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Quantitative Genetics of Relative Toe Lengths

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Abstract: In 187 males and 150 females of the Pattusali population of Tirupati, the right foot especially in females showed an increased frequency of the relatively longer second toes in comparison to the first. The female sex and younger generations displayed an increased proportion of feet with longer first toe. Two toes at the cost of that with longer first toe. A quantitative measure of the increased length of toe I over toe II gave a trit-modal distribution, a higher estimate of heritability and better fit with the hypothesis of a pair of additive alleles and better classification. The lower correlation between relatives involving females might suggest sex-influence and inactivation of one X-chromosome in females.

INTRODUCTION

Quantification permits more objective phenotypical classification than apparent categories and may facilitate genetical analysis as in the case of ability to taste phenylthiocarbamide. In this paper a quantitative approach is employed to reexamine the mode of inheritance of relative lengths of first and second toes in man.

Hawkes (1914) has suggested an autosomal inheritance of the trait, but also dominance of longer first toe (type L) in males and dominance of shorter first toe (type S) in females. Further complications are introduced by preponderance of type S in children (Huizinga and Vetten 1967). Kaplan (1963, 1964) has obtained a good fit of phenotype frequencies with that expected in dominance of type S on the assumption of random mating. But such agreements may be purely mathematical.

Regarding frequency distribution, data are available from a few population of Africa (Wells 1931, Pales 1960), Europe (Huizinga and Vetten 1963), Japan (Miani 1952) and north east region of India. The present series represents a small endogamous population of 1152 individuals of Tirupati town of southern Andhra Pradesh.

MATERIALS AND METHODS

337 individuals, 187 males and 150 females, of 69 families have been examined for relative lengths of first and second toes. Of these, data on 141 males and 131 females are analysed for bilateral asymmetry.

From 55 families both parents have been available and only one parent from the rest. The estimated ages of the subjects range from 5 to 65 years, the average being 20.37 years for males and 20.06 years for females.

Metric distances of the tips of first and second toes of each foot from pterion were recorded by placing the foot on the osteometric board with its axis along the length of the board. To obtain a measure of the difference between the first two toes independently of the size of the foot and age variation (Huizinga and Votten 1967), an index has been calculated by using the following formula.

Index of relative length
of toe I over toe II,

$$(IRL) = (T_1 - T_2) / T_2 \times 100$$

where, T_1 = length of toe I from pterion

and T_2 = length of toe II from pterion.

Positive and negative values of the index indicate greater length of toe I and toe II respectively. The zero value of the index could mean absolute equality of toe I and toe II. No allowance for small differences have been given in classifying this middle category to minimise arbitrariness (Das and Mukherjee 1962). It has been assumed that the errors still occurring balance themselves statistically on both sides of the mean values.

The qualitative categories of digital formulae have been derived from the metric data. The three categories of relative toe lengths denoted by digital formulae $1 > 2$, $1 = 2$ and $1 < 2$ (Wood Jones 1945) have been scored as +1, 0 and -1 in order to arrange them in a graded scale.

RESULTS AND DISCUSSION

Variability of the trait: The Pattusali shows the highest frequency of grade 0 or equal lengths of first two toes, and the lowest frequency of grade I or the longer first toe among populations studied so far (table 1). However, scoring of relative toe lengths in other populations without measurements and standard orientation of the axis of the foot, may not be strictly comparable with the present data.

TABLE 1
Comparison of available data from different populations of the world

Contingent	Population	Number of individuals tested	Right foot			Author
			-1	0	+1	
INDIA	<i>Caste Populations:</i>					
	(a) Brahman	225	8.25	5.75	86.00	Das (1969)
	(b) Kalita	475	4.85	4.35	90.80	"
	(c) Vaishya	161	8.85	6.25	84.90	"
	(d) Kaibarta	205	8.20	4.65	87.15	"
Assam	(e) Pattusali	337	13.05	29.97	59.98	Present study
	<i>Tribal Populations:</i>					
	(a) Khasi	118	17.60	0.30	82.10	Das & Uzir (1961)
	(b) Mikir	220	11.00	7.35	81.65	Das & Das (1968)
	(c) Rabha	600	17.40	11.40	71.20	Das & Uzir (1959)
Orissa	(d) Juang	43	3.49	4.65	91.86	Sarkar (1958)
	(e) Oraon	44	5.68	1.14	93.18	"
	(f) Pahira	29	12.07	8.62	79.31	"
	(g) Dogon	338	6.21	?	?	Huizinga et al. (1959)
	(h) N. W. Africa	?	11.20	?	?	Pakes et al. (1960)
AFRICA	(i) Malagassy	?	7.40	?	?	"
	(j) London	2,300	6.10	8.40	83.10	Lake (cited by W. Jones)
	(k) England	over 1,000	7.99	5.00	85.50	Hawkes (1914)
	(l) Germany	50	30.30	4.75	64.95	Wissenberg (cited by Wood Jones)
	(m) Dutch (foetuses)		54.00	?	?	Huizinga et al. (1967)

