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A NEW APPROACH TOWARDS THE STUDY OF HERITABILITY OF SOMATOMETRIC CHARACTERS OF TWINS

INTRODUCTION

Identical twins seem at first sight to provide for man a means of measure of genotypic variance. They provide individuals of identical genotype, just as inbred lines, or crosses between lines, do for laboratory animals or for plants. The phenotypic variance within pairs of identical twins should, therefore, estimate the environmental variance and so allow the partition of the phenotypic variance into genotypic and environmental components to be made.

Genetic causes, however, are not the only reasons for resemblance between relatives, there are also environmental circumstances that tend to make relatives resemble each other, some sorts of relatives more than others. If members of a family are reared together, as with human families, they share common environment. This means that some environmental circumstances that cause differences between unrelated individuals are not a cause of the difference between members of the same family. In other words, there is a component of environmental variance that contributes to the variance between means of families but not to the variance within the families, and it therefore contributes to the covariance of the related individuals. This between-group component is usually called common environment. The remainder of the environmental variance arises from the causes of difference that are unconnected with whether the individuals are related or not. It therefore appears in the within-group component of variance, but does not contribute to the between-group component, which is the variance of the true means of the groups. This division of environmental variance holds completely also for the twins.

MODEL, METHODS AND MATERIAL

MODEL

If anthropometric measurement is carried on pairs of like-sexed twins, for each measure character on each pair of twins we receive a pair of values (X_1, X_2), where X_1 represents the measurement on one member of a pair and X_2 on the other. As we could not distinguish the "first" and the "second" twin we speak about the disarranged pair of values. We assume that (X_1, X_2) is a twodimensional random vector with a symmetrical normal distribution having probability density

$$F(x_1, x_2) = (2\pi\sigma^2 \sqrt{1 - \varrho^2})^{-1} . \exp \{-[2\sigma^2(1-\varrho^2)]^{-1} . \cdot [(x_1 - \mu)^2 - 2\varrho(x_1 - \mu)(x_2 - \mu) + (x_2 - \mu)^2]\} \quad (1)$$

The vector of the expected values is (μ, μ) and the covariance matrix is

$$\begin{pmatrix} \sigma^2, \varrho\sigma^2 \\ \varrho\sigma^2, \sigma^2 \end{pmatrix}$$

It means that both X_1 and X_2 random variables are connected by the correlation coefficient ϱ and the probability behaviour of the character in both twins is the same.

Further we assume for identical twins the validity of the model:

$$_IX_j = \mu + G + es_j + ec \qquad \text{for } j = 1, 2 \quad (2)$$

where $_IX_j$ is the measure value of j^{th} twin $(j = 1, 2)$ in identical pairs of twins

μ is the constant given by the age of the twins

G is the random quantity representing the influence of the genotype of the parents and for which the expected value $E(G) = 0$ and variance

$D(G) = \sigma_G^2$ (variance of genetic deviations)

es_j represents random differences among people due to the influence of environment and not depending on the relationship for which $E(es_j) = 0$ and $D(es_j) = \sigma_{es}^2$ $(j = 1, 2)$, it means that σ_{ec}^2 is the variance of deviations due to micro-environment (the within-pair component)

and ec is the random quantity describing the influence of common environment springing from the relationship and for which the expected value $E(ec) = 0$ and variance $D(ec) = \sigma_{es}^2$ it means that

σ_{es}^2 is the variance of deviations due to common environment (the between-pairs component)

We also assume that G, ec and es_j are uncorrelated and do not depend on age.

For the fraternal twins from this is analogically valid:

$$_FX_j = \mu + G_j + es_j + ec \qquad \text{for } j = 1, 2$$

where G_j is the random quantity describing the influence of the genotype of the parents and which have the probability characteristics as the same as G for identical twins that means that

$$E(G_j) = 0 \text{ and } D(G_j) = \sigma_G^2 \text{ for } j = 1, 2.$$

We suppose that $G_1 = \frac{G}{2} + G_1'$ and

$$G_2 = \frac{G}{2} + G_2'$$

Where G is common genotype and G_1' and G_2' are different part of genotype of fraternal twins. The G, es_j and ec are the same as in the preceding model and G, G_1', G_2', es_j and ec are also uncorrelated. It means that $E(_IX_j) = \mu$ and

