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Determinants of Ridge Counts in MZ Twin Kinships

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The inheritance of total ridge count (TRC) was studied in 967 individuals from the families of 111 pairs of MZ twins. The sample included data on 47 male half-sibships with 227 offspring and 64 female half-sibships with 306 offspring. The males in this sample had a mean ridge count of 135 ± 2 and the females a mean ridge count of 124 ± 2. The distribution of scores for females showed evidence for significant skewness. For this reason, prior to the analysis, the data were corrected for sex and adjusted to normality using a power transformation. Nested analyses of variance were performed on the ridge counts from male and female half-sibships separately to derive estimates of among, between, and within-variance components. These estimates were then used in a nonlinear least squares program to estimate genetic and environmental parameters and to determine the goodness of fit of various models. A model which included additive genetic and dominance effects could not be rejected (P = 0.67) but did not fit the data as well as a simple additive genetic-random environmental model (P = 0.81). The addition of maternal effects to the latter model also provided a satisfactory fit (P = 0.68). However, there was no improvement in the goodness of fit over the simple model, and the estimated magnitude of the maternal effect was not significantly different from zero.

Key words: Total ridge count, MZ twin kinships, Additive genetic effects

INTRODUCTION

Finger ridge count has long been considered a classic example of a quantitative trait of high heritability in man. Although the finger print patterns of monozygotic (MZ) twins need not be identical, the total ridge counts (TRCs) of such twins are remarkably similar [4]. In general, MZ twins are more similar in their total ridge count than are dizygotic (DZ) twins, and close relatives have a higher degree of similarity in dermatoglyphic patterns than do unrelated individuals, suggesting a strong genetic influence on ridge count.

Various methods have been used to estimate the sources of observed variation in quantitative traits in man. The present study utilizes MZ twin kinships to assess the genetic and environmental influences on total ridge count. This research design allows for the compari-

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son of individuals who have all, one-half, one-fourth, and none of their genes in common, thus permitting the separation of many important genetic and environmental components of variation, as well as the detection of maternal effects [9]. Estimates of the additive, dominance, additive epistatic, maternal, and environmental effects can be obtained from a nested analysis of the offspring data by a weighted least-squares procedure.

MATERIALS AND METHODS

The study population consisted of 967 members of 111 MZ twin kinships, including 47 male half-sibships with 227 offspring and 64 female half-sibships with 306 offspring. Zygosity of the twins was confirmed by typing twin pairs for nine polymorphic blood group systems.

Rolled finger prints were obtained from each individual using printer's ink. Fingertip counts were taken as the number of ridges that touched a straight line drawn from the center of the pattern to the triradius. Total ridge count was calculated as the sum of the scores over the ten fingers of an individual.

Prior to data analysis, the distribution of total ridge counts for the study population was tested for any departures from normality. Mean total ridge counts were obtained separately for the males and females in the population. Data were corrected for sex and adjusted to normality using a power transformation [1].

Nested analyses of variance were performed separately on the ridge counts derived from the children of male and female twins to obtain estimates of variation among half-sibships, between full-sibships nested within half-sibships, and within full-sibships. These estimates were then set equal to their expected values under several different models, and estimates were obtained for genetic, maternal, and environmental parameters using a weighted least-squares procedure. Since previous experience has indicated that the inclusion of constraints to adjust for the correlation between correlations does not appreciably alter parameter estimates [3], they were not included in the least-squares procedure. Alternate models were evaluated by a comparison of the χ^2 goodness-of-fit, the standard error of parameter estimates, and their biologic plausibility.

RESULTS

The distribution of total ridge count scores for males and females is given in the Figure. Because the mean total ridge count for females (125 ± 2) was significantly less than that for males (135 ± 2), the raw values were corrected to remove the effect of sex. There was no evidence of any significant departure from normality for the distribution of TRC scores for males; however, the distribution of scores for females was significantly skewed. The scores for females were therefore adjusted to normality using a power transformation prior to the analysis.