As the frequency distribution obviously deviates from normality, the variability of the index must be influenced by a few major factors such as a small number of genes. Therefore, the simple hypothesis of a single autosomal pair of alleles has been tested on the basis of frequency distributions of qualitative grades and quantitative classes.

Inheritance: Several alternative hypotheses of dominant inheritance of particular grades or combination of two grades have been tested for agreement between observed and expected phenotype frequencies (table 4). Good agreement of the frequencies with both dominance and recessiveness of a particular phenotype cancels each other and suggests additive effects of a pair of genes. But if additive inheritance is assumed, the observed frequencies of grades differ significantly from expected genotype frequencies estimated indirectly on the assumption of random mating or by direct

TABLE 4

Test for dominant/recessive inheritance of grades of toe I length

Grades	+1	0	-1	
	$\bar{G}$		$\bar{L}$	χ^2 2 d.f.
Phenotype frequencies				
Observed ($G = +1; L = 0 \text{ \& } -1$)	57	43		
Expected	4	43.5		
dominant $\bar{L}$ (1)	56.5			0.010
dominant $\bar{G}$ (2)	57.0	43.0		0.000
Observed ($L = -1; G = +1 \text{ \& } 0$)	.87	13		
Expected	86.9	13.1		0.001
dominant $\bar{L}$ (3)	87.0	13.0		0.000
dominant $\bar{G}$ (4)				
Gene frequencies	pG	qL		
Case 1	0.755	0.245		
2	0.341	0.659		
3	0.932	0.168		
4	0.360	0.640		

Phenotypes involving 0 & -1 are shown in between the columns of 0 and -1. Phenotypes involving +1 & 0 are shown between columns +1 and 0.

counting (table 5). The segregational analysis of the grades (table 6) does not also fit with an assumption of two 'dominant/recessive alleles'.

TABLE 5

Test for additive inheritance of grades of toe I length

Grades	+1	0	-1
Genotypes	GG	GL	LL
Frequencies Observed	57	30	13
Expected			
case 1	56.50	36.98	6.52
case 2	40.96	46.08	12.96
case 3	51.84	40.32	7.84
Gene frequencies	Method	pG	qL
case 1	$p^2 = 0.570$	0.755	0.245
case 2	$q^2 = 0.130$	0.640	0.360
case 3	Counting	0.720	0.280
chi-square	Case 1	case 2	case 3
at 2 d.f.	7.761	11.890	6.560

TABLE 6

Segregational analysis of three grades of relative lengths of toe I

Mating Fa $\times$ Mo	Families <i>n</i>	Son			Daughter			offspring		
		-1	0	+1	-1	0	+1	-1	0	+1
+1 $\times$ +1	17	1	2	25	2	7	24	3	9	49
+1 $\times$ 0	9	1	5	10	2	4	6	3	9	16
0 $\times$ +1	8	1	4	10	1	4	3	2	8	13
0 $\times$ 5	5	0	4	0	1	5	0	1	9	0
0 $\times$ -1	1	1	0	0	0	0	0	1	0	0
-1 $\times$ 0	5	2	8	4	1	7	1	3	15	5
-1 $\times$ -1	2	3	1	1	1	1	0	4	2	1
+1 $\times$ -1	5	4	1	9	0	0	5	4	1	14
-1 $\times$ +1	3	1	1	2	0	1	2	1	2	4
Total	55	14	26	61	8	29	41	22	55	102

On the other hand, estimation of gene frequencies either on the assumption of genetic equilibrium or by direct gene counting from the three segments of the trimodal frequency distribution of the index (IRL) leads to a close agreement with the two allele hypothesis of additive inheritance of the trait (table 7). The genotypes are provisionally identified as (A) below 0.5, (B) 0.5 to 4.5 and (C) above 4.5 values of IRL (fig. 1).