$D(_IX_j) = {_I\sigma^2} = \sigma_G^2 + \sigma_{es}^2 + \sigma_{ec}^2$
for identical

and $E(_FX_j) = \mu$ and
$D(_FX_j) = {_F\sigma^2} = \sigma_G^2 + \sigma_{es}^2 + \sigma_{ec}^2$
for fraternal twins,

respectively, (Falconer, 1960) so that the following holds:

$$_I\sigma^2 = {_F\sigma^2} = \sigma^2$$

Under presumption of the validity of this model we receive coefficients of correlation

$$\varrho_I = \varrho(_IX_1, {_IX_2}) = \frac{E(_IX_1 - \mu)\,(_IX_2 - \mu)}{_I\sigma^2} =$$

$$= \frac{E(G + es_1 + es)\,.\,(G + es_2 + ec)}{_I\sigma^2} =$$

$$= \frac{\sigma_G^2 + \sigma_{ec}^2}{\sigma^2} \tag{3}$$

for identical and

$$\varrho_F = \varrho(_FX_1, {_FX_2}) = \frac{E(_FX_1 - \mu)\,(_FX_2 - \mu)}{_F\sigma^2} =$$

$$= \frac{E(G_1 + 1/2G + es_1 + ec)\,(G_2 + 1/2G + es_2 + ec)}{_F\sigma^2}$$

$$= \frac{\sigma_{ec}^2 + 1/4\sigma_G^2}{\sigma^2} \tag{4}$$

for fraternal twins. These coefficients of correlation will be called intrapairs correlation coefficients. The quantity h^2 given by the formula

$$h^2 = \frac{\sigma_G^2}{\sigma^2} \tag{5}$$

is called the coefficient of heritability and from (3), (4) and (5) we receive

$$\varrho_I - \varrho_F = \frac{\sigma_G^2 + \sigma_{ec}^2}{\sigma^2} - \frac{\sigma_{ec}^2 + 1/4\sigma_G^2}{\sigma^2} =$$

$$= \frac{3/4\sigma_G^2}{\sigma^2} = 3/4h^2$$

For the determination of the coefficient of heritability we than receive the formula

$$h^2 = 4/3(\varrho_I - \varrho_F) \tag{6}$$

NOTICE: *It is necessary to realise that the coefficient heritability determined in this way impresses itself the estimation of the upper level of this parameter because the real coefficient of the heritability is the ratio of the additive and phenotypic variance (σ_A^2/σ^2) whilst in this way we calculated with the ratio σ_G^2/σ^2, or as quoted for instance by Falconer (1960), with the degree of genetic determination of the character. The level of agreement of this parameter with the true one depends on the share of nonaditive components of variability for each character counted.*

METHOD

In the next paragraph we shall discuss the estimation of the parametres ϱ_I, ϱ_F, σ^2, σ_G^2, σ_{ec}^2 and σ_{es}^2 under the above mentioned model. As it has been said that mean value μ of the twins depends on age. This fact usually complicates the situation, because the investigation with twins of the same age is very rare. The estimation of variance counted direct from the data would be distorted by the different age of the twins. Also for the estimation of the correlation coefficient it is not possible to use the standard formula for Pearson's correlation coefficient because the data consist of disarranged pairs.

To diminish the error due to different ages of the twins, in our case the expected value μ for each age group was estimated from the random sample of the Czechoslovak population and this value was substracted from our data. By this manner we received normalized data with the distribution under formula (1) and we can suppose that really $\mu = 0$, so that the influence of the different age was eliminated.

Let n_I or n_F be the number of pairs for each character counted in identical or fraternal twins, respectively. Let the random sample be in the forms

$$\begin{array}{ll} X_{11}, X_{12} & X_{11}, X_{12} \\ X_{21}, X_{22} & X_{21}, X_{22} \\ \cdot \quad \cdot \quad \text{and} & \cdot \quad \cdot \\ \cdot \quad \cdot & \cdot \quad \cdot \\ \cdot \quad \cdot & \cdot \quad \cdot \\ X_{n_I1}\ X_{n_I2} & X_{n_F1}\ X_{n_F2} \end{array}$$

Let the pair measurement (x_{i1}, x_{i2}) in each pair of twins be arranged randomly. We suppose that each pair of measurement is independent on the other. To eliminate the influence of arrangement we shall work with the quantities independent on the arrangement. These quantities are established for both identical and fraternal twins in a similar way. If this reality has to be distinguished we shall do it, as done, by the subscript F or I on the right down part of apparent quantity. In our computations we have used these quantities: $\bar{X}_i = \frac{X_{i1} + X_{i2}}{2}$
the mean value of the character for each pair

$$W_i = \sum_{j=1}^{2} (X_{ij} - \bar{X}_i)^2 = 1/2\,(X_{i1} - X_{i2})^2$$

sum of squares within the i-th pair

$$W = \sum_{i=1}^{n} W_i$$

sum of squares within pairs

$$\bar{X} = \frac{1}{2n} \sum_{i=1}^{n} \sum_{j=1}^{2} X_{ij}$$

mean value of the character in all pairs

$$B = 2 \sum_{i=1}^{n} (\bar{X}_i - \bar{X})^2$$

sum of squares between pairs

$$T = \sum_{i=1}^{n} \sum_{j=1}^{2} (X_{ij} - \bar{X})^2$$

sum total of squares
Is evidently $T = B + W$.
As it was said, Pearsons correlation coefficient

