Evolution, Heredity and Gene-Localization of Interdigital Patterns

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Dermatoglyphy is a character peculiar to primates. Interdigital patterns (IDPs) are the most representative dermatoglyphies. At beginning of the primates' evolution pathway, there are several unconnected muscle pads with patterns in each interdigital area. Latter primates keep only one pad in each area, but they have kept different pads, which suggests they departed quite early. The habit of ground-inhabited makes the patterns indifferent areas develop equally, while tree-inhabited unequally. Pattern intensity is direct ratio to the rate of utilization of interdigital areas. So Old World monkeys' IDPs are most developed and those of apes' are most retrograde. Humankind has secondary developed a kind of various pattern in the palm area opposite to the third finger for labor. The types of this pattern on one hand can be clustered into 4 lots by curve and merge transformations. They are 4 combinations of 2 states (pattern or no pattern) in area III and IV. Pedigree analysis shows that pattern genes controlling area III or IV are mosaic dominant, and the corresponding area patterns on left and right hands are controlled by the same allele. Some of these alleles express symmetric patterns, while others express asymmetric patterns. This is the major gene locus of IDP. There are still loci of a kind of original patterns inherited from human-like apes, on which the pattern genes are recessive. So IDP fit a left-right asymmetric, mosaic dominant, major gene inheritance model. The study of IDP may inspire the studies of other left-right asymmetric characters such as brain, hand habit, etc. The linkage relationship between IDP and phenylthiocarbamide (PTC) tasting is found in our pedigrees($\theta = 0.113$). The gene of PTC tasting is considered on chromosome 7q, so the gene of IDP may be on a locus nearby. Whole genome scan with 304 short tandem repeat polymorphism (STRP) markers throughout 23 chromosomes has been done in 223 individuals of 11 pedigrees. The linkage between these STRP markers and IDP has been tested. D7S821 is found tightly linked with IDP genotype. Thus, IDP gene is initially localized near 109.12 cM of chr.7.

Key words: Interdigital patterns (IDPs) , evolution , heredity, gene-localization

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Skin ridges, which appear on the palm and sole of primates, including human being, can form all kinds of designs. These skin ridges enhance the frictional force, increase the sense area, which makes primates hold tree branch firmer, touch things more sensitive. This must have acted an important role on the pathway of primates to the summit of evolution.

The beginning of scientific study of dermatoglyphy is the systematic classification by Pukinje in 1823. In 1892, Galton proved that skin ridge pattern is characteristic, constant and hereditary.^[1] From then on, dermatoglyphics has developed vigorously, and is always applied in medical science and anthropology. *Finger-prints, Palms and Chromosomes* by L.S.Penrose on *Nature* 197(1963) gave a minute description on characteristic dermatoglyphies of some hereditary diseases such as Down's Syndrome.^[1] Now, the interrelationship between dermatoglyphies and hereditary disease has been approved generally, and has been applied on infants' early diagnosis. In the field of anthropology, researchers find that there are divergences of different degrees between races, nationalities, and even populations. Diagnosis on individuals of different nationalities. Clustering of these data can even reflect the genetics relation between different populations. *A Dermatoglyphic Study of the Chinese Population* III by Zhang Haiguo on *Acta Genetica Sinica* 25(1998) calculated the genetics relation between 52 minority nationalities of China with dermatoglyphies successfully.^[2]

Anthropologists are also aware of the dermatoglyphies of other primates, and have described those of several species. From Ayer (1948),^[3] many anthropologists have studied a great deal of primates' dermatoglyphies. But there has never been one who analyzed exhaustively and audaciously the evolutionary



Figure 1. Position of IDPs on a Left Palm Interdigital area II is between point a and b; interdigital area III is between point b and c; interdigital area IV is between point c and d.

pathway of the dermatoglyphies among all the primates and the factors influence it. $^{\left[4,5\right] }$

The most perplexing thing is the specific inheritance model of dermatoglyphy. The genetics studies on the size, trend or shape of skin ridge patterns always turn to self-contradictory conclusions. From 1920 to 1965, scholars of many countries did a lot of work to advance all kinds of theories about the inheritance of individual characters.^[6] But that is far from the foundation of an inheritance model of dermatoglyphy. The opinion that is now generally accepted is that the dermatoglyphy accord with a polygenic inheritance model. A lot of genes determine the appearance of dermatoglyphy jointly; each of them only effects insignificantly.

