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The M Quadruplets
II. The Interpretation of Quantitative Differences

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The first part of this two-part paper reviewed the evidence on zygosity of a set of female quadruplets born in Lansing, Michigan, in 1930 (Allen, 1960a). Calculations based upon simple qualitative traits, presumed to be chiefly genetic, indicated a probability of less than one per cent that the girls originated from more than one zygote. The probability of a three- or four-egg origin was entirely negligible. Quantitative traits had been considered by previous authors as consistent with monozygotic origin, but some of the quantitative differences were considerable. An attempt will be made here to show how quantitative variations may be brought into the zygosity calculations, and to draw some inferences from the quantitative variation in this set of quadruplets.

Heights, weights and cephalic indices of the girls at age 10 were recorded by Gardner and Newman (1943) (see Table 1). Adult statures based on the average

Table 1 - Measurements of the M quadruplets at age 10, from Gardner and Newman (1943)

	A	B	C	D
Height (cm)	133	129	132	126
Weight (lbs)	54	51	53	49.5
Cephalic Index	70.6	73.9	70.6	70.6

of two sets of measurements are A, 159 cm.; B, 156 cm.; C, 157 cm.; and D, 153 cm. The last-born girl, D, is clearly the smallest, but the differences between her and the next are equalled or exceeded in other pairs. A and C were very close at age 10 in height, weight and cephalic index. D had the same cephalic index as A and

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C, while B was somewhat less dolichocephalic. Although Gardner and Newman claimed that the differences in height and weight were no greater than the average of monozygotic twins, they may have considered only the three serial differences. If the heights are taken in six pairs, the differences are 1, 3, 3, 4, 6 and 7 cm. Newman's collected twin data as reproduced by Smith and Penrose (1955) show that, for adult twins, a difference in stature of three cm. is equalled or exceeded by less than 30 per cent of identical pairs, and a difference of seven cm., by less than four per cent. The difference in cephalic index between B and the other three, 3.3, is exceeded by only about ten per cent of monozygotic pairs.

Dermatoglyphic characters are more stable and some are more accurately quantified than height, weight and cephalic index. Ridge count data, in particular, are available on a large number of twins, and in the M quadruplets it happens that ridge counts provide even stronger suspicion of a two-egg origin than do the anthropometric data.

The ridge-count differences

The quantitative variation to be expected in monozygotic quadruplets is not known empirically. Only one other set of identical quadruplets has been reported with reasonable supporting evidence (Searle and Denny, 1953), and relevant quantitative data were not given. Triplets are of course more numerous than quadruplets, but only twin data are voluminous enough to permit generalizations. Yet, direct comparisons between twins and quadruplets are bound to be misleading. Apparently Gardner and Newman (1943) arranged the quadruplet measurements in sequence and compared the largest single interval with differences of identical and fraternal twins. When compared with twins in this way, variation in a set of quadruplets would be underestimated because any large interval would be likely to *include* one or both of the other values, and would thus be eliminated from consideration. In twins, however, both large and small intervals would be recognized. Equally unreliable is the extreme difference in a set of quadruplets; this will tend to be larger than the difference between twins just as in any small sample the expected range is a function of sample size.

The extreme ridge counts in the M quadruplets, those of B and D, differ by 41; in twins this would constitute strong evidence of dizygotic origin. Even when D is compared with the *average* of the other three, the difference is 38, a value exceeded in only 1.2 per cent of 324 identical twins in the combined series of Smith and Penrose (1955) and of Lamy et al. (1957). However, the ridge count is not the only quantitative description of dermatoglyphic anatomy. Two other characters that would seem to be nearly independent of ridge count are the individual pattern score (Wendt, 1955) and the sum of left and right maximal *atd* palmar angles (Penrose, 1949). Table 2 gives ridge counts for left hand, right hand, and total, together with the pattern scores and summed palmar angles. The last were measured on prints published by MacArthur and MacArthur (1937). It is apparent that the isolated

position of D suggested by ridge counts is not reflected in the other two characters.