$$r = \frac{n \sum_{i=j}^{n} X_{i1}X_{i2} - \left(\sum_{i=1}^{n} X_{i1}\right)\left(\sum_{i=1}^{n} X_{i2}\right)}{\left[\left(n \sum_{i=1}^{n} X_{i1}^2 - \left(\sum_{i=1}^{n} X_{i1}\right)^2\right)\left(n \sum_{i=1}^{n} X_{i2}^2 - \left(\sum_{i=1}^{n} X_{i2}\right)^2\right)\right]^{1/2}} \qquad (7)$$

is not suitable for the estimation of ϱ because of disarrangement within pairs and so as a measure of the level of statistical linkage within pairs (for the estimation of ϱ) we apply the so-called sample intraclass corelation coefficient and we denote it as r_R (see Rao, 1968, p. 173). At first we arranged pairs within the random sample in all possible combinations and so we received $2n$ of pairs in the form

$$\begin{array}{l} X_{11}, X_{12} \\ X_{12}, X_{11} \\ X_{21}, X_{22} \\ X_{22}, X_{21} \\ \cdot \quad \cdot \\ \cdot \quad \cdot \\ \cdot \quad \cdot \\ X_{n1}, X_{n2} \\ X_{n2}, X_{n1} \end{array}$$

and for these $2n$ pairs we computed Pearson's correlation coefficient according to formula (7) and so received the correlation coefficient r_R which is the estimation of correlation coefficient for this case. It is evident that the value of r_R is independent on the arrangement within pairs. It is also possible to show that for r_R the following formula is valid:

$$r_R = \frac{2B - T}{T} \qquad (Rao,\ 1968) \qquad (8)$$

From the assumption that the random samples are from the distribution given by the probability (1) it is possible to derive that the statistic $W/[(1 - \varrho)\,\sigma^2]$ has Pearson's χ^2 distribution with n degrees of freedom. the statistic $B/[(1 + \varrho)\,\sigma^2]$ has Pearson's χ^2 distribution with $n-1$ degrees of freedom, and that statistic W and B are independent (*Rao*, 1968). The expected values of W and B are

$$E(W) = (1 - \varrho)\,\sigma^2 . n \quad \text{and} \quad E(B) = (1 + \varrho)\,\sigma^2 . . (n - 1)$$

because the expected value of statistic with Pearson's χ^2 distribution equals to the number of degrees of freedom. Therefore W/n is the unbiased estimation of the quantity $(1 - \varrho)\,\sigma^2$ and $B/(n - 1)$ is unbiased estimation of the quantity $(1 + \varrho)\,\sigma^2$.

From the (2) and (3) it follows that

$$(1 - \varrho_I)\,\sigma^2 = \left(1 - \frac{\sigma_G^2 + \sigma_{ec}^2}{\sigma^2}\right)\sigma^2 = \sigma_{es}^2$$

and analogically

$$(1 - \varrho_F)\,\sigma^2 = \left(1 - \frac{\sigma_{ec}^2 + 1/4\sigma_G^2}{\sigma^2}\right)\sigma^2 = \sigma_{es}^2 + 3/4\sigma_G^2$$

and further

$$(1 + \varrho)\,\sigma^2 + (1 - \varrho)\,\sigma^2 = 2\sigma^2$$

In other words if we designate the estimate of parameter by the row over the relevant litter we received

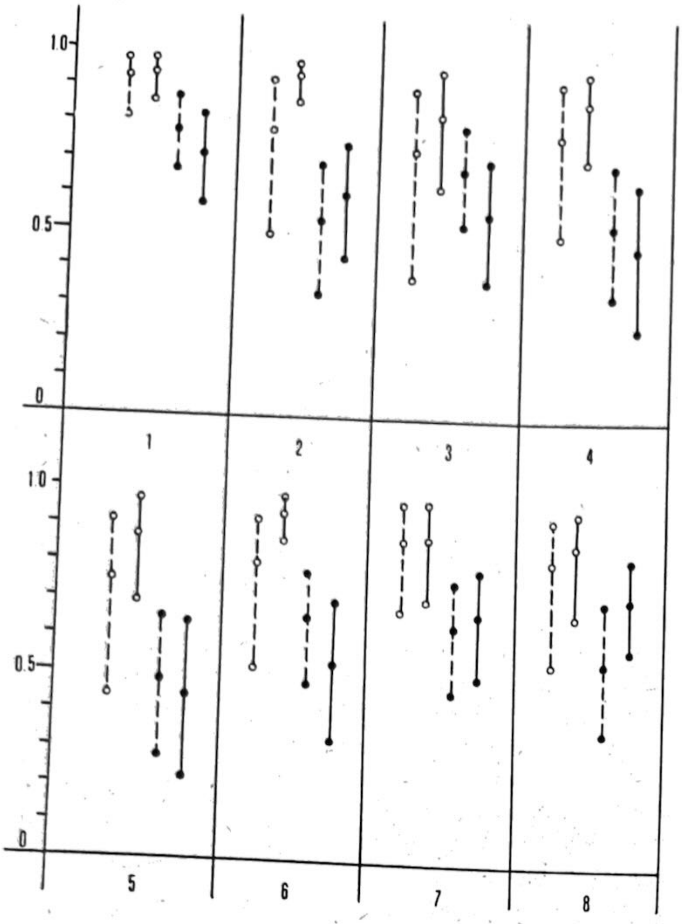
$$\hat{\sigma}_{es}^2 = \frac{W_I}{n_I}, \ \hat{\sigma}_{es}^e + 3/4\hat{\sigma}_G^2 = \frac{W_F}{n_F} \qquad (9)$$

