

# The Inheritance of Accessory Triradii on Palmar Interdigital Areas II and IV

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Handprints provide a very useful tool for the geneticist and the physical anthropologist. They are especially valuable in twin diagnosis and as an important criterion in the estimation of degrees of genetic relationship between ethnic groups (Rife, 1958). Ridge counts on finger tips have a heritability of 90% (Newman, 1930), probably the highest heritability recorded for common, non-pathological quantitative variations in man.

MacArthur (1938), in a careful study of the reliability of dermatoglyphics in twin diagnosis, rated the reliabilities of various aspects of hand prints in the following order: (1) ridge counts on finger tips, (2) finger tip patterns, (3) patterns on palms and (4) palmar main lines. While palmar patterns are characterized by relatively high heritabilities, their exact modes of inheritance are unknown. Gene penetrance is incomplete, and expressivity is highly variable, as manifested in bimanual and sexual variations.

Patterns on the radial areas (thenar/first and second interdigital) appear to be more highly heritable than those on the ulnar side of the palm. Weninger, (1935), in a careful study of the thenar/first interdigital area in 290 families concluded that the inheritance is too complex to be explained on the basis of a single pair of genes. Weinand (1937) investigated the inheritance of patterns in interdigital area II in 57 families, and concluded that the presence of a pattern is dominant to its absence, with 97.5% penetrance. Similar results were obtained by Pemberton (1953).

The objective of the investigation recorded herewith was to make a further study of the inheritance of patterns on interdigital area II. Patterns on this area are almost invariably associated with an accessory tri-radius, and are thus free from the complication arising in areas III and IV, where L patterns are common. Patterns in this area occur much more frequently on right than on left palms. The occurrence of a pattern in area II shows a high degree of association with the occurrence of accessory triradii in area IV. The expression of the gene or genes concerned varies from patterns with high ridge counts on both hands to only a vestige on one hand.

The high degree of association between patterns on areas II and IV leads one to suspect that the same genes may be responsible for patterns in both areas. Four simple types inheritance are analyzed and compared in this paper; simple domi-

nance of patterns in area II, simple recessiveness of patterns in area II, a single dominant gene for patterns in either one or both areas II and IV, a single dominant gene for patterns in either one or both areas II and IV, a single recessive gene for patterns in either one or both areas II and IV.

### Source Material

The senior author collected hand prints from 53 families of Panjabi Khatri, of whom one or more members of each family were characterized by at least one accessory triradius or vestige in interdigital area II. She also collected hand prints of 1,000 Panjabi Khatri, unselected for pattern types and obtained quite independently of the family data.

### Analysis of the Data

Table I shows the incidence of individuals within complete families (those from which prints were obtained from both parents and children), possessing one or more patterns or vestiges in interdigital area II, as well as those lacking them. D denotes individuals possessing patterns or vestiges, and d denotes those who lack them. This symbolization will be used throughout the tables.

Table 2 shows the incidence of individuals within complete families possessing one or more patterns or vestiges in either or both areas II and IV.

Table 3 gives the result of an analysis for association between the incidence of patterns in interdigital areas II and IV within individuals. These data were taken from the individuals comprising the 53 families. It can readily be seen that there is a highly significant association between the incidence of patterns on interdigital areas II and IV.

Gene frequency analysis was employed for testing the possible modes of inheritance. These frequencies were obtained from the 1,000 unselected individuals. The following percentages of individuals possess patterns on areas II and IV. (Henceforth in this article the term pattern will include both true patterns and vestiges).

|                                  |       |
|----------------------------------|-------|
| Patterns on interdigital area II | 16.7% |
| Patterns on interdigital area IV | 38.0% |
| Patterns on either or both areas | 44.3% |
| Lack patterns on both areas      | 55.7% |

The expected proportion of recessive phenotypes among children in families where both parents have the dominant phenotype is  $\frac{q^2}{(1+q)^2}$ , where  $q$  = the frequency of the recessive gene. As  $q^2$  = frequency of recessive phenotypes in the general population, the value of  $q$  is easily obtained.