A more informative treatment of quantitative differences would be one that employed them as estimates of variance. A difference between MZ twins is a single observation of *nongenetic variance*. This variance can be estimated accurately for a given genotype only from an isogenic population. In inbred laboratory animals variance is generally found to be greater in some genotipes than in others, but

Table 2 - Quantitative dermatoglyphic data on the M quadruplets, based upon MacArthur and MacArthur (1937)

	A	B	C	D
Ridge counts, right hand	48	44	47	29
left hand	51	58	51	32
total	99	102	98	61
Wendt pattern scores	43	40	40	41
Sum of palmar atd angles	101	104	93	93

human material has not yet provided evidence for this. In fact, Richter and Geisser (1960) have shown that inter-pair differences in variance for identical twins do not contribute an appreciable part of the variation in ridge-count differences, which can be entirely accounted for in terms of sampling errors. This means that, if there are genotypic differences in variance of ridge count, twin data are too crude to reveal them.

For the 324 twin pairs mentioned above, the average estimate of within-pair variance is 93. If this is, as Richter and Geisser suggest, the approximate true variance for any pair of identical twins, it should also be the approximate true variance for a set of identical quadruplets. However, the variance observed in the M quadruplets is 377. This corresponds to a Chi-square of 12.2 on the basis of an assumed variance of 93 (obtained as follows: $\frac{3 \times 377}{93}$), which, for three degrees of freedom, has a probability of .0065. The probability of such a deviation from the mean variance in either direction has twice this probability, or .013.

It might be supposed that ridge count would depend on size of the embryonic fingers when the ridges were determined. If so, the ridge count discrepancy in these quadruplets should represent a large early growth deficit of D to which her birth weight and subsequent growth bore testimony. However, when ridge counts on the toes are examined (MacArthur and MacArthur, 1937), A is found to have the lowest ridge count, although she was the largest at birth and as an adult.

Utilization of quantitative traits in quadruplet zygosity calculations

Despite the high apparent probability of monozygotic origin of the M quadruplets judged from qualitative traits in the earlier paper, the above quantitative data call for a second examination of this probability. The use of theoretical segregation ratios in the computation of probability of dizygosity is open to certain objections. First, actual segregation ratios do not always conform to theory. Second, there is evidence that at least a small proportion of dizygotic twins are chimeras with respect to their red blood cells. Third, some observations on twins (Osborne, 1957) indicate the possibility that, with respect to the ABO blood groups, concordance in surviving dizygotic twins differs considerably from expectation. Finally, any of these sources of doubt may be accentuated in higher orders of plural birth.

In theory, therefore, the best normative data for zygosity diagnosis from either quantitative or monofactorial traits would be empirical probabilities. Ideally these should be based on large numbers of twins in whom zygosity diagnosis was established without reference to the trait in question. Because such ideal data are not available, theoretical probabilities must be used in the analysis of monofactorial traits, and questionable empirical data must be used for quantitative traits. In some instances even these empirical data may be superior to theoretical probabilities, and in any event it is sometimes necessary to go beyond the monofactorial traits in zygosity diagnosis.

The analysis of quantitative traits in triplets and quadruplets entails some computational problems that do not arise in similar calculations on twins. A common procedure in the past has been simply to compare the average difference in a set of quadruplets with the averages for MZ and DZ twins, respectively. This may decide in favor of one zygote when the average is smaller than that for MZ twins, or in favor of four zygotes when the average is greater than that for DZ twins, but it gives no quantitative estimate of the probability and it does not permit a decision in favor of a two- or three-zygote origin.

For a set of same-sex twins there are only two possible hypotheses about zygotic origin; for triplets there are five and for quadruplets there are fifteen. The hypotheses to be entertained for a set of same-sex quadruplets may be represented as follows, with uniovular partners appearing side-by-side on the same line, multiovular partners on different lines:

One-egg:	ABCD			
Two-egg (2 : 2):	AB CD	AC BD	AD BC	
Two-egg (3 : 1):	A BCD	B ACD	C ABD	D ABC

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Three-egg:	AB C D	AC B D	AD B C	A BC D	A BD C	A B CD
Four-egg:	A B C D					

Insofar as probabilities or weights are to be based on observed quantitative differences, all fifteen hypotheses are equally probable, and the weights should reflect only the goodness of fit of the respective hypotheses to the quantitative observations. It may often be found that monofactorial traits eliminate one or more zygosity types from serious consideration. Thus, in the M quadruplets three-egg and four-egg origins were shown to be virtually incompatible with the observed concordance in qualitative traits, so that only the one monozygotic and seven dizygotic hypotheses remain.

