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Short Note

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Quantitative Twin Analysis of Radial and Ulnar Ridge Counts and Ridge Count Diversity

Terry Reed, Joe C. Christian

Department of Medical Genetics, Indiana University School of Medicine, Indianapolis

Analysis of variance was performed on the radial and ulnar finger ridge counts and ridge count diversity index in 360 twin sets from which estimates of genetic variance were obtained. Findings for radial and ulnar counts paralleled those previously obtained for finger pattern type and ridge count (larger of radial and ulnar count). In contrast, ridge count diversity showed no indication of unequal total variances, as previously found for the total ridge count. One must be cautious not to exclude genetic influences on traits, such as the thumb variables in this study, where there are unequal total variances between monozygotic and dizygotic twins and the more conservative estimate of genetic variance is not significant.

Key words: Dermatoglyphics, Twin study, Analysis of variance, Ridge count

INTRODUCTION

We previously reported on the twin analysis of 71 dermatoglyphic variables [5]. Included in that analysis on the fingertips were variables for pattern type, ridge count, and the total ridge count (TRC). Subsequently, we and others [4, 7, 10] have obtained evidence that radial and ulnar ridge counts of the fingers load on different factors extracted from multivariate analyses. These findings also indicated that, particularly on the thumbs, prenatal environmental influences may have unequal effects on radial and ulnar ridge counts [8, 9]. We therefore now report on the twin analysis of the radial and ulnar counts of the fingers. Ridge count diversity is also analyzed for comparison with the TRC data previously reported.

MATERIALS AND METHODS

The twin pairs studied were presented in detail previously [5]. In the present instance, all subjects needed complete print data for calculation of the diversity index and, therefore, only those sets without missing data (224 monozygotic, or MZ, and 136 like-sexed dizygotic, or DZ, twin pairs) were

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further analyzed. The reader is referred to Schaumann and Alter [11] for a succinct description of ridge counting rules. The diversity index was calculated after Holt [3:p 67 ff] where only the larger of the radial or ulnar count is used and equals $S/\sqrt{10}$ where S^2 is the sum of squares of the ten finger ridge counts minus the square of the TRC divided by 10.

One-way analysis of variance was performed for each variable on the MZ and DZ sets separately and the resulting among- and within-pair mean squares were utilized to obtain and test the estimates of genetic variance. The means of the MZ and DZ twins for each variable were compared by the t' test of Christian and Norton [2]. None of the 21 variables were found to display significant ($P < 0.05$) differences between MZ and DZ twin means.

RESULTS AND COMMENTS

The table displays the results of the analysis of variance and the application of the twin model [1]. The left half of the table presents the among- and within-pair mean squares for both twin groups. The right half displays the probability that the total variances of the MZ and DZ twins are equal, followed by the within-pair and among-pair component estimates of genetic variance and their significance.

The within-pair estimate is tested by the F ratio of the within-DZ mean square to the within-MZ mean square. This ratio would, however, be expected to be biased upward if the environmental variance of DZ twins is greater than that of MZ twins [1]. The generally more conservative among-pair component estimate is designed to be unbiased by unequal environmental variances and should be used when the probability of equal total variances is less than 0.20 [1].

As seen in the table the within-pair estimate of genetic variance is highly significant ($P < 0.01$) for all 21 variables, but employing the criteria of Christian et al [1], 7 variables show evidence of unequal total variances indicating that the among-pair component estimate should be used. Of these 7, 4 (left and right, radial and ulnar counts of the thumb) have nonsignificant among-pair component estimates of genetic variance.

The findings in the thumb parallel those seen previously for ridge count (larger of radial or ulnar count) and pattern type variables on this digit L where there were larger total variances in DZ twins and subsequent nonsignificant estimates of genetic variance [5]. Factor analysis has shown that the radial and ridge counts of the thumb load on the same factor and likewise ulnar counts and pattern type have similar loadings, so the present results were expected. However, the thumb variables were previously found to be among the best discriminators of MZ from DZ twins [6], and useful in discriminating dichorionic and monochorionic MZ twins [8]. Study of family members of MZ twins and their offspring, which are the equivalent of half-siblings, have indicated that there are both genetic and environmental influences in determining dermatoglyphic variables of the thumb [9]. Therefore one must be cautious, when there is a significantly larger total variance of DZ twins compared to MZ twins and a nonsignificant among-pair component estimate of genetic variance, to not completely eliminate the possibility of genetic influences on such a trait.