and

$$\hat{\sigma}^2 = 1/2\left(\frac{B}{n - 1} + \frac{W}{n}\right) \qquad (10)$$

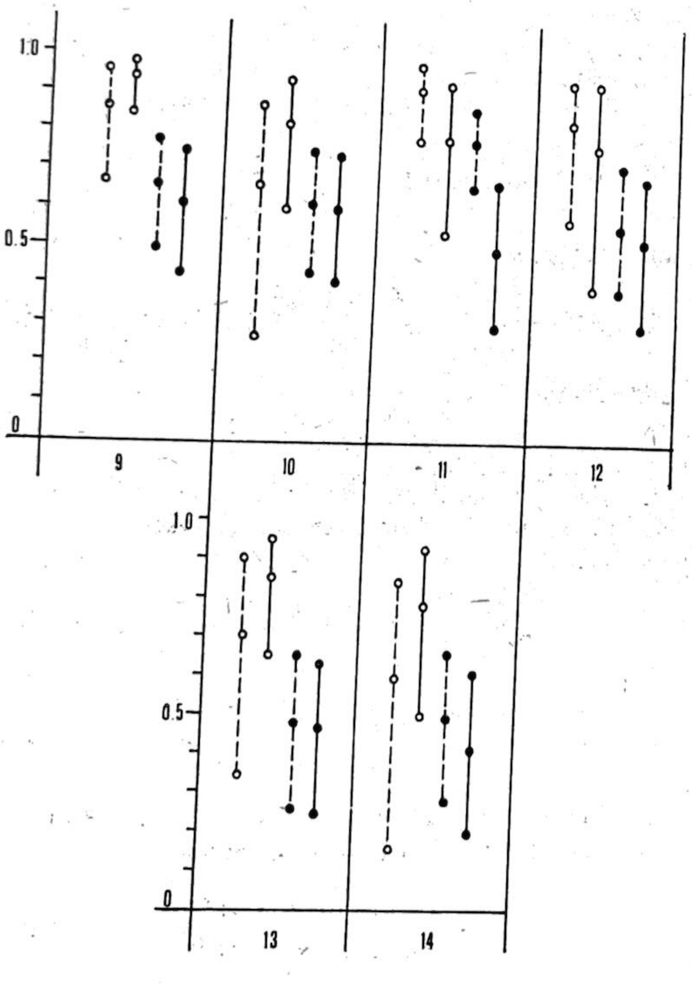
and by the formal introduction into (3) and (4) and (4) from (9) and (10) we received

$$\hat{\varrho}_I = \frac{n_I B_I - (n_I - 1)\,W_I}{n_I B_I + (n_I - 1)\,W_I} \qquad (11)$$



▲ FIG. 1

▼ FIG. 2



and

$$\hat{\varrho}_F = \frac{n_F B_F - (n_F - 1)\, W_F}{n_F B_F + (n_F - 1)\, W_F} \tag{12}$$

NOTICE: *Estimation $\hat{\varrho}$ of correlation coefficient ϱ given by this manner is called the sample intraclass correlation coefficient in the analysis of variance.*

In comparison of the just received estimation of correlation coefficients with the r_R given by the formula (8) we can see that they are asymptotically equivalent because it is possible to write the formula for estimation of r_R in the form

$$r_R = \frac{B - W}{B + W} \tag{13}$$

and then the estimate of $r_R \leqq \hat{\varrho}$.

It is possible to apply the coefficient r_R also to the test of the hypothesis $\varrho = 0$ because from (13) it follows that

$$\frac{1 - r_R}{2} = \frac{W}{T} = \frac{W}{W + B}$$

and from what was said on the statistics W and B above follows that $\frac{W}{T}$ has under hypothesis $\varrho = 0$ β-distribution with $n/2$ and $(n-1)/2$ degrees of freedom.