In the case of twins, probabilities of zygosity may be calculated from known distributions of quantitative traits (Essen-Möller, 1941; Smith and Penrose, 1955; Bulmer, 1958). In the case of quadruplets, prior probabilities are not known directly, but it seems possible to use data from twins. Richter and Geisser (1960) suggested that twin data might be used to predict the distribution of variances in each type of quadruplets; namely, according to Chi-square with three degrees of freedom based upon the average variances found in MZ and DZ twins. This method has certain disadvantages. First, it requires the assumption that all genotypes have the same variance. This is contradicted by the evidence from inbred laboratory animals. While it may be a sufficiently accurate assumption in the case of twins, where sampling errors of the variance estimates are very large, it is likely to be misleading in the case of quadruplets. As the number of replications of a genotype increases, accuracy of estimation of variance increases, so that the distribution of quadruplet variances predicted as sampling errors becomes relatively narrow. The true distribution, depending partly upon the differences of genotype, may be much broader.

A second disadvantage of the method of Richter and Geisser is its inefficient use of the individual measurements in a set of triplets or quadruplets. Thus all hypotheses under each zygosity type must be weighted together and accepted or rejected together, and this will often discard useful information. In the M quadruplets, for example, D is widely separated from the other three in ridge counts, while B is the isolated member in cephalic index. By the method of variances the two traits would support a dizygotic hypothesis in a cumulative manner, when in fact they are mutually inconsistent.

The method of combined likelihoods of separate pair differences

Unless individual variation is very different in quadruplets than in twins, a question to be discussed below, any one pair within a set of quadruplets should conform to the distribution of differences found in twins. From a set of quadruplets six such pairs can be made up, and each of the resulting six differences can be assigned two likelihoods of occurrence, one as among MZ and one as among DZ twins. For each difference, only one of the two likelihoods will be appropriate in any given hypothesis about origin of the set as a whole. For the hypothesis of monozygosity, all six differences are assigned likelihoods as in MZ twins. For the hypothesis that D has a separate origin, the differences of D from A, B and C have likelihoods corresponding to the distribution of DZ twins, while for the other three differences the likelihoods correspond to the distribution of MZ twins. Similarly, when B is considered to be of separate origin, the differences between B and the others are treated as in DZ twins.

The question now arises as to how the six likelihoods selected under each hypothesis are to be meaningfully combined. This will determine the relative magnitudes of the likelihoods assigned to the fifteen hypotheses, and in some instances even their rank order. At present no rigorous mathematical basis has been found for any particular method of combination. However, one method is convenient and gives values comparable to the likelihoods found in twin problems. This measure is the square root of the six-fold product. If the likelihood of a given difference is denoted by Lm for monozygotic pairs and by Ld for dizygotic pairs, and if the six possible pairs taken in alphabetical order are denoted by subscripts 1 through 6, then the resulting measures of likelihood for the first four hypotheses listed previously are as follows:

Hypothesis	Index of likelihood
ABCD	$(Lm_1.Lm_2.Lm_3.Lm_4.Lm_5.Lm_6.)^{1/2}$
AB CD	$(Lm_1.Ld_2.Ld_3.Ld_4.Ld_5.Lm_6)^{1/2}$
AC BD	$(Ld_1.Lm_2.Ld_3.Ld_4.Lm_5.Ld_6.)^{1/2}$
AD BC	$(Ld_1.Ld_2.Lm_3.Lm_4.Ld_5.Ld_6)^{1/2}$

In practice, six individual likelihoods need not be used in each computation. Every hypothesis will contain, for the (i)th difference, either Lm_i or Ld_i. Either of these can be divided by Lm_i so as to reduce Lm_i to unity or Ld_i to the " relative chance in favor of dizygosity ", in the terminology of Smith and Penrose. Since the tables of Smith and Penrose are all reduced to this form, the values they give may be used directly in the above formulas. All factors of the type Lm become unity

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and can be omitted, and the only factors that have to be multiplied are the relative chances in favor of dizygosity as given by Smith and Penrose.