In a previous analysis [5] DZ twins had a significantly larger total variance than MZ twins for TRC, although the estimate of genetic variance was significant at $P < 0.05$. In the present study, the ridge count diversity index did not show a similar trend and yielded highly significant ($P < 0.01$) estimates of genetic variance. Since Holt [3] found the diversity index to be less heritable than the TRC, the findings may be in part reflective of the difference in variances of MZ twins of known placental type found for the TRC but not for the diversity index [8].

TABLE. Analysis of Variance, Test of the Equality of Total Variance, and Estimates of Genetic Variance

Variable	MZ pairs (n=224)		DZ pairs (n=136)		$(\sigma^2 MZ = \sigma^2 DZ)^a$	Estimates of genetic variance	
	AMS	WMS	AMS	WMS	P-value	With-in-pair[b]	Among-component[c]
Finger ridge counts, Radial							
L thumb	49.03	5.61	64.41	19.26	0.00[d]	13.66**	−0.86
R thumb	49.59	6.10	64.23	21.07	0.00[d]	14.97**	0.16
L index	63.32	11.51	53.00	28.31	0.88	16.80**	13.56**
R index	72.80	12.07	42.86	32.63	0.33	20.56**	25.25**
L middle	63.78	8.26	55.04	21.68	0.61	13.42**	11.08*
R middle	53.02	6.15	46.41	17.51	0.54	11.37**	8.99*
L ring	57.92	5.37	51.27	24.23	0.16[d]	18.86**	12.76**
R ring	66.79	7.62	51.77	21.86	0.94	14.23**	14.63**
L little	42.89	4.82	33.93	13.91	0.98	9.09**	9.02**
R little	46.78	6.50	35.40	15.79	0.75	9.29**	10.33**
Finger ridge counts, Ulnar							
L thumb	63.12	14.03	71.52	34.30	0.01[d]	20.27**	5.93
R thumb	75.08	14.43	77.25	33.74	0.08[d]	19.30**	8.56
L index	82.84	16.45	78.67	42.11	0.10[d]	25.66**	14.91*
R index	96.15	13.60	78.76	38.90	0.57	25.30**	21.34**
L middle	54.37	8.23	43.31	27.18	0.33	18.95**	15.01**
R middle	60.20	8.85	41.98	19.46	0.35	10.61**	14.41**
L ring	71.79	9.23	46.59	34.12	0.98	24.88**	25.04**
R ring	85.38	10.31	46.68	30.17	0.07[d]	19.86**	29.28**
L little	16.95	3.45	13.18	9.49	0.37	6.04**	4.91**
R little	22.64	3.36	12.89	10.10	0.31	6.73**	8.24**
Ridge count diversity	4.11	0.56	2.97	1.61	0.88	1.06**	1.10**

AMS = among-pair mean squares; WMS = within-pair mean squares. R = right; L = left.

*$P < 0.05$; **$P < 0.01$.

[a] $\sigma^2_{MZ} = AMS_{mz} + WMS_{mz}$; $\sigma^2_{DZ} = AMS_{dz} + WMS_{mz}$.

[b] $WMS_{dz} - WMS_{mz}$.

[c] $[(WMS_{dz} - WMS_{mz}) + (AMS_{mz} - AMS_{dz})]/2$.

[d] Among-component estimate should be used if the probability of equal total variances is less than 0.20.

These analyses reinforce the conclusions that multiple factors affect dermal ridge development and that twins are a sensitive tool for resolving sources of developmental variation. Total ridge count, the classic example of an additive genetic trait, upon closer inspection is the sum of multiple variables influenced by both genetic and environmental factors. This finding, although not minimizing the importance of the TRC in past dermatoglyphic studies, perhaps should promote careful interpretation of results from other variables that cannot be so readily broken into different components.

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Correspondence: Dr. T. Reed, Department of Medical Genetics, Indiana University, 1100 W. Michigan St., Indianapolis, IN 46223.