The expected proportion of recessive phenotypes among children in families where one parent is of dominant phenotype, and the other is recessive is  $\frac{q}{1+q}$ .

### **Test for Dominance of D on Area II**

In this case  $q = .912$ . Inspection of Table 4 reveals that although the observed and calculated frequencies agree closely in families where both parents have patterns, there is a highly significant deviation within families in which one parent only possesses patterns.

### **Test for Recessiveness on Area II**

Here  $q = .408$ . Somewhat the reverse situation is revealed in this analysis. There is a highly significant difference between the calculated and observed numbers within families in which both parents lack patterns, whereas there is close agreement within families in which only one parent lacks patterns. But it appears clear that neither simple dominance or recessiveness for patterns on area II are in close accord with the family data.

### **Test for Dominance of Patterns on Areas II and IV**

The obvious correlations between the occurrence of D patterns on areas II and IV strongly suggests the same gene or genes may be responsible for patterns on both areas. Assuming a simple dominant gene to be operative,  $q = .557$ . Inspection of Table 6 shows no significant deviations between observed and calculated frequencies in the family data, although the differences are on the border of significance within families in which only one parent possesses patterns.

### **Test for Recessiveness on Areas II and IV**

In this case  $q = .443$ . Here we observe highly significant deviations within families in which both parents lack patterns, but agreement within families in which only one parent has patterns.

It is obvious that the hypothesis that a simple dominant gene is responsible for D patterns in areas II and IV is the only one of the four proposed which agrees closely with the family data.

An examination of Table 2 reveals that among 35 complete families, there are four in which both parents lack D patterns, although some of the children in each have patterns. Assuming dominance of the gene for D patterns, this gives an estimate of approximately 88% full penetrance.

Table 8 gives the expected numbers of children within families in which only one parent possesses patterns, when adjustment is made for 88% penetrance of the dominant gene. It can readily be seen that the agreement between observed and calculated frequencies is indeed close.

The data thus strongly support the hypothesis that a simple dominant gene with approximately 88% full penetrance, and highly variable in expressivity, is responsible for patterns in interdigital areas II and IV. The expressivity ranges from a vestige on only one of the four areas of an individual, to well developed patterns on all four areas.

### Summary

Data obtained from 53 Panjabi Khatri families were tested for mode of inheritance of patterns on palmar interdigital area II. Gene frequencies were obtained from 1,000 unselected Panjabi Khatri.

Analysis of the data indicate that a single dominant gene, with approximately 88% penetrance, is responsible for D patterns in both the second and fourth interdigital areas of the palm.

### Literature

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**Tab. 1. The incidence of individuals within complete families possessing one or more patterns (including vestiges) on interdigital area II. D signifies persons possessing patterns, d those lacking it**

| Type of Parents |            |            | d × d         |            |            |
|-----------------|------------|------------|---------------|------------|------------|
| D × D           |            |            | Family Number | D Children | d Children |
| Family Number   | D Children | d Children |               |            |            |
|                 |            |            | 1             | 1          | 3          |
| 6               | 3          | 1          | 2             | 0          | 6          |
| 11              | 2          | 3          | 3             | 1          | 3          |
| 34              | 4          | 0          | 7             | 1          | 2          |
| 38              | 4          | 2          | 14            | 1          | 3          |
|                 |            |            | 21            | 1          | 2          |
| Total           | 13         | 6 (31.5%)  | 25            | 1          | 3          |
|                 |            |            | 30            | 1          | 3          |
|                 |            |            | 33            | 3          | 3          |
|                 |            |            | 43            | 3          | 3          |
|                 |            |            | Total         | 13         | 31 (70.5%) |
| D × d           |            |            |               |            |            |
| Family Number   | D Children | d Children |               |            |            |
| 1               | 1          | 2          |               |            |            |
| 2               | 0          | 1          |               |            |            |
| 4               | 1          | 4          |               |            |            |
| 5               | 2          | 3          |               |            |            |
| 10              | 0          | 1          |               |            |            |
| 16              | 3          | 3          |               |            |            |
| 17              | 1          | 1          |               |            |            |
| 18              | 2          | 2          |               |            |            |
| 19              | 1          | 3          |               |            |            |
| 22              | 1          | 2          |               |            |            |
| 23              | 1          | 4          |               |            |            |
| 24              | 0          | 6          |               |            |            |
| 26              | 2          | 1          |               |            |            |
| 29              | 0          | 2          |               |            |            |
| 31              | 0          | 4          |               |            |            |
| 35              | 1          | 1          |               |            |            |
| 39              | 2          | 0          |               |            |            |
| 41              | 2          | 4          |               |            |            |
| 42              | 0          | 4          |               |            |            |
| 49              | 1          | 3          |               |            |            |
| 50              | 0          | 3          |               |            |            |
| 52              | 1          | 5          |               |            |            |
| 53              | 1          | 2          |               |            |            |
| Total           | 23         | 61 (76.4%) |               |            |            |