The index of likelihood described above can be extended to triplets and quintuplets. In a set of quadruplets there are six differences and the following three independent contrasts: $A - B$, $\frac{A+B}{2} - C$, and $\frac{A+B+C}{3} - D$. The index for quadruplets is the 3/6 power of the six-fold product. If the index for any type of multiple birth is defined thus in terms of the numbers of differences and independent contrasts, then for triplets it would be the 2/3 power of the three-fold product and for quintuplets it would be the 4/10 power of the ten-fold product. However, unless they can in the future be validated mathematically, all of these indices must be regarded as arbitrary. An attempt is now underway to validate them empirically.

Final estimate of probability of monozygosity for the M quadruplets

The calculation of relative likelihoods or relative chances of different hypotheses in relation to a given quantitative trait starts with a table that compares the distributions of differences in MZ and DZ twins. Ideally, the relative chances should be obtained from the ordinates corresponding, in the distribution, to each observed difference. Smith and Penrose and also Lamy *et al.* broke their observed distributions into segments and used the areas of these segments as proportional to the ordinates for all differences within the respective limits. This method is satisfactory in the central part of the distribution of monozygotic differences, where the frequency curves are nearly horizontal, but at the extremes it gives rather sharp discontinuities or inconsistencies. Since the ridge count differences of the M quadruplets include some at the extreme of the monozygotic range, this defect of the tables might vitiate the probability calculations.

A somewhat better approximation to the ordinates on a curve is given by areas of overlapping segments, each one extending equally to left and right of the points at which ordinates are desired. If the segments are of the same width for the MZ and DZ distributions, then for any given difference the ratio of their areas will be nearly the same as the ratio of the respective ordinates.

In the construction of Table 3, the MZ twin data of Lamy *et al.* were combined with those of Smith and Penrose after it was determined that the two distributions satisfied several tests of homogeneity. The 185 DZ twins of Lamy *et al.* were not homogeneous with the siblings in the Smith and Penrose table, and the former were taken by preference. In the table, individual differences in the lower and upper part of the MZ range are represented by areas of overlapping segments; in the middle of the distribution and beyond the expected MZ range the values are grouped, as in the Smith and Penrose tables. The data of Wendt on pattern score for 100 identical and 100 fraternal twins are reproduced in Table 4, again with overlapping segments. In both tables, as in those of Smith and Penrose, relative chance of occur-

Table 3 - Relative chances in favor of dizygosity according to differences in total finger ridge count (after Smith and Penrose, 1955; Lamy et al., 1957)

Difference in total count	Range of differences used	Percentage of pairs		Relative chance in favor of dizygosity (d/m)
		Monozygotic (m)	Dizygotic (d)	
0	0-1	10.80	5.41	.501
1	0-2	16.98	7.57	.446
2	1-3	21.30	8.65	.406
3	2-4	18.52	5.41	.292
4	3-5	16.36	5.41	.331
5	4-6	16.67	5.95	.357
6	5-7	13.89	5.95	.428
7-12	7-12	25.00	11.35	.454
13-24	13-24	26.85	18.38	.685
25	22-28	7.10	5.95	.838
26	23-29	6.79	7.57	1.115
27	24-30	6.48	7.03	1.085
28	25-31	4.94	8.65	1.75
29	26-32	4.94	10.27	2.08
30	26-34	5.56	12.43	2.24
31	27-35	4.01	13.51	3.37
32	28-36	3.70	13.51	3.65
33	29-37	2.78	14.05	5.05
34	30-38	2.78	14.59	5.25
35	31-39	2.16	14.05	6.50
36	32-40	2.47	11.89	4.81
37	33-41	2.16	9.73	4.50
38	-43	2.16	12.97	6.01
39	-45	2.16	14.05	6.51
40	-47	2.16	15.67	7.26
41	-49	2.16	17.83	8.25
42	-51	2.16	19.46	9.01
43	-53	2.16	21.08	9.76
44	-55	2.16	21.08	9.76
45+	33 +	2.16	43.78	20.29

rence of any given difference in MZ twins is arbitrarily taken equal to one and only the relative chances in dizygotic twins are listed.