We chose interdigital pattern, which is the most representative in the dermatoglyphies, collected a lot of samples of random populations and pedigrees, studied for about one year. Now, we have tentatively made it clear the pathway and the factors of the evolution, the inheritance model of IDPs.

IDPs are the patterns on the part of the palm connected with fingers. The palm area between thumb and the first finger is called interdigital area I, so is the other areas called interdigital area II, III, IV. The demarcation between two close interdigital areas is the tripartite point of different skin ridge trends. There are always all kinds of patterns such as arch, loop, and whorl with different trends in a certain interdigital area.

IDPs differ severely among primates, also among individuals of humankind. IDPs are quite more various

than other dermatoglyphies. The observation and analysis of them is simpler than that of fingerprints. So they are suited to be a model for studying dermatoglyphy. IDPs are also left-right asymmetric characters. The foundation of inheritance model of them can also inspire the genetics studies of other left-right asymmetric characters.^[7,8]

1. Origin and Evolution of IDPs among Primates

1.1.Origin of IDPs

General opinion about how dermatoglyphy come into being is that primates need to enhance the frictional force and sense of the palms and soles for tree-inhabited lives. IDP is one of the earliest dermatoglyphies. When interdigital patters have just taken shape, those in different area did not contact each other. There were still large fur areas between dermatoglyphy areas. On palms of *Tupaia*,^[9,10] there are always 3 to 4 muscle pads, fairly close to each other, opposite to each finger, with simple arch patterns on each pad. Ridge trends are different from one pad to another. During latter primates' development, some of these pads expand, and others get narrowed. Neighboring pads contact each other. Dermatoglyphies are distributed all over the palm. There is a tripartite point left at the demarcation of each three pads. On the pads, appear more complicated patterns.

1.2.Evolutionary Pathways of IDP

Commonly speaking, there is only one biggest pad in each interdigital area of those species senior to *Tupaia*. Analyzing the ridge trends and the positions of tripartite points, we find that primates have reserved different pads according to *Tupaia*, which suggests some big categories split up quite more early than we think. So the evolutionary pathway of primates is bush-like.

There are mainly 5 evolution branches out of *Tupaia*. ① Tarsidae. There is only one pad in each interdigital area, and fairly big space between pads. On the pads, there is only simple arch pattern.^[11] (2)Lemur and Lorisidae, one pad in each area, too, small gap between pads. On the pads, equally develop out primitive pattern, loop or small whorl.^[12,13] ③New World monkey.^[14] Side interdigital areas are developed while central areas are retrograde. In Cebidae's interdigital area II is a big whorl, and in area IV is a loop. In Hapalidae's area I is a big whorl, area IV also loop. Interdigital areas have completely connected. ④Old World monkey. The IDPs of Old World monkey are the most developed. There are loops in different sizes in Colobidae.^[15,16] In Macaca's area II, III and IV, are all big obvious whorls.^[17,18,19] ⑤Human-like ape. Their IDPs are quite retrograde. Gibbons have no IDP.^[20] Chimpanzees occasionally have some little loops. Humankind has developed out of ape. So the original IDPs are also retrograde. But opposite to the third finger, appears a new various pattern.



Figure 2. IDPs of the Primates

1.3.Evolution Factors of IDP

Comparing the categories of primates, we find interdigital areas of tree-inhabited primates developed rather unequally, while ground-inhabited are on the contrary. Equality of IDPs is direct ratio to the ground-inhabited tendency. It is possibly because palms need to touch ground equally when ground-inhabit, but when tree-inhabit, palms must press the branch from both sides. So interdigital areas of tree-inhabit primates are side developed and central retrograde. Pattern intensity is also direct ratio to the rate of utilization. This is reflected very well in human-like apes. Gibbons use fingers to seize hold of branches, and seldom use interdigital area (so that to be nimble when seize or release). Then there are no patterns in their interdigital



Figure 3. Bush-like Evolution of Primates

various and inheriting distinctively.

areas. When chimpanzees are walking, they let finger back touch ground. Only when they seize hold of something occasionally, they will use IDP. So their IDP are very retrograde. Only few individuals have small loop in their interdigital areas.