The results of the nested analyses of variance of the offspring data are shown in Table 1. As can be seen from the table, there appear to be no differences in the partitioning of variation among and within half-sibships, differences that would be dependent on the sex of the twin pair. Although estimates of among, between, within, and total variances for male twin kinships were slightly greater than those estimated for female twin kinships, these differences were not significant.

Maternal effects can be examined by contrasting the analyses of variance for male and female twin kinships. To the extent that maternal effects influence a trait, the offspring of female MZ twins would be expected to be more similar than the offspring of male twins. Thus, if a maternal effect is present, the among half-sibship component of variance will be inflated in the analyses of female MZ kinships, and since the children of male twins are born to genetically unrelated mothers, the between full-sibship/within half-sibship component of variance will be increased in the analyses of male MZ twin kinships. Comparison of the manner in which the variation is partitioned among and between the male and female kinships revealed no significant evidence for the influence of maternal effects on TRC in this sample.

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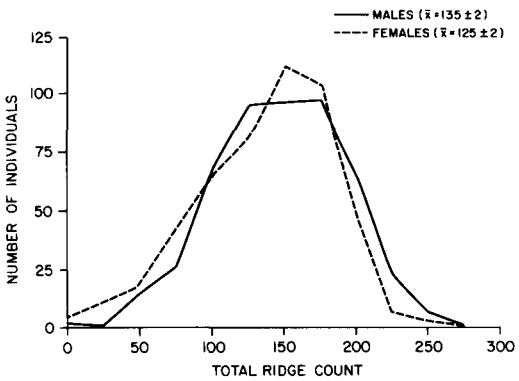

Figure. Distribution of total ridge count by sex.

TABLE 1. Results of Nested Analyses of Variance

Source of variation	df	Mean square	Variance component
Among ♂ half-sibships	46	88077.1	9896.1
Between full-sibships/within ♂ half-sibships	47	38061.7	7361.1
Within full-sibships	311	19803.8	19803.8
Between full-sibships/within ♀ half-sibships	64	33248.3	6562.9
Among ♀ half-sibships	63	77480.0	8874.5

The correlations between members of male and female twin pairs, as well as the intraclass correlation coefficients for half-sibships and full-sibships, are shown in Table 2. The observed pattern of correlations strongly suggests a major genetic effect. The close agreement between the correlations of male and female twins also suggests that sex does not have an influence on the degree of similarity between pair members for this trait. The magnitude of the correlations for full-sibs and half-sibs agree quite well with their expectations under a simple genetic model, since full-sibs share approximately one-half of their genes and half-sibs share about one-quarter of their genes.

As shown in Table 3, the correlations between first-born half-siblings combined over male and female kinships did not differ appreciably from the observed half-sib correlation for either male or female kinships. This finding is contrary to what would have been expected if parity were a factor important in the determination of total ridge count.

Mean-squares from the analyses of variance among, between, and within half-sib kinships were used to obtain estimates of genetic, maternal, and environmental components through an iterated weighted least-squares procedure. Models including additive (V_A), dominance (V_D), additive epistatic (V_{AA}), maternal (V_M), and three environmental (V_{EH}, V_{ES}, V_{EW}) effects were fit to the observed mean squares as part of the model-fitting procedure.

Preliminary analysis revealed no significant contribution of dominance effects to the genetic variance, nor were the environmental components that take into account the differences among half-sibships (V_{EH}) and between full-sibships/within half-sibships (V_{ES})

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TABLE 2. Comparison of Observed Correlations (R) for TRC in MZ Twin Kinships

	Male twins		Female twins		Pooled	
Relationship	N	R	N	R	N	R
Twin-twin	47	0.95*	64	0.95*	111	0.95*
Full-sibs	94	0.44*	128	0.44*	222	0.45*
Half-sibs	47	0.25	64	0.27*	111	0.26*

*Significant at the 0.01 level.