Table 5 gives the results of the previous calculations on qualitative traits (Allen, 1960a) together with indices of likelihood for the quantitative traits under the eight most likely hypotheses. The three types of origin have different initial odds, shown in the first line of the table. In the calculations based on unit traits, the two types of dizygotic origin did not need to be separated and were together assigned initial

odds of three, relative to the monozygotic hypothesis. Here the two dizygotic types must be considered separately, and their individual probabilities are smaller. According to a recent estimate (Allen, 1960), the initial relative odds are 1 for monozygotic quadruplets, 2.2 for dizygotic quadruplets of the 3 : 1 type and 0.8 for dizygotic quadruplets of the 2 : 2 type. It should be noted that even though the initial

Table 4 - Relative chances in favor of dizygosity according to differences in pattern score (after Wendt, 1955)

Difference in score	Range of differences used	Percentage of pairs		Relative chance in favor of dizygosity (d/m)
		Monozygotic (m)	Dizygotic (d)	
0	0-1	49	16	.327
1	0-2	70	22	.314
2	1-3	65	24	.369
3	2-4	43	19	.442
4	3-5	30	20	.667
5	4-6	16	20	1.25
6	5-7	8	20	2.50
7	-9	8	30	3.75
8	-11	8	35	4.38
9 +	5 +	8	65	8.13

odds for all dizygotic hypotheses are collectively only 3, the relative probability, 2.2, applies in each test of a 3:1 hypothesis, and the relative probability, 0.8, applies in each test of a 2 : 2 hypothesis.

The " qualitative traits " grouped together in line b of Table 5 are those described in the earlier paper: sex, seven blood factors, and two traits of uncertain genetic causation, hair color and a bony anomaly of the wrist. Since the manner of quadruplet formation (2 : 2 *vs.* 3: 1) would not alter concordance or discordance in genetic traits of two zygotes initially present, the relative chances from monofactorial traits in favor of a dizygotic origin apply alike to all the dizygotic hypotheses.

The most useful and most nearly independent dermatoglyphic traits appear in lines c, d and e, and their cumulative products in line h. The indices of likelihood corresponding to ridge counts were obtained as in Tables 6 and 7, and illustrate the method used for the other traits.

The likelihoods for ridge counts and for Wendt scores were obtained from Tables 3 and 4, those for palmar *atd* angles, stature and cephalic index, from the tables of Smith and Penrose. Some of the tables, particularly those for stature and cephalic index, are based on very scanty material. With possible exception of the ridge counts, therefore, the derived probability estimates may be very inaccurate. More appropriate data have recently become available (Osborne and De George, 1960).

Table 5 - Relative chances of the monozygotic and dizygotic hypotheses judged by both qualitative and quantitative traits

	Hypothesis							
	ABCD	AB CD	AC BD	AD BC	A BCD	B ACD	C ABD	D ABC
a. Initial odds	1	.8	.8	.8	2.2	2.2	2.2	2.2
b. Qualitative traits	1	.00313	.00313	.00313	.00313	.00313	.00313	.00313
c. Ridge counts	1	2.71	1.62	2.20	.88	.89	.81	14.93
d. Pattern scores	1	.129	.129	.139	.269	.213	.213	.191
e. Palmar *atd* angles	1	1.09	.65	.65	.64	1.10	.80	.80
f. Adult stature	1	1.62	5.07	2.43	2.36	.603	1.89	7.40
g. Cephalic index	1	.704	.704	.704	.622	1.45	.622	.622
h. Dermatoglyphics, cumulative product (*c.d.e*)	1	.381	.136	.199	.153	.209	.139	2.28
i. Quantitative traits, cumulative product *f.g.h.*	1	.435	.485	.340	.225	.183	.163	10.49
j. All traits, cumulative product *a.b.i*	1	.0011	.0012	.0008	.0015	.0013	.0011	.072

According to available normative data, the quantitative traits (line i) clearly favor a dizygotic hypothesis in which D is of separate origin from A, B and C. However, this depends entirely on ridge count and stature; the other three quantitative traits, in lines d, e and g, argue that this hypothesis is less likely than that of monozygotic origin. If it is correct to combine the estimates of relative likelihood based on qualitative and quantitative traits as in the last line of Table 5, the likelihood of dizygosity is only 7.2 per cent as great as the likelihood of monozygosity.

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The likelihoods given at the bottom of Table 5 are all relative. In the case of twins, absolute probability of a zygosity hypothesis is easily obtained as the ratio of its relative chance to the sum of the relative chances. The same is true for triplets or quadruplets as long as the hypotheses correspond to zygosity types. In both of these situations each hypothesis represents a definite fraction of a real population.