IDPs of humankind, corresponding to those of human-like apes, are also very retrograde. They are all inperfectible dominant or recessive small loops. It does not fit for the high frequency and intensive use of interdigital areas when we are laboring. So at the force focus of human palm when seizing something,^[21] opposite to the third finger, appears a new pattern. This kind of new pattern is

2. Clustering of the Secondary Developed IDPs of Humankind

2.1. The Old Classification of IDPs

In 1943, H.Cummins establish the methods of classification and statistics about all the dermatoglyphies including IDPs.^[22] He regarded the patterns obviously in a certain interdigital area X as "area X patterns", the patterns open to tripartite point c as "patterns across area III and IV", and no obvious true patterns as "no pattern". There are still two occasions left, "tripartite point c or d absent". He also recorded loops or whorls *etc* in each area. This classification only pays attention to appearance, mingles all kinds of elements, is useful to population genetics study, but not for classic genetics study.

2.2. Types of IDPs

The small loops in interdigital area II, III or inclined to ulnar side in area IV are patterns reserved from human-like apes. We haven't studied them detailedly for they are not various.

The IDPs in area III and IV opposite to the third finger are secondary developed in humankind. They are quite various in shapes. On one palm only, there can be 20 types. A single pattern in one area may be in three states: ①parallel to the fingers, ②head of the pattern turns to the third finger, vertical to the fingers, ③the whole pattern inclines to the third finger, head of it still parallel to the fingers. When there are patterns both in area III and IV, they will turn or incline to the third finger together in a certain degree, Which form 11 types of patterns appearances. Area IV pattern interacts with the ulnar original pattern will form 3 types: separating, leaning, and merging. Tripartite point d



Figure 4. Transformations of IDPs of the right hands. Interdigital areas III are on the left side, and areas IV are on the right sides.

absent is another type, which shows a state that all the ridges in area III and IV lead to ulnar side.

2.3. Transformations among the Types of IDPs

When there are patterns both in area III and IV, and they are not curved, both of them can be seen clearly. When curved slightly, we can see two patterns leaning to each other. When both two patterns incline to the third finger's axis, a "shoulder by shoulder" pathway of merging turns out. First, both two patterns keep part of their shapes, then one of the patterns with fewer ridges entirely merge into the other pattern, which forms a pattern type across two area but also with a small pattern in one area. At the end, two patterns deeply merge into a pattern across area III and IV. When two patterns both turn their heads to the third finger's axis, a "head to head" pathway of merging turns out. The top of one pattern merges into the other first, then both two patterns lose their top-ridges with a gap at the demarcation line. At last the ridges of two patterns get joint entirely, and the tripartite point c disappears. When both two patterns turn to the third finger's axis but directions of them are not in the same line, they will brush past each other. Area III pattern enters area IV and area IV pattern also enters area III. When patterns cross the third finger's axis, they push against each other as the space is too narrow and reduce the ridge number of their waist, which makes the heads of the patterns become little whorls. All kinds of transitions in these pathways are discovered. The type that tripartite point d absents or only a ulnar loop in area IV is the real no-pattern type.

2.4. Significance of the Clustering

According to the classification and the transformations, the pattern types on one hand in the third finger root area are actually clustered into 4 lots. They are 4 combinations of 2 states (pattern or no pattern) in either area. Studying the distribution of these states in pedigrees, we can find out the inheritance law determining the number of patterns fairly easily.