TABLE 3. Correlations (R) for Half-Siblings and First-Born Half-Sibs Partitioned Within and Over Sexes

	Male twins		Female twins		Pooled	
Relationship	N	R	N	R	N	R
Half-sibs	47	0.25	64	0.27*	111	0.26*
First-born half sibs	47	0.24	64	0.20	111	0.22*

*Significant at the 0.01 level.

found to be significant. The results of fitting several alternative models that include additive, epistatic, maternal, and random environmental effects are shown in Table 4.

The simple additive model (I) gave a satisfactory fit, which was further improved when additive epistatic effects were included in the model (II). The addition of random environmental effects to the model (VI) also provided a good fit, although the standard error of V_{AA} was large when it was estimated simultaneously with V_A and V_{EW}. The simple additive genetic-random environmental model (III) provided the best fit and was considered to give a reasonable explanation for the data. When maternal effects were included in the solution (IV, V, VII), a reduced fit was obtained, and because it could not be shown that V_M was significantly different from zero, the inclusion of a maternal component could not be justified.

These results support previous findings of a large additive genetic influence on total ridge count and suggest that about 89% of the total variation in this trait can be attributed to genetic factors.

DISCUSSION

The sex difference in mean total ridge count found in this analysis is in agreement with the results of studies conducted by several other investigators [4, 12, 15]. The nature of these differences has been explained in various ways. Finger ridges in the female are generally finer than those in the male, a trend correlated with the tendency to smaller hand size in females [2]. Ohler and Cummins [11] found a significant difference in the mean number of ridges per centimeter in young adult males (20.7) compared to young adult females (23.4), a further reflection of the narrower ridge size in females than in males.

Dermatoglyphic differences between the sexes have also been attributed to a higher frequency of pattern types that yield low ridge counts in females than in males. Holt [6] has shown that females tend to have a higher frequency of arches, fewer radial loops, and

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TABLE 4. Genetic Analysis of Total Ridge Count

	Alternative models						
Parameters	I	II	III	IV	V	VI	VII
V_A	3.74 ± 0.16	2.91 ± 0.55	3.17 ± 0.35	2.83 ± 1.04	2.94 ± 0.66	4.13 ± 1.23	3.93 ± 1.39
V_{AA}	...	0.66 ± 0.44	...	0.71 ± 0.31	...	1.89 ± 2.24	1.92 ± 2.24
V_M	...	...	...	0.03 ± 0.31	0.12 ± 0.30	...	0.11 ± 0.27
V_{EW}	...	...	0.30 ± 0.23	...	0.50 ± 0.37	1.34 ± 1.13	1.46 ± 0.11
χ^2	2.05	1.0	0.73	0.99	0.66	0.39	0.31
df	4	3	3	2	2	2	1
p	0.73	0.80	0.87	0.61	0.72	0.82	0.58
h^2	1.0	1.0	0.89	0.99	0.83	0.82	0.79

fewer whorls on their fingertips than do males. Since arches are scored as a zero ridge count, this greater occurrence of arches in females further contributes to their lower ridge counts.

Further evidence for an inherent sex difference is given by the distortion of dermal ridge arrangements associated with certain sex chromosome aberrations, particularly Turner syndrome and Klinefelter syndrome. Females with Turner syndrome generally have fewer arches and fewer radial loops on their fingers than normal females. This deficiency of arches and radial loops is compensated for by an increased frequency of large whorls and ulnar loops [7], patterns that tend to give Turner females higher total ridge counts.

Although males with Klinefelter syndrome tend to be of tall stature with long hands and feet, there is a slight tendency for their fingertip patterns to be smaller, with lower ridge counts than normal males [6]. Studies of seven cases of males with an XXYY chromosome complement revealed small fingertip patterns, with 20% being arches [16]. Thus, the general trend in sex chromosome anomalies seems to be toward a reduced ridge count in individuals who bear extra X chromosomes and higher ridge count in those who have only one X chromosome [12].