**Tab. 2. The incidence of individuals within complete families possessing one or more patterns (including vestiges) on interdigital areas II and IV. D signifies individuals possessing patterns, d those lacking it**

| <i>Type of Parents</i> |            |            |               |            |            |
|------------------------|------------|------------|---------------|------------|------------|
| Family Number          | D × D      |            | Family Number | d × d      |            |
|                        | D Children | d Children |               | D Children | d Children |
| 30                     | 2          | 2          | 1             | 1          | 3          |
| 6                      | 4          | 0          | 3             | 1          | 3          |
| 11                     | 2          | 3          | 14            | 5          | 2          |
| 34                     | 4          | 0          | 33            | 4          | 2          |
| 38                     | 4          | 2          |               |            |            |
| Total                  | 16         | 7 (30.4%)  | Total         | 11         | 10 (41%)   |

  

| Family Number | D × d      | d Children |
|---------------|------------|------------|
|               | D Children |            |
| 2             | 4          | 2          |
| 4             | 2          | 3          |
| 5             | 2          | 3          |
| 10            | 0          | 1          |
| 12            | 3          | 1          |
| 13            | 1          | 2          |
| 16            | 4          | 2          |
| 17            | 2          | 0          |
| 18            | 2          | 2          |
| 19            | 1          | 3          |
| 22            | 2          | 1          |
| 23            | 2          | 3          |
| 24            | 0          | 6          |
| 25            | 2          | 2          |
| 26            | 3          | 0          |
| 27            | 1          | 2          |
| 29            | 0          | 2          |
| 35            | 1          | 2          |
| 39            | 2          | 0          |
| 41            | 2          | 4          |
| 42            | 1          | 3          |
| 43            | 4          | 3          |
| 49            | 2          | 2          |
| 50            | 2          | 1          |
| 52            | 2          | 4          |
| 53            | 3          | 0          |
| Total         | 50         | 54 (53%)   |

**Tab. 3. Test for association between patterns (including vestiges) on palmar interdigital areas II and IV**

| Patterns                  | Observed | Calculated |
|---------------------------|----------|------------|
| Present on both II and IV | 102      | 71.2       |
| Present on II only        | 20       | 50.8       |
| Present on IV only        | 86       | 116.8      |
| Absent on both II and IV  | 114      | 83.2       |
| Chi-square = 48.709       | df = 1   |            |

**Tab. 4. Tests for dominance of D on Area II**

| a.   |          |            |
|--|----------|------------|
| Families in which both parents have patterns   |          |            |
| Type of Children                               | Observed | Calculated |
| With patterns                                  | 13       | 14.82      |
| Without patterns                               | 6        | 4.18       |
| Total  | 19       | 19         |
| Chi-square = 1.015                             | df = 1.  |            |
| b.   |          |            |
| Families in which only one parent has patterns |          |            |
| Type of Children                               | Observed | Calculated |
| With patterns                                  | 23       | 44.52      |
| Without patterns                               | 61       | 39.48      |
| Total  | 84       | 84         |
| Chi-square = 20.044                            | df = 1.  |            |

**Tab. 5. Tests for recessiveness of D on area II**

a.