3.Left-right Asymmetric Mosaic Dominant Inheritance of Humankind's

Secondary Developed IDPs

3.1. Linkage Analysis of Pedigrees and the Gene Frequencies

Regarding area III and IV of two hands of a certain individual as 4 characters, and pattern as dominant character, no pattern recessive, each character is monogenic inheriting. This is concluded from the analysis of 101 nuclear families with 135 parents-child sets, nearly 99% of which can be explained with monogene inheritance model. When studying one hand only, characters of area III and IV are found entirely linked. That is to say the genes of area III and IV patterns are on the same locus. There are only 3 kinds of linkage: ① pattern in area III and no pattern in area IV, ②pattern in area IV and no pattern in area III, ③no pattern in either area. So we know there may be only 3 alleles, area III pattern allele, area IV pattern allele, and no pattern in both areas. This is a mosaic dominant inheritance model.^[23] By the statistics of a random population with 1200 individuals, rough gene frequencies of these 3 alleles are calculated, area III pattern allele 0.23, area IV pattern allele 0.71, no pattern allele 0.069.

We also find the entire linkage between the left and right hands. So there is only one gene locus



Figure 5. One of the Pedigrees studied. (C is area III symmetric allele. c¹ is area III asymmetric allele showing pattern on the left. c^r is area III asymmetric allele showing pattern on the right. D is area IV symmetric allele. d¹ is area IV asymmetric allele showing pattern on the left. d^r is area IV asymmetric allele showing pattern on the right. (1)~(20) are the same pattern type numbers as in figure 4.Right hand type is before comma, and the other is left hand type.)

controlling the patterns both in area III and IV, left and right hands. The linkage between a pair of hands has 6 types. Area III patterns both on the left and right hands, one area III pattern only on one side of the hands, area IV patterns both on the left and right hands, one area IV pattern only on one side of the hands. So there are 6 corresponding alleles. These alleles all control the corresponding area pairs of two hands, don't control the different areas of two hands. There is symmetric alleles controlling a pair of patterns' appearance in the corresponding area of two hands and asymmetric alleles controlling one side pattern's appearance on only one side of an area pair. In one area, symmetric allele is dominant to asymmetric allele. Alleles of different areas, no matter whether symmetric or not, are mosaic dominant. This is the left-right asymmetric mosaic dominant inheritance of IDP. The gene frequencies are calculated roughly from the random population.

Area III, symmetric 0.1, asymmetric 0.2; area IV, symmetric 0.6, asymmetric 0.1.

3.2.Inperfectible Dominant Allele

In the pedigrees studied, we find very occasionally an inheritance phenomenon that can not be explained even with one area monogenic dominant model. For example, parents have patterns only in area IV, but in their child's hand there appears an area III pattern. It may be because there is an inperfectible dominant allele on the same locus we just talked about, controlling a rhombus loop appears in area III of





Inperfectible an

inperfectible dominant allele in either one of the parents or their child. It expresses in the child but doesn't express in his father or mother.

3.3. Inheritance of the Original Patterns

The original patterns can also be recognized by appearances. They are smaller than the secondary developed patterns. Their heads are always out of the tripartite points. The genes of different areas are not on the same locus. So patterns of different areas are not mosaic dominant inheriting. There are only 3 alleles on a locus of one area, and they are still fit the left-right asymmetric

inheritance model. The pattern alleles are recessive, not like those of the secondary developed pattern. So the original patterns seldom express. When they express, they won't effect the major gene's expression. These



Figure 7. The Original Patterns (a,b), Comparing with the Secondary Developed Patterns (c,d).

original pattern genes are inherited from human-like apes.

Though on the major gene locus of the IDP there are 6 alleles, every allele may still be polymorphous. The polymorphous types of one allele defer from each other in quantity, and the different alleles in quality.

Other genes or other factors during the embryo development may control all kinds of the curve states of IDPs. It is pending further study and discussion.

4. Linkage Relationship between IDPs and PTC tasting

4.1. Survey of the Genetics Study of PTC Tasting

Difference of PTC taste sensibility among people was found by Fox in 1932. Some have a bitter taste to a certain PTC dilution, while others would never have any taste. In 1989, two research groups send up the inheritance model of PTC tasting respectively. Reddy and Rao believed that PTC tasting is controlled by an inperfectible dominant gene^[24]. But Olson believed there is a PTC tasting gene and a bitter gene joining forces to control the PTC tasting ^[25]. In our pedigrees, there is no difference of common bitter taste sensitivity. Thus, inheritance of PTC tasting can be interpreted with a monogenic model.