If $\varrho \neq 0$ then the quantity

$$F = \frac{B}{(1+\varrho)\,\sigma^2(n-1)} \Big/ \frac{W}{(1-\varrho)\,\sigma^2 n} =$$

$$= \frac{B}{W}\,\frac{1-\varrho}{1+\varrho}\,\frac{n}{n-1} = \frac{1+r_R}{1-r_R}\,\frac{1-\varrho}{1+\varrho}\,\frac{n}{n-1}$$

has Fisher-Snedecor's F distribution with $n-1$ and n degrees of freedom. The quantity F may be also applied to the test of hypothesis $\varrho = \varrho_0$ and to the construction of confidence interval for ϱ.

If we designate $F_\alpha(n_1, n_2)$ the α-quantile of Fisher-Snedecor's distribution with n_1 and n_2 degrees of freedom then

$$1 - \alpha = P\Big(F_{\alpha/2}(n-1, n) \leqq \frac{1+r_R}{1-r_R}\,\frac{1-\varrho}{1+\varrho}\,\frac{n}{n-1} \leqq$$

$$\leqq F_{1-\alpha/2}(n-1, n)\Big) =$$

$$= P\left(\frac{1 + r_R - F_{1-\alpha/2}(n-1, n)\,.\,\frac{n-1}{n}\,.\,(1-r_R)}{1 + r_R + F_{1-\alpha/2}(n-1, n)\,.\,\frac{n-1}{n}\,.\,(1-r_R)} \leqq \varrho\right.$$

$$\left.\leqq \frac{1 + r_R - F_{\alpha/2}(n-1, n)\,.\,\frac{n-1}{n}\,.\,(1-r_R)}{1 + r_R + F_{\alpha/2}(n-1, n)\,.\,\frac{n-1}{n}\,.\,(1-r_R)}\right) \tag{14}$$

and from this it follows that $100\,(1-\alpha)$ % confidence interval for ϱ is created by the quantities on both sides of unequality in formula (14). We reject the hypothesis $\varrho = \varrho_0$ on the level of significance α, if the ϱ_0 is not inside the confidence interval for ϱ.

From the estimation of ϱ the coefficient of heritability was received by means of formula (6).

$$\hat{h}^2 = 4/3(\hat{\varrho}_I - \hat{\varrho}_F) \quad \text{or} \quad \hat{h}^2_r = 4/3(r_{R_I} - r_{R_F})$$

As it was said from the quality of r_R and $\hat{\varrho}$ it follows that both estimations of the coefficient of heritability are asymptotically equivalent and so we work with the estimation estabilished on the coefficient r_R.

MATERIAL

The material used in this work consisted of random sample of 33 pairs of identical twins (EZ ♂♂ = 16, EZ ♀♀ = 17) and 132 pairs of fraternal twins (ZZ ♂♂ = 64, ZZ ♀♀ = 68) originating from the South Moravian Region. These twins were anthropologically investigated during the semilongitudial research of twins conducted at the Paediatric Research Institute in Brno. The age of the twins studied varies from 7 to 14 years and only healthy children were included in this sample.

The criterion for the determination of zygotic characters was an examination of the blood and serum systems (ABO, MNS, Pp, Rh, Lewis, Kell-Cellano) and the diagnosis of zygosity was completed by the dermatoglyphic analysis on fingers, palms and soles, by the clinical picture of the twins, and by the polymorphism of amylasis.

The 14 anthropometric characters were examined on each of the pairs using conventional anthropological methods of Martin-Saller (Fetter et al., 1967):

(1) Body height
(2) Body weight
(3) Total arm length
(4) Biacromial diameter
(5) Biiliocristal diameter
(6) Bitrochanter diameter
(7) Chest circumference
(8) Abdomen circumference (umbilical level)
(9) Head length
(10) Head breadth
(11) Morphological face height (nasion-gnation)
(12) Bizygomatic diameter
(13) Nose height
(14) Nose breadth

