Commentary on "Are intelligence differences hereditarily transmitted?" (Pierre Roubertoux and Christiane Capron)

ON THE ALLEGED INDEPENDENCE OF VARIANCE COMPONENTS AND GROUP DIFFERENCES

Eric Turkheimer

University of Virginia, Department of Psychology
Gilmer Hall, Charlottesville, VA 22903-2477, U.S.A.
E-mail: ENT3C@VIRGINIA.EDU

I will focus my commentary on two related themes of the target article. The authors contend that the contribution of genetic factors is on the one hand "not disputable" (p. 585), but on the other hand not convincingly quantifiable. Moreover, they assert that two aspects of genetic analysis -- partitioning of phenotypic variance and explanation of mean differences between groups -- are independent. The second claim, I will show, is true only in a very narrow sense. An examination of the fundamental relations underlying both variance partitioning and mean differences leads to suggestions about how the indisputable contribution of genetic factors might be better quantified.

Consider first a strictly algebraic example. Suppose a quantity $Y$ is completely determined (i.e., no error and no interaction) by two causes, $X_1$ and $X_2$, according to the unstandardized regression equation:

$$ Y = b_1 X_1 + b_2 X_2 + I $$

(1)

where $I$ is a regression intercept.

Suppose two experiments are conducted to elucidate this relationship. In the first, the object is to partition the variance of $Y$ into two independent parts attributable to $X_1$ and $X_2$. These proportions are equal to the squares of the
standardized coefficients corresponding to $b_1$ and $b_2$ in Equation 1, which are determined by multiplying the unstandardized coefficients by the ratio of the variance of $Y$ to that of $X_1$ and $X_2$, respectively:

$$
\hat{b}_1^2 = \frac{\hat{b}_1}{\hat{b}_1} \left( \frac{s_Y^2}{s_{X_1}^2} \right); \quad \hat{b}_2^2 = \frac{\hat{b}_2}{\hat{b}_2} \left( \frac{s_Y^2}{s_{X_2}^2} \right)
$$

(2)

The object of the second experiment is to compare the mean $Y$ values of two groups exposed to different levels of $X_1$ and $X_2$. In two groups A and B, the mean value of $Y$ will equal,

$$
\bar{Y}_A = b_1 \bar{X}_{1A} + b_2 \bar{X}_{2A} + I; \quad \bar{Y}_B = b_1 \bar{X}_{1B} + b_2 \bar{X}_{2B} + I
$$

(3)

so,

$$
(\bar{Y}_A - \bar{Y}_B) = b_1 (\bar{X}_{1A} - \bar{X}_{1B}) + b_2 (\bar{X}_{2A} - \bar{X}_{2B})
$$

(4)

A comparison of Equations 2 and 4 demonstrates that the variance components and the mean differences share one determinant: the unstandardized regression coefficients $b_1$ and $b_2$, which are the quantities both studies were designed to estimate, and each has a unique determinant. The proportion of variance attributable to $X_1$ and $X_2$ is function of the magnitude of the variances of $X_1$ and $X_2$; the mean differences in $Y$ between groups A and B is a function of the magnitude of the group differences in the mean of $X_1$ and $X_2$. Note that the common determinants are given by the hypothetical scientific law in Equation 1, while the unique determinants are expected to vary from study to study.

Figure 1. Intragroup difference implies positive slope of $T$ on environment.
Figure 1 is a slightly rearranged version of Roubertoux and Capron’s Figure 2. Notice that the difference in trait T between the two groups of twins implies a positive slope of the regression of T on the environment. Our Figure 2 is another rearrangement of Roubertoux and Capron’s Figure 2, from a genetic perspective. The fact that the correlation within groups is 1.0 implies that the regression of T on genotype also has a positive slope. These two slopes are completely independent of the variance of genotype or the amount of environmental difference between the groups.

Figure 2. Correlation of 1.0 within groups implies positive slope of T on genotype.

Figure 3 combines Figures 1 and 2 above. The relationship between genotype, environment, and T is represented as a response surface. Each point on the plane represents the expected value of T for a particular combination of genotype and environment, i.e.,

\[ T = b_1 (GENOTYPE) + b_2 (ENVIRONMENT) + R + I \]  

where R is a residual variance and I is a regression intercept.

In genetics, the response surface relating genotype, environment, and a phenotype is called a reaction norm (Dobzhansky, 1955; Gottesman, 1963; Turkheimer & Gottesman, in press). Although restriction of the variance of genotype or environment in a particular study limits the proportion of the phenotypic variance that can be explained, the slopes of the reaction norm, as estimated by the unstandardized regression weights, are not affected. The reaction norm, rather than variance components or mean differences, is the appropriate object of analysis in genotype-environment research.

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1. The standard error of the estimates (but not their expected value) does increase as the variance of a predictor approaches zero. If there is zero variance for a predictor, the slope cannot be estimated. Zero variance is unlikely in actual data.
In the "intragroup" described in the target article (p. 586), it would be misleading to reach exclusively genetic conclusions simply because the genetic variance happens to be greater than the environmental variance. Instead, one could conclude in terms of the reaction norm, as follows: "Each increase of 1 point in genotype resulted in an increase of x points in T; each increase of 1 point in environment resulted in an increase of y points in T; because of the restriction of environmental variance, little of the variation in T was explained by the environment." Conversely, in the "intergroup" study, it would be a mistake to interpret the large mean difference between the groups as evidence for an exclusively environmental effect. Rather, one could conclude, "Each increase of 1 point in genotype resulted in an increase of x [The same x as in the intragroup study!] points in T; each increase of 1 point in environment resulted in an increase of y points in T; the mean environments of the two groups differed by 12.5 points, so the mean difference in T was 12.5y."

Roubertoux and Capron are correct when they suggest that heritability is not a particularly useful measure of genetic effects in natural populations. Their confidence in the mean difference analyses of Schiff and his colleagues (e.g., Schiff & Lewontin, 1986) and Capron and Duyne (1989) is misplaced, however. Analyses of differences between groups share all of the interpretive complexities of heritabilities, in that they confound the important effect (the slope of phenotypes on the environment) with local concerns (the degree of environmental difference between the groups being compared). As I have shown elsewhere (Turkheimer, submitted), when the data from the French adoption studies are reanalyzed in terms of unstandardized coefficients, the results, while...
still encouraging, are not nearly as dramatic as the large mean differences might lead one to believe.

High heritabilities do not preclude successful environmental interventions. The reason this is true is not that means and variance components are independent in terms of their causes, but because high heritabilities can result if genetic variance is considerably greater than environmental variance, as may often be the case in adoption studies. If high heritabilities need not be a concern for the environmentally-minded, small intragroup relationships between the environment and the trait of interest ought to be. Typically, even studies that demonstrate mean differences which appear to be attributable to the environment are unable to demonstrate intragroup relations between environment and phenotype if genetic effects are properly controlled (e.g., Skodak & Skeels, 1949; see Turkheimer, submitted, for an intragroup analysis of Schiff et al.).

I do not wish to join the authors of the target article (and, to be sure, many geneticists) in prolonging the turf war between genes and environment. Both genes and environment affect IQ; both kinds of effects are very difficult to measure; and the difficulty of measuring something is not evidence that it does not exist. Abandoning heritability and naive interpretations of mean differences between groups reared in contrasting environments would be a step in the right direction. Both of these outmoded methods of analysis could easily be replaced with unstandardized analyses of the type that have been very briefly described here. Although a great many complexities would remain, unstandardized analyses would at least express within and between group relationships on the same scale, thus establishing some common ground for future discussions about nature and nurture.

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