Table 6 - Likelihoods of the separate pair differences in ridge count

Pair	Difference	Relative chance in favor of dizygosity
AB	3	.292
AC	1	.446
AD	38	6.01
BC	4	.331
BD	41	8.25
CD	37	4.50

When quantitative traits are used for quadruplets (or triplets), however, the several hypotheses under one zygosity type are equivalent and appear to have no separate counterparts in the quadruplet (or triplet) population. Concepts of absolute probability may therefore be inapplicable to the present situation.

Significance of the large quantitative differences in the M quadruplets

Earlier in this paper it was stated that the variance in ridge counts for the M quadruplets was 377, which is greater at the .01 probability level than the average for two large series of MZ twins. If the monozygotic origin of the quadruplets is accepted, then this high variance may be taken as evidence for either or both of two suppositions: (1) Different human genotypes have different variances with respect to ridge count and these differences are highly significant in quadruplets, though not discernible in twin data. (2) Variance in identical quadruplets may be, on the average, greater than in identical twins because of more marked disturbances in their prenatal development. By analogy, the average variance observed in identical twins might be an overestimate of the phenotypic variance of the same genotypes if they had been replicated in single births. This analogy is misleading, however. Differences in the intrauterine environment between gestations may contribute as

much or more variance than do the special intrauterine factors that act differentially on members of a twin pair. In the case of ridge count, it is known that correlation between single-born siblings is equal to that between fraternal twins (Holt, 1954), so that in this instance the two sources of variance appear to contribute equally or

Table 7 - Combined likelihoods of the monozygotic and dizygotic hypotheses based on dermal ridge counts

Hypothesis	Relative chance
ABCD	$1 \frac{1}{2} = 1$
AB CD	$(.446 \times 6.01 \times .331 \times 8.25)^{\frac{1}{2}} = 2.71$
AC BD	$(.292 \times 6.01 \times .331 \times 4.50)^{\frac{1}{2}} = 1.62$
AD BC	$(.292 \times .446 \times 8.25 \times 4.50)^{\frac{1}{2}} = 2.20$
A BCD	$(.292 \times .446 \times 6.01)^{\frac{1}{2}} = 0.88$
B ACD	$(.292 \times .331 \times 8.25)^{\frac{1}{2}} = 0.89$
C ABD	$(.446 \times .331 \times 4.50)^{\frac{1}{2}} = 0.81$
D ABC	$(6.01 \times 8.25 \times 4.50)^{\frac{1}{2}} = 14.93$

not at all. However, identical twins may be subject to more potent difference-producing factors in utero.

If quadruplets vary more than twins, tables on quantitative differences in twins used in the diagnosis of zygosity of triplets or quadruplets must be regarded as biased against monozygotic hypotheses. Thus, a ridge count difference of 41 is only occasionally found in MZ twins, but it may be frequent in MZ quadruplets.

Summary

Early students of the M quadruplets considered that the dermatoglyphic traits and physical measurements corroborated a monozygotic origin. More careful analysis in terms of variance shows that the ridge counts, at least, are quite inconsistent with data from monozygotic twins. However, when several quantitative measures are considered together by a method of combined relative likelihoods of separate pair differences, the evidence against monozygosity is less impressive than the contrary evidence from qualitative traits including blood groups. It is concluded that quadruplets tend to vary more than twins and/or that some genotypes are much more variable than others, at least with respect to dermal ridge counts.

References

ALLEN, G. 1960 a: The M quadruplets: I. Probability of uniovular origin judged from qualitative traits. A.Ge. Me. Ge., 9: 240-254.

— 1960 b: A differential method for estimation of type frequencies in triplets and quadruplets. Amer. J. Human Genet., 12: 210-224.

BULMER, M. G. 1958: A note on monozygotic twin diagnosis. Ann. Human Genet., 22: 340-341.

ESSEN-MÖLLER, E. 1941: Empirische Ahnlichkeitzdiagnose bei Zwillingen. Hereditas, 27: 1-50.

GARDNER, I. C., and NEWMAN, H. H. 1943: Studies of quadruplets: V—The only living one-egg quadruplets. J. Hered., 35: 83-88.

HOLT, S. B. 1954. Quantitative genetics of finger-print patterns. Proc. 9th Intern. Congr. Genetics. Caryologia, 6, Suppl.: 624-625.