RESULTS AND DISCUSSION

For all the 14 characters examined in each of the four groups of twins (monozygotic girls, monozygotic boys, dizygotic girls and dizygotic boys) sums of squares of deviations were calculated as well as the respective mean values and corrected mean values (*Tab. 1*). As the individual somatic parameters change considerably with age, which is fully reflected in further statistical investigation (Wilson 1975), in our case a correction was carried out in each character with respect to the corresponding population mean values of the individual age groups. The corrected mean values have several consequences, above all the fact that they inform us about body growth and the development of the set of twins under investigation with respect to general population. It is logical that in the case of perfect correction the resulting mean value should equal zero. In our case this did not happen even once. Some parameters show negative deviations from among which particularly character No. 8 is conspicuous (belt circumference), others, on the other hand positive deviations, they are characters No. 5, 11, 12, and 13 (i.e., biiliocristal diameter, morphological face height, bizygomatic diameter, and nose height). Even though the significance of those deviations was not statistically tested, it seems to be biologically conspicuous and it would give testimony to the fact that the twins during their growth and development somewhat lag, as far as the body is concerned, behind the children of general population. This retarded development whose reason is probably a lower birth weight (multiple births), is reflected above all in the length-breadth proportions of the trunk and the limbs. The balancing comes shortly after puberty (Beneš 1973). The conditions are somewhat different in the head dimensions, where a rather opposite trend appears.

In *Tab. 2* and *3* estimates of the strength of linkage in monozygotic and dizygotic pairs of twins for both sexes are given, as well as estimate statistic $\frac{1-\varrho}{2}$ and differences between ϱ_I and ϱ_F. In all cases the strength of the statistical linkage is higher in monozygotic twins than in dizygotic ones. As follows from formulae 3 and 4, this difference is due to the fact that the correlation coefficient ϱ_I of monozygotic twins includes in the numerator besides others the whole variation due to genetic influences (σ^2_G), while the correlation coefficient of dizygotic twins only one quarter of it. The difference between ϱ_I and ϱ_F results in, as has been stated in our model, the estimate of only 3/4 of coefficient of heritability. The comparison of $1 - r_B$ with the critical values of the β-distribution has confirmed the fact that all correlation coefficients are significantly different from zero both for monozygotic and dizygotic pairs of girls and boys at the level of significance $\alpha = 0.01$.

The estimates of correlation coefficients including the confidence intervals of monozygotic and dizygotic twins (girls and boys) are graphically represented in Fig. 1. From it 3 items of information important for us follow: (1) The strength of the statistical linkage in the majority of the characters under investigation is higher in monozygotic boys than in monozygotic girls. This is testified above all by a range of the values of correlation coefficients which in monozygotic boys vary between 0.778 and 0.948, while in monozygotic girls within the range of 0.568 and 0.932. The same trend can also be observed in dizygotic pairs of twins, but it is not so marked. (2) The significance of the correlation coefficients moved by means of the β-distribution is verified by the construction of confidence interval, from whose not a one reaches zero. (3) The difference between $\hat{\varrho}_I$ and $\hat{\varrho}_F$ is, as a rule, higher in boys than in girls, which will be reflected in the heritability estimate (see below).

TABLE 1

Sums of squares and corrected mean for monozygotic and dizygotic twins

Character	Sum of squares within pairs (W)				Sum of squares between pairs (B)				Corected mean value			
	EZ		ZZ		EZ		ZZ		EZ		ZZ	
	♀♀	♂♂	♀♀	♂♂	♀♀	♂♂	♀♀	♂♂	♀♀	♂♂	♀♀	♂♂
1	22.055	41.135	484.249	436.154	626.270	1362.102	4008.690	2682.763	—3.189	—1.353	—1.765	—1.143
2	31.815	11.430	625.319	359.409	273.554	432.239	2100.511	1502.236	—3.154	—2.669	—1.862	—1.536
3	16.600	20.865	205.685	192.405	106.721	245.433	1139.170	699.497	—1.338	—1.431	—1.010	—0.700
4	3.210	4.780	77.920	71.635	27.972	78.109	259.359	196.076	—0.614	—0.928	—0.308	—0.480
5	2.950	3.515	74.270	52.890	20.943	50.720	209.755	137.080	0.099	—0.087	0.313	—0.195
6	3.330	1.775	40.490	46.005	29.406	59.500	190.778	151.206	—0.934	—0.685	—0.468	—0.430
7	19.125	24.000	374.645	293.625	278.348	367.482	1656.035	1458.407	—3.943	—3.409	—2.932	—2.571
8	47.250	30.375	500.000	315.000	452.665	403.635	1730.726	1952.940	—6.886	—6.797	—6.582	—4.323
9	56.500	37.500	860.500	1009.500	811.565	1174.277	4204.734	4143.754	—0.321	—1.350	—0.872	—2.473
10	81.000	89.000	976.500	1005.500	397.487	943.099	4018.202	3995.625	—2.479	—2.225	—3.268	—2.050
11	31.500	82.500	701.500	573.000	742.503	701.526	5669.555	1706.633	3.864	2.981	3.407	—5.089
12	38.500	78.500	971.000	724.000	405.618	792.036	3573.289	2262.555	0.307	2.544	1.912	1.280
13	51.000	25.500	409.625	398.000	290.595	304.729	1136.109	1076.984	2.732	4.178	2.749	4.582
14	23.000	22.500	151.125	177.625	88.077	179.822	437.300	425.355	—0.275	—0.141	0.312	0.480