Comparison of the mean total ridge counts for males and females in the half-sib families to mean ridge count values in the general population revealed no significant deviation from the population norms. Thus, factors that predispose to twinning do not appear to exert an obvious effect on the formation of fingertip ridge patterns. That the offspring of identical twins fall into the normal range of TRC values further suggests that the presence of a twin parent does not alter the ridge counts of the offspring.

Because finger ridge patterns are established prenatally, one might expect to find evidence for significant maternal effects on total ridge count. A possible explanation for the failure to detect maternal effects might be in the strong genetic control of ridge count, such that the effects of prenatal influences are largely overridden.

The finding of a significant correlation in total ridge counts between members of MZ twin pairs suggests a major genetic component in the determination of ridge patterns. In the past, the strong link between genetic factors and the determination of dermatoglyphic patterns has been illustrated by the occurrence of particular types of dermal ridge configurations in association with certain genetic syndromes. Holt [5] found that the characteristic ridge pattern in trisomy 21 is a high, L-shaped ulnar loop and that there are fewer whorls and arches. There appears to be less variation in fingerprint patterns of individuals who are trisomic for chromosome 21 than in the general population, and in contrast to normal populations, there seems to be no discernible sex difference in the frequency of pattern types in individuals with trisomy 21. A second chromosomal disorder with characteristic dermatoglyphic features is trisomy 18. The high frequency of arches is so striking in this syndrome that fewer than six arches or more than two whorls would argue against a diagnosis of trisomy E [13]. Unusual dermatoglyphic configurations have also been associated with syndromes resulting from single gene defects. The occurrence of eight or more whorls is unusual in a normal individual but is found in over one-third of patients with Smith-Lemli-Opitz syndrome [13].

Previous investigators [8] have indicated a parental age effect on the heritability of total ridge count in man. In the present analysis, comparison of the correlations between first-born half-sibs with the intraclass correlations for male and female kinships revealed no significant differences. However, the tendency for correlations between first-born half-sibs to be somewhat lower than the half-sib correlations is consistent with a change in the

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heritability of TRC with parental age. The trend appears to be more striking in the female half-sibships than in the male half-sibships, suggesting that the reputed change in heritability may reflect a change in maternal effects with age and/or parity of the mother.

The present analysis is in agreement with earlier findings that the genetic factors influencing total ridge count are largely additive [14]. In regard to the various environmental components under consideration, models that include V_{EH} or V_{ES} generally gave a poor fit. This is not surprising since it is unlikely that among half-sibship and between full-sibship/within half-sibship environmental components would contribute to a trait that is determined during the first trimester of pregnancy. However, the within-sibship environmental component (V_{EW}) proved to have an important influence on TRC.

While early studies suggested no significant dominance effect on total ridge count [4, 14], later studies have suggested a small but significant dominance contribution to account for the residual nonadditive variation [15]. In the present analysis, the addition of a dominance component did not improve the fit over the simple additive genetic-random environmental model. Past studies have also suggested an additive epistatic effect on the total ridge count [10]. In the present investigation, although a positive estimate for V_{AA} was obtained, the standard error of the estimate was large, especially when random environmental effects were included in the model (Table 4, VI). Although the inclusion of additive epistatic effects results in a biologically plausible model for a trait with such a high degree of additive genetic determination, the present analysis suggests that a larger sample size will be required to distinguish unambiguously between the simple and more complex genetic model.

CONCLUSION

The analysis of total finger ridge count in 111 monozygotic twin kinships supports previous observations that this trait has major genetic determinants and that the genetic effect is largely additive. The best-fitting model was one that included additive genetic and random environmental effects, with no evidence for significant maternal influence. The results of this analysis suggest that as much as 89% of the total variation in total ridge count may be attributable to genetic factors.

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