In 1984, M.A.Spence found the linkage relationship between PTC tasting and Kell blood group ($\theta = 0.14$) whose gene has been localized on chromosome 7q33. So, the PTC tasting gene is considered on chr.7q.^[26]

4.2. Test of PTC Tasting and Genotype Determination

PTC dilution of 1g/l is regarded as dilution [#]1, then dilute it into a half consistency to get dilution [#]2. Every time a certain dilution should be half diluted. At last, dilution [#]14 will be gotten. One shall taste from dilution [#]14 until to a certain dilution he finds bitter. The number of this bitter dilution stands for his PTC taste sensitivity.^[27]

Pedigree study shows that [#]1-[#]4 individuals are PTC tasting blinds whose PTC alleles are recessive and homozygous; [#]5-[#]8 individuals are heterozygote; [#]10-[#]14 individuals are PTC complete taster whose alleles are dominant and homozygous. [#]9 individuals are on the threshold line, and should be judged in the very pedigree.

4.3. Linkage Observation between IDPs and PTC tasting

The linkage relationship between these two characters was analyzed in 101 nuclear families. There are 115 times of haplotype inheritance confirmed, with 13 times of recombination ($\theta = 0.113$). The true recombination rate shall be from 0.067 to 0.184 with such an observed rate. It shows that the genes of PTC tasting and IDPs are fairly tightly linked. The gene of IDPs may also be on the chromosome 7q, and near 7q33. Analyzing the linkage with the polymorphism genome markers on chromosome 7q may accurately localize it.

5. Localization of IDP Gene with Whole-Genome Scan and Linkage Analysis

5.1. STRP Markers Used in Whole Genome Scan

Short tandem repeat sequences can be found throughout the whole human genome. On a certain locus, there are a series of alleles repeating a short tandem in different numbers. We used 304 STRP markers to scan 223 individuals' whole genome in 11 pedigrees. 26 of those markers are on chromosome 7.

5.2. Chromosomes' Structure Analysis of the Pedigrees

There are about 0.5% error data among the original data of whole genome scan. They disrupt the genetic structures of the pedigrees. *Cyrillic* program of Cherwell Scientific Publishing Ltd. can find out these errors.

This program can also draw haplotype of every individual's every chromosome, showing the recombination. There are about 0.04 times of recombination per cM each individual. All the pedigrees' recombination density is 4.6 per cM. It is far more than the need of scanned markers' density. Enough recombination times are prerequisite of gene localization.

5.3. Linkage Analysis between STRP Markers and IDP Gene

With the *Linkage* programs of Columbia University (NY), we got a series of lod scores on every supposed link levels. Lod score is the common logarithm of the ratio between possibility of the supposition of a certain link level being true and that of being false while the observed link level appears. When the lod score is negative, the supposition must be false. When the lod score is positive, the supposition may be true. When the lod score is big than 3, the supposition must be true.

We find the lod score of most STRP markers are negative or small than 1, only that of D7S821 is 1.43 on the link level of 0.05. Then, it is quite possible that IDP gene and D7S821 are linked and there is 0.05cM between them.

So IDP gene may be near 109.12cM of chr.7, the locus of D7S821, and between D7S2204 (90.95cM) and D7s1799 (113.92cM).

5.4. Possibility of Gene Cloning and Application of this Study

To cloning the IDP gene, two kinds of work must be done in advance. ① Collect more pedigrees from the same population to aggrandize the whole recombination density. ② Test more STRP markers between D7S2204 and D7S1799. Then, we might find the marker even tightly linked with IDP gene. If there are rather little genes near it known from the Human Genome Project's database, candidate cloning can be done.

Most detailed known genes are found poly-effective. It's quite possible IDP gene being a poly-effective gene. Dermotoglyphies are shaped by the distribution of nerve capillary under the skin. IDP gene may also controls other organs of nerve system including brain. The study of IDP gene may become a breakthrough point of studies of brain growth, inheritance of intelligence and nerve capillary growth. Nerve capillary deformity is one of the main causes of human fetal death. If some alleles of IDP gene are proved related to nerve capillary deformity, the study of them will greatly effect the development of eugenics and medical sciences. In these points, IDP gene is worth further study.

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