Sexual and bilateral difference: In the sample of each sex there are greater frequencies of grades 0 and -1 in the right foot than that in the left (table 2). As the relative length of toe II over toe I increases the probability of occurrence of grades lower than +1 in the right foot also increases, and in the left foot there is a greater bias for relatively longer toe I. The χ^2 value for right-left difference is significant at $p = 0.05$ only in females. But frequency of a symmetrical combinations are not negligible. Therefore, the right foot has been selected for the present analysis due to greater incidence of the rarer grades in that foot, adding further data from 46 male and 19 female individuals (table 3). The sex difference is not significant.

TABLE 2

Combinations of grades of relative toe I length in right (R) and left (L) feet in each sex

L/R	Male			Female		
	-1	0	+1	-1	0	+1
+1	4	10	78	0	19	66
0	4	29	5	6	32	2
-1	8	2	1	4	1	1
	<i>n</i>			<i>n</i>		
	115			102		
	%			%		
	81.6			77.9		
Symmetry						
Asymmetry (relatively longer toe II)	R	18	12.8	25	19.1	
	L	8	5.7	4	3.0	

χ^2 (2 d.f.) for side difference = 4.94; $0.10 < p < 0.05$

Age difference: There is a consistent increase of grade 0 in the younger generation accompanied with small decrease of extreme grades (1 and -1), specially in females (table 3). Age difference is insignificant and does not show an increased incidence of grade 1 as in earlier samples (Huizinga and Vetten 1967). The average values of the IRL which is corrected for foot-growth also do not display any systematic change in different age groups in either sex to need correction for age or sex.

Distribution of IRL: The frequency distribution of the index shows a trimodal curve, especially in males (figure 1). The mode at lower end of the distribution has a higher frequency in the female sample. The higher peaks increase in the male. This is consistent with sexual varia-

TABLE 3
Frequency distribution of the three grades of relative lengths of toe I over toe II in the right of two generations in each sex

Grades	Total	n			%		
		-1	0	+1	-1	0	+1
MALES:							
Generation I	59	10	14	35	17.2	23.9	59.9
Generation II	128	16	35	77	12.5	27.5	60.0
Total	187	26	49	80	13.9	26.2	59.9
FEMALES:							
Generation I	65	9	20	36	13.7	30.8	55.5
Generation II	85	9	32	44	10.6	37.7	51.7
Total	150	18	52	80	12.0	34.6	53.3

χ^2 (2 d.f.) for sex difference = 2.93; $0.30 > p > 0.20$

tion in qualitative grades of relative toe lengths. The position of the first antinode at 0.5 indicates that grades -1 and 0 can be combined together as one phenotype. Half of the frequencies at each antinode has been included in the lower range and half in the higher range for further analysis. The male antinode at 4.5 has been provisionally used for classification because of more adequate data in the higher range in males.