LAMY, M. et al. 1957: Le nombre de dermatoglyphes dans un échantillon de jumeaux. Ann. Human Genet., 21: 374-385.

LERNER, I. M. 1954. Genetic Homeostasis. New York: John Wiley; London: Oliver and Boyd. 134 pp.

MACARTHUR, J. W., and MacArthur, O. T. 1937. Finger, palm and sole prints of monozygotic quadruplets. J. Hered., 28: 147-153.

MATHER, K. 1953. Genetical control of stability in development. Heredity, 7: 297-336.

OSBORNE, R. H. 1957: Selective survival in dizygotic twins in relation to the ABO blood groups. Amer. J. Human Genet. 9: 321-330.

— and De George, F. V. 1960. Genetic Basis of Morphological Variation. Cambridge, Mass.: Harvard Univ. Press.

SEARLE, W. N., and DENNY, F. 1953. A case of uniovular quadruplets. J. Obst. Gynec. Brit. Emp., 60: 31-36.

SMITH, S. M., and PENROSE, L. S. 1955: Monozygotic and dizygotic twin diagnosis. Ann. Human Genet. 19: 273-289.

RICHTER, D. L., and GEISSER, S. 1960: A statistical model for diagnosing zygosis by ridge-count. Biometrics, 16: 110-114.

WENDT, G. G. 1955: Der individuelle Musterwert der Fingerleisten und seine Vererbung. A. Ge. Me. Ge., 4: 330-337.

RIASSUNTO

I primi studiosi che hanno esaminato i quadrigemini M pensavano che le caratteristiche dermatoglifiche e le misurazioni fisiche fossero in favore di una origine monozigotica. Una analisi più dettagliata dei dati di varianza dimostra che almeno il numero dei dermatoglifici è incompatibile con i dati forniti dai gemelli monozigotici. Tuttavia, quando si analizzi un insieme di diverse misurazioni quantitative, mediante il metodo di probabilità relativa di variazione fra le diverse coppie, le prove di una origine non-monozigotica diventano meno convincenti delle prove contrarie, quelle fornite dalle caratteristiche qualitative, compresi i gruppi sanguigni. Si conclude che i quadrigemini presentano una tendenza a variare più accentuata dei gemelli e che, al contempo, alcuni genotipi tendono a variare più di altri, almeno per quanto riguarda il numero dei dermatoglifici.

RÉSUMÉ

Les premiers investigateurs des quadruplés M étaient d'avis que les caractéristiques dermatoglyphiques et les mesurations physiques corroboraient une origine monozygotique. Une analyse plus détaillée des données de variance démontre qu'au moins le nombre des dermatoglyphes est tout-à-fait incompatible avec les données fournies par les jumeaux monozygotiques. Toutefois lorsqu'on analyse un groupement de diverses mesurations quantitatives à l'aide de la méthode de probabilité relative des différences entre les diverses paires, les preuves d'une origine non monozygotique sont moins convaincantes que les preuves contraires, celles qui sont fournies par les caractéristiques qualitatives, y compris les groupes sanguins. On arrive à la conclusion que les quadruplés ont une tendance à varier plus que les jumeaux et, en même temps, que certains génotypes tendent à varier plus que d'autres, tout au moins en ce qui concerne le nombre des dermatoglyphes.

ZUSAMMENFASSUNG

Die frühen Forscher auf dem Gebiet der M-Vierlinge betrachteten die Papillarleistenmerkmale und die körperlichen Masse als Bestätigung eines eineiigen Ursprungs. Sorgfältigere Untersuchung, im Sinne der Varianz, zeigt, dass die Leistenzahl schon gar nicht mit den Angaben über eineiige Zwillinge übereinstimmt. Wenn man jedoch verschiedene quantitative Werte gemeinsam anhand einer Methode von kombinierten relativen Wahrscheinlichkeiten der einzelnen Paarunterschiede in Betracht zieht, dann imponiert der Beweis gegen Eineiigkeit weniger als der entgegengesetzte Beweis qualitativer Merkmale, einschliesslich der Blutgruppen. Es ergibt sich, dass Vierlinge zu grösserer Variation neigen als Zwillinge, bzw. dass manche Genotypen variabler sind als andere, zumindest in Bezug auf die Hautleistenzahl.

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