.000
	N	96	96	96	96	96	96
FP_7M	Pearson Correlation	.642**	.461**	.398**	.361**	.541**	.607**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96

Correlations

		FP_7R	FP_8R	FP_9R	FP_10R	FP_1M	FP_2M
FP_8M	Pearson Correlation	.633**	.703**	.351**	.327**	.427**	.586**
	Sig. (2-tailed)	.000	.000	.000	.001	.000	.000
	N	96	96	96	96	96	96
FP_9M	Pearson Correlation	.347**	.413**	.552**	.424**	.534**	.372**
	Sig. (2-tailed)	.001	.000	.000	.000	.000	.000
	N	96	96	96	96	96	96
FP_10M	Pearson Correlation	.401**	.322**	.426**	.503**	.547**	.405**
	Sig. (2-tailed)	.000	.001	.000	.000	.000	.000
	N	96	96	96	96	96	96

Correlations

		FP_3M	FP_4M	FP_5M	FP_6M	FP_7M	FP_8M
FP_1R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_2R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_3R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_4R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_5R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_6R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_7R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_8R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_9R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_10R	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_1M	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_2M	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_3M	Pearson Correlation						
	Sig. (2-tailed)						
	N						
FP_4M	Pearson Correlation	.631**					
	Sig. (2-tailed)	.000					
	N	95					
FP_5M	Pearson Correlation	.626**	.774**				
	Sig. (2-tailed)	.000	.000				
	N	95	96				
FP_6M	Pearson Correlation	.559**	.653**	.579**			
	Sig. (2-tailed)	.000	.000	.000			
	N	95	96	96			
FP_7M	Pearson Correlation	.598**	.604**	.582**	.667**		
	Sig. (2-tailed)	.000	.000	.000	.000		
	N	95	96	96	96		

Correlations

		FP_3M	FP_4M	FP_5M	FP_6M	FP_7M	FP_8M
FP_8M	Pearson Correlation	.553**	.569**	.516**	.529**	.599**	
	Sig. (2-tailed)	.000	.000	.000	.000	.000	
	N	95	96	96	96	96	
FP_9M	Pearson Correlation	.571**	.658**	.661**	.538**	.500**	.503**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	95	96	96	96	96	96
FP_10M	Pearson Correlation	.516**	.631**	.710**	.593**	.661**	.504**
	Sig. (2-tailed)	.000	.000	.000	.000	.000	.000
	N	95	96	96	96	96	96

Correlations

		FP_9M	FP_10M
FP_1R	Pearson Correlation Sig. (2-tailed) N		
FP_2R	Pearson Correlation Sig. (2-tailed) N		
FP_3R	Pearson Correlation Sig. (2-tailed) N		
FP_4R	Pearson Correlation Sig. (2-tailed) N		
FP_5R	Pearson Correlation Sig. (2-tailed) N		
FP_6R	Pearson Correlation Sig. (2-tailed) N		
FP_7R	Pearson Correlation Sig. (2-tailed) N		
FP_8R	Pearson Correlation Sig. (2-tailed) N		
FP_9R	Pearson Correlation Sig. (2-tailed) N		
FP_10R	Pearson Correlation Sig. (2-tailed) N		
FP_1M	Pearson Correlation Sig. (2-tailed) N		
FP_2M	Pearson Correlation Sig. (2-tailed) N		
FP_3M	Pearson Correlation Sig. (2-tailed) N		
FP_4M	Pearson Correlation Sig. (2-tailed) N		
FP_5M	Pearson Correlation Sig. (2-tailed) N		
FP_6M	Pearson Correlation Sig. (2-tailed) N		
FP_7M	Pearson Correlation Sig. (2-tailed) N		

Correlations

		FP_9M	FP_10M
FP_8M	Pearson Correlation Sig. (2-tailed) N		
FP_9M	Pearson Correlation Sig. (2-tailed) N		
FP_10M	Pearson Correlation Sig. (2-tailed) N	.714** .000 96	

**. Correlation is significant at the 0.01 level (2-tailed).

*. Correlation is significant at the 0.05 level (2-tailed).

DISTRIBUTION BY LEVEL OF INHERITANCE RESULTS

H %	1p	1r	1m	2p	2r	2m	3p	3r	3m	4p	4r	4m	5p	5r	5m
0	1819	734	824	936	734	1240	2510	691	1263	1265	653	883	2933	665	1374
.0625	1	1	1	0	0	2	1	1	3	2	0	1	3	0	0
.125	11	3	5	2	1	11	14	6	13	15	1	6	18	1	10
.25	43	17	17	21	18	30	61	23	33	52	10	22	74	12	26
.5	79	24	30	37	37	47	74	27	56	70	30	31	101	26	46

H %	6p	6r	6m	7p	7r	7m	8p	8r	8m	9p	9r	9m	10p	10r	10m
0	2145	627	1086	828	672	1561	2180	701	1234	1972	680	1379	3141	788	1704
.0625	1	0	2	1	1	2	1	0	1	3	0	1	3	1	1
.125	11	3	6	3	4	14	10	3	5	14	2	5	21	4	8
.25	57	15	22	26	23	33	49	13	32	54	13	20	75	18	38
.5	80	20	35	40	37	53	81	25	47	76	28	55	104	28	60

*p=pattern type
r=ridge count
m=minutiae count

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