TABLE 2

Estimates of the strength of linkage in monozygotic and dizygotic pairs of girls

Character	$\hat{\varrho}_I$	$\frac{1-\hat{\varrho}_I}{2}$	$\hat{\varrho}_F$	$\frac{1-\hat{\varrho}_F}{2}$	$\hat{\varrho}_I - \hat{\varrho}_F$
1	0.932	0.034	0.784	0.108	0.148
2	0.792	0.104	0.541	0.229	0.251
3	0.731	0.135	0.694	0.153	0.037
4	0.794	0.103	0.538	0.231	0.256
5	0.753	0.123	0.477	0.261	0.276
6	0.979	0.102	0.650	0.175	0.147
7	0.871	0.064	0.631	0.185	0.240
8	0.811	0.095	0.552	0.224	0.259
9	0.870	0.065	0.660	0.170	0.210
10	0.661	0.169	0.609	0.196	0.052
11	0.919	0.041	0.780	0.110	0.139
12	0.827	0.087	0.573	0.214	0.254
13	0.701	0.149	0.470	0.265	0.231
14	0.586	0.207	0.486	0.257	0.100
	n = 17		n = 68		

TABLE 3

Estimates of the strength of linkage in monozygotic and dizygotic pairs of boys

Character	$\hat{\varrho}_I$	$\frac{1-\hat{\varrho}_I}{2}$	$\hat{\varrho}_F$	$\frac{1-\hat{\varrho}_F}{2}$	$\hat{\varrho}_I - \hat{\varrho}_F$
1	0.941	0.029	0.720	0.140	0.221
2	0.948	0.026	0.614	0.193	0.334
3	0.843	0.078	0.569	0.216	0.274
4	0.885	0.058	0.465	0.268	0.420
5	0.870	0.065	0.443	0.278	0.427
6	0.942	0.029	0.533	0.233	0.409
7	0.877	0.061	0.665	0.168	0.212
8	0.860	0.070	0.722	0.139	0.138
9	0.938	0.031	0.608	0.196	0.330
10	0.828	0.086	0.598	0.201	0.230
11	0.790	0.105	0.497	0.251	0.293
12	0.778	0.111	0.515	0.242	0.263
13	0.846	0.077	0.460	0.270	0.386
14	0.778	0.111	0.411	0.295	0.367
	n = 16		n = 64		

TABLE 4

Estimation of some components of variance in monozygotic and dizygotic twins

Character	monozygotic twins					dizygotic twins				
	$\hat{\sigma}^2$	$\hat{\sigma}^2_{es}$	$\hat{\sigma}^2$	$\sigma^2_{es+3/4}\hat{\sigma}^2_C$	$\dot{\sigma}^2_C$	$\hat{\sigma}^2$	$\hat{\sigma}^2_{es}$	$\dot{\sigma}^2$	$\hat{\sigma}^2_{es+3/4}\hat{\sigma}^2_C$	$\hat{\sigma}^2_C$
1	20.2196	1.297	33.476	7.121	7.765	46.689	2.571	24.699	6.659	5.451
2	9.4843	1.871	20.273	9.196	9.767	17.765	0.714	14.730	5.616	6.536
3	3.8232	0.976	10.014	3.025	2.732	8.833	1.304	7.055	3.006	2.269
4	0.9685	0.189	2.508	1.146	1.276	2.753	0.299	2.116	1.119	1.093
5	0.7412	0.174	2.111	1.092	1.224	1.801	0.220	1.501	0.826	0.808
6	1.0169	0.196	1.721	0.595	0.532	2.039	0.111	1.559	0.719	0.811
7	9.2608	1.125	15.113	5.509	5.845	12.999	1.500	13.869	4.588	4.117
8	15.5355	2.779	16.592	7.353	6.099	14.404	1.898	17.960	4.922	4.032
9	27.0232	3.324	37.706	12.654	12.440	40.314	2.344	40.774	15.773	17.905
10	14.8038	4.794	37.167	14.360	6.392	34.218	5.563	39.567	15.711	13.531
11	24.1297	1.853	47.468	10.316	11.284	25.962	5.156	18.022	8.953	5.063
12	13.8079	2.265	33.806	14.279	16.019	16.875	4.280	23.613	11.312	9.376
13	10.5811	3.000	11.490	6.239	4.319	10.955	1.594	11.657	6.219	6.167
14	3.6642	1.353	4.375	2.222	1.159	6.697	1.406	4.763	2.775	1.825