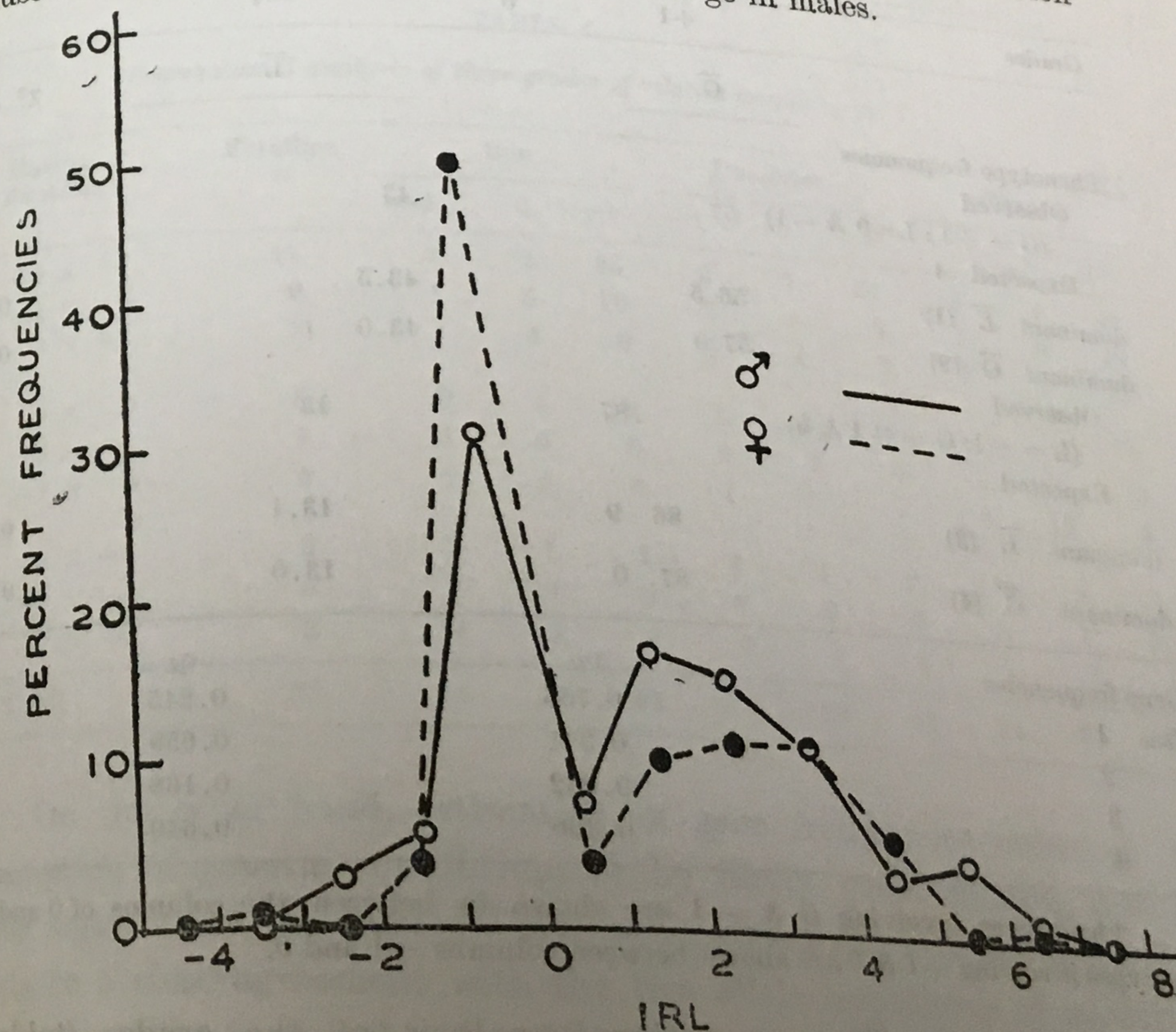


Fig. 1. Frequency distribution of Index of relative length (IRL) among males and females Pattusali.

TABLE 7

Test for additive inheritance of IRL

Genotype frequencies	LL (below 0.5)	LG (0.5-4.5)	GG (above 4.5)
Observed	0.486	0.498	0.016
Expected (1)	0.486	0.422	0.092
(2)	0.541	0.390	0.070
Chi square with 2 d.f. = 0.079 for (1) & (2) each; $0.98 < p < 0.95$			
Gene frequencies	PL		
estimate (1)	p = 0.486		
(2)	by counting		
		qg	
		0.697	0.303
		0.735	0.265

A biometrical genetical analysis is attempted on both qualitative grades and quantitative phenotypic classes A, B, C to find out the relative degrees of hereditary influence on either system of phenotypes. The difference of mean values of IRL between parents and children are not statistically significant except in the case of fathers and sons (table 8). Variability of the values are always greater in parents than in children.

TABLE 8

Mean (M) with standard error (SE), standard deviation (S.D.) and variance of IRL among parents (P) and offspring (O)

	n	M ± S.E.	S.D.	V	t
Fathers (F)	99	1.02 ± 0.73	2.69	7.28	2.59
Sons (Z)	99	0.37 ± 0.30	1.74	3.04	
Fathers (F)	57	0.76 ± 0.87	2.56	6.54	0.73
Daughters (D)	57	0.98 ± 0.39	1.71	2.94	
Mothers (M)	107	0.71 ± 0.49	2.26	5.10	0.70
Sons (Z)	107	0.58 ± 0.35	1.91	3.65	
Mothers (M)	58	0.80 ± 0.69	2.29	5.25	0.81
Daughters (D)	58	1.02 ± 0.47	1.89	3.60	

This agrees more with additive rather than dominant inheritance of the quantitative variation. Coefficients of correlation between various combinations of parents and children for both gradational and quantitative variations are compared in table 9. The heritability estimates obtained are 0.78 and 0.56 respectively for quantitative and qualitative classes, on the basis of parent: offspring correlations.