Families in which both parents lack patterns

| Type of Children | Observed | Calculated |
|------------------|----------|------------|
| Without patterns | 31       | 40.48      |
| With patterns    | 13       | 3.52       |
| Total            | 44       | 44         |

Chi-square = 27.751      df = 1

b.

Families in which only one parent lacks patterns

| Type of Children | Observed | Calculated |
|------------------|----------|------------|
| Without patterns | 61       | 60.48      |
| With patterns    | 23       | 23.52      |
| Total            | 84       | 84         |

Chi-square = 0.004      df = 1

**Tab. 6. Tests for dominance of patterns on areas II and IV combined**

a.

Families in which both parents possess patterns

| Type of Children | Observed | Calculated |
|------------------|----------|------------|
| With patterns    | 16       | 18.63      |
| Without patterns | 7        | 4.37       |
| Total            | 23       | 23         |

Chi-square = 1.95      df = 1

b.

Families in which only one parent possesses patterns

| Type of Children | Observed | Calculated |
|------------------|----------|------------|
| With patterns    | 50       | 59.80      |
| Without patterns | 54       | 44.20      |
| Total            | 107      | 104        |

Chi-square = 3.76      df = 1



**Tab. 7. Tests for recessiveness of patterns on areas II and IV combined**

| a.   |          |            |
|--|----------|------------|
| Families in which both parents lack patterns     |          |            |
| Type of Children                                 | Observed | Calculated |
| Without patterns                                 | 9        | 17         |
| With patterns                                    | 11       | 3          |
| Total  | 20       | 20         |
| Chi-square = 25.09      df = 1                   |          |            |
| b.   |          |            |
| Families in which only one parent lacks patterns |          |            |
| Type of Children                                 | Observed | Calculated |
| Without patterns                                 | 54       | 62.4       |
| With patterns                                    | 50       | 41.6       |
| Total  | 104      | 104        |
| Chi-square = 2.82      df = 1                    |          |            |

**Tab. 8. Tests for dominance of II and IV combined in families in which only one parent possesses patterns. Adjustment is made for 88% penetrance in heterozygous offspring**

| Type of Children               | Observed | Calculated |
|--------------------------------|----------|------------|
| With patterns                  | 50       | 49.43      |
| Without patterns               | 54       | 54.57      |
| Total                          | 104      | 104        |
| Chi-square = 0.123      df = 1 |          |            |

#### RIASSUNTO

Sono stati studiati i dati ricavati da 53 famiglie Khattris del Panjab, al fine di esaminare il modo di trasmissione del tracciato della II regione interdigitale palmare. Le frequenze geniche sono state ricavate da 1.000 individui

Khattris del Panjab non selezionati.

L'analisi dei dati indica che un solo gene dominante, con una penetranza di circa 88%, è responsabile del tracciato D sia nella II che nella IV regione interdigitale della palma.

#### RÉSUMÉ

Les empreintes obtenues de 53 familles Khattris du Panjab ont été étudiées au sujet du processus héréditaire du dessin de la palme interdigitale de la surface II. La fréquence du gène a été constatée chez 1.000 Khattris du Panjab non sélectionnés. Les ana-

lyses des empreintes indiquent qu'un gène dominant unique, avec une pénétrance approximative de 88%, est responsable du dessin D de la palme dans la deuxième et quatrième surface de la palme interdigitale.

#### ZUSAMMENFASSUNG

Daten von 53 Panjabi Khattris-Familien wurden untersucht, um den Erbmodus der Handflächenzeichnung am II. Interdigitalraum zu bestimmen. Es wurden die Genfrequenzen von 1.000 auslesefreien Panjabi Khattris gewonnen.

Die Analyse der Daten zeigen, dass ein einzelnes dominantes Gen mit ungefähr 88% Penetranz für die Fingerzeichnungen sowohl am II. als am IV. Interdigitalraum verantwortlich ist.