TABLE 5 *Heritability estimate in girls and boys*

Character	♀♀		♂♂	
	h^2 (I)	h^2 (II)	h^2 (I)	h^2 (II)
1	0.197	0.8179	0.295	0.6139
2	0.335	0.7965	0.445	0.8729
3	0.049	0.6774	0.365	0.5662
4	0.341	0.8351	0.560	0.7328
5	0.368	0.8406	0.569	0.7336
6	0.196	0.6706	0.545	0.8456
7	0.320	0.7958	0.283	0.6731
8	0.345	0.6220	0.184	0.6144
9	0.280	0,7373	0.440	0.8514
10	0.069	0.6662	0.307	0.6459
11	0.185	0.8204	0.391	0.4241
12	0.339	0.8414	0.351	0.6216
13	0.308	0.5192	0.515	0.7372
14	0.133	0.3911	0.489	0.4933

$h^2 \text{ (I)} = 4/3(\varrho_I - \varrho_F)$

$$h^2 \text{ (II)} = \frac{s_d^2 - s_m^2}{s_d^2} = \frac{\frac{W_F}{n_F} - \frac{W_I}{n_I}}{\frac{W_F}{n_F}}$$

The above model enabled also estimates of some components of the variation and total variation σ^2, as given in *Tab. 4*. The test of agreement of total variation $\hat{\sigma}^2$ for monozygotic and dizygotic twins was not carried out.

Coefficient of heritability in the breadther sense of the word (or genetic determination of the character σ_G^2/σ^2) is estimated according to our model from the difference ϱ_I and ϱ_F end it is marked as h^2 (I). In *Tab. 5*, where it is stated, it can be seen that the values of h^2 (I) are substantially (sometimes even by orders) lower than the values of h^2 (II) which were obtained in way current in literature according to the formula

$$h^2 = \frac{s_d^2 - s_m^2}{s_d^2} \tag{15}$$

where $s_d^2 = \frac{W_F}{n_F}$ is the intrapair variance of dizygotic twins of the same sex and $s_m^2 = \frac{W_I}{n_I}$ is the intrapair variance of monozygotic twins (Nakata et al. 1973).

Before we deal with this difference following from different interpretation it is necessary to mention the fact that the valus of h^2 (I) were always higher in boys than in girls. The greatest share of the genetic component appears in the breadth proportions of the trunk: biacromial diameter (4), biiliocristal diameter (5), and bitrochanter diameter (6), in the face it was nose breadth (14). In all those characters the values of h^2 (I) exceeded the value of 0.5. As for girls, the values of h^2 (I) for the individual characters fell deep below the value of 0.5, universally within the range of 0.1 and 0.3.

The differences observed between h^2 (I) and h^2 (II) are explained above all by the fact that by the application of formula (II) s_d^2 is found in the denominator, which magnitude is not equivalent to σ^2 but, according to formula (10) it represents only the estimate $\sigma_{es}^2 + 3/4\sigma_G$. Thus the value of the denominator is substantially lowered on the value of σ_{ec}^2 which, as shown in *Tab. 4*, is very essential in most of the characters. This method, of course, results in the overestimation of the share of genotype in creating the individual characters where, according to our results, it is rather the influence of common environment that makes itself felt to a decisive extent. Therefore it is necessary to look at the hitherto high estimates of the share of heritability very carefully.

Briefly it can be said that the genetic component of variability manifested itself mostly in those characters by which the breadth proportions of the body are characterised and, to a certain extend, also body weight. In the remaining characters, such as stature, etc., which are traditionally said to be significantly influenced by the genetic component, the determining component proves to be the common environment. Generally a high value of the correlation coefficient need not result in a high value of heritability, as shown by character No. 1 (stature).

According to the results of our investigation, another perspective trend of processing the material of twins appears to be above all the appliction of of multivariate analysis (Nakata et al. 1974 a, b, Vandenberg 1970, 1971). These very methods seem to be capable of leading to possible revelation of a factor or group of factors (e.g., the factor of stature, the factor of breadth or of valume, etc.,) acting in the same direction on some groups of characters a we could observe in the course of our work.

SUMMARY

For reasons stated in the introduction of the present paper it is no genitable to use the conventional methods for the evaluation of the linkage of relation between pairs of twins. In this paper a new model was, therefore, suggested which is based on the sample intraclass correlation coefficient, and which was verified on a set of twins (EZ ♂♂ 16, EZ ♀♀ 17, ZZ ♂♂ 64, ZZ ♀♀ 68) originating from the South Moravian Region.

In comparing these two models considerable differences were found in the results obtained. If the coefficient of heritability (h^2) of most of the characters estimated by the conventional method was, on the whole, high (in monozygotic twins it varied about 0.8), then, on the other hand, according to the newly suggested model it was substantially lower. In the discussion it is stated that the conventional approach miss the influence of common environment which, of course, results in the overestimation of the genetic component of variability.

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