TABLE 9

Coefficients of correlation between pairs of relatives for quantitative and qualitative measures of relative toe lengths

Pairs of relatives	n	Quantitative IRL r ± S.E.	n	Qualitative grades r ± S.E.
P : O	321	0.39 ± 0.03	392	0.28 ± 0.05
Sib pair	156	0.55 ± 0.06	474	0.26 ± 0.05
F : O	165	0.23 ± 0.02	198	0.36 ± 0.06
M : O	99	0.58 ± 0.07	204	0.21 ± 0.04
F : Z	57	0.50 ± 0.10	108	0.36 ± 0.06
F : D	107	0.23 ± 0.09	80	0.36 ± 0.10
M : Z	58	0.22 ± 0.12	121	0.24 ± 0.07
M : D	—	—	83	0.16 ± 0.08
B : B	—	—	225	0.40 ± 0.06
S : S	—	—	110	0.21 ± 0.09
B : S	—	—	139	0.17 ± 0.08

However, father: offspring correlation is higher than mother: offspring for both types of variation. Brother: sister and sister: sister correlations are also low. This is difficult to explain if the possibility of misrepresentation of females in the pedigrees is excluded or Lyon hypothesis of inactivation of one X-chromosome in females is not assumed. Lower correlation between opposite sexes, may suggest sex influence.

The values of parent: offspring or sibpair correlations for qualitative grades are significantly different from the theoretical value of 0.5 for additive genes, but not so from the expected value of 0.33 for dominant/recessive inheritance. But dominant/recessive inheritance would require higher values of sibpair correlation than parent: offspring correlation which is not the case. The parent: offspring correlation for quantitative measurement of the trait is significantly higher than that expected for dominant/recessive inheritance and it approaches the theoretical value for additive inheritance. The father: offspring correlation alone agrees perfectly with the expected value for completely additive inheritance.

Thus, the results of the present analysis based on objective classification of relative lengths of toes I and II, suggest that the variation is inherited by additive autosomal genes which may be subject to sex influence. Inactivation of one X-chromosome in females may reduce the resemblance between female relatives. Three grades of longer, equal and shorter first toe display a smaller degree of heritability and less clear pattern of inheritance.

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Variation in the Termination of Polymorphous C Line in Palmar Dermatoglyphs of the Khyntiam of Shillong

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Abstract: The present paper manifests the C line termination situation in palmar dermatoglyphs of Khyntiam. The result showed that among the four modal types, Ulnar type occurs in 62.3%, Radial types in 23.4%. Proximal and Absent types in 8.0% and 6.3% respectively. There is no significant sexual difference. Bimanual difference is higher in males than in females. A comparison with other populations shows that the Khyntiam along with all other mongoloids cluster with high frequency of Ulnar (I) type.

INTRODUCTION

Dermatoglyphic studies created a keen interest in the field of Physical Anthropology for its marked contributions in population variation studies. C line termination polymorphism has been proved to be a potential tool for studying population discrimination. Rife in his recent reports on the Seminole Indians (Rife 1968) and the Puerto Ricans (Rife 1969) stressed the importance of C line termination in terms of pattern for variation in the III and IV inter-digital areas, and also to the measure of transversality. He also emphasized on the geographic and bimodal variation of the C line termination. Later on, Plato (1970) pointed out its significance. According to him C line is the only main line which is truly polymorphic in nature, as it demonstrates qualitative as well as quantitative variation in terms of transversality and termination, because it may have any direction as ulnar, radial or proximal or it may be completely absent. In India Bansal and Bhattacharya (1972), Bhanu (1971), Bhanu and Malhotra (1972), Tyagi and Maselkar (1972) have reported the palmar C line sequence among several populations.

In accordance with the above stated polymorphism the modal types of C line, these are: (1) U