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The application of heritabilities in personnel selection –

A comment on Velden

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More than 30 years ago, studying for my doctorate in human behavioral genetics, I came to the same conclusions as Velden and for exactly the same reasons (in retrospect, Weiss, 1986). The biometrical doctrine seeks to measure all the variation in a characteristic and to partition the differences observed into fractions (variances, heritabilities) ascribable to the effects of genetic and environmental factors. The biometrical paradigm asserts that continuous variation implies the determination of characters by many genes with small effects. However, the usual notion of small and additive effects of many genes for polygenic inheritance is violated by the hierarchical nature of biochemical conversions in metabolic pathways and needs to be replaced by Mendelian molecular genetics (Weiss, 1995, 2000).

Starting in 1974, in the former East Germany, I became involved in basic research for the selection of top athletes. Selective breeding was not the aim, but we had in personnel selection the task of long range prediction for different specialities. The problem was especially difficult, when we had to select children at the age of 5 or 10, for example, and we had to predict their final stature, arm length, and achievement in the long jump and endurance running (Weiss, 1979a), which are of importance in both athletics and ice skating (or to predict IQ, which is of importance for team players) In effect we were trying to select for sports for which ten years and more of training is required through childhood and youth children in order to reach top performance and Olympic gold standard. Ideally we aimed for a single classification battery of measurements and tests which, by means of differential weighting based on the multiple correlations between criterion and predictor variables, would enable us to predict success in each of a variety of specialities. In order to calculate true final scores and to minimize error variance, a second weighting was applied, which maximized the heritability of the battery. Why did we do this and how did we do it?

There exists an analogy between test theory and quantitative genetics. In classical test theory, the following linear model is assumed:

$X = T + E$,

where X is the observed test score of an individual, T is the true score, and E is the error of measurement. In quantitative genetics the following is assumed:

$P = G + E$,

where P is the observed phenotypic value, G is the genotypic value, and E is the environmental deviation (including error of measurement).

Two tests are said to be parallel if they yield identical true scores and if the errors are uncorrelated. The analogous situation in quantitative genetics is the case of monozygotic twins reared in random environments. In such a case, members of the twin pair would have identical genotypical values and environmental deviations would be uncorrelated. From the above model of test theory it follows that

$\mathrm{Var}(X) = \mathrm{Var}(T) + \mathrm{Var}(E)$,

where Var is variance. The proportion of the variance in observed scores owing to variation in true scores is defined as the reliability $p_{xx'}$ of a test X. It may be shown that reliability has the following equivalent forms:

$$p_{xx'} = \frac{\mathrm{Var}(T)}{\mathrm{Var}(X)} = r^2_{xt} = b_{tx} = r_{xx'},$$

where r_{xt} is the correlation between true and observed scores, b_{tx} is the regression of true score, and $r_{xx'}$ is the correlation between performances on parallel forms of a test.

From the model of quantitative genetics it follows that Var (P) = Var (G) + Var (E),

when G and E are uncorrelated (if correlated, see Weiss, 1979b). The proportion of the phenotypic variance due to variation in genotypic values is defined as "heritability in the broad sense" h and has the following equivalent forms:

$$h_{pp'} = \frac{\text{Var (G)}}{\text{Var (P)}} = r^2_{gp} = b_{gp} = r_{pxpx'},$$

where px and px' are measures of members of monozygotic twin pairs. Therefore, test-retest reliability provides an upper-bound-estimate of heritability.

If there is a time interval of one, two, or even ten years between test and retest, we do not speak of test-retest reliability, but of the longitudinal correlation between the two measurements. Evidently, in long range prediction it is better to weight the variables with these longitudinal correlations rather than with the test-retest reliabilities at the starting point of prediction. But longitudinal correlations over ten years can only be measured in longitudinal studies lasting at least this long. Quicker results are often required. From the analogy between test theory and quantitative genetics we can conclude that longitudinal correlation and "heritability in the broad sense" are equivalent expressions for the reliability in the long run. However, heritabilites can be measured immediately, without longitudinal study. In East Germany the total population at age 10 was measured each year, and a representative sample of 3000 twin pairs was drawn in 1974. This basic research was not secret (as were some later applications), but was published in detail (Weiss, 1977).

From the information about heritabilities and the matrix of intercorrelations of the variables for each child, a score of the heritability index I (Weiss, 1980) was calculated:

$I = a_1h_1X_1 + a_2h_2X_2 + \ldots + a_nh_nX_n$, Where $X_1, \ldots, X_n$ are the tested scores, $h_1, \ldots, h_n$ are heritabilities, and $a_1, \ldots, a_n$ are weights depending on the regression of predictor and criterion variables. For different chronological ages the heritabilities are different. By using standardized scores and by standardizing I-scores, we can not only predict relative performance, compared with other individuals, but also absolute performance. Because it was, for example, very important to predict some final values (Weiss, 1979a) as accurately as possible (for example, the height of ice skating pairs, separately for male and female partners, or the IQ of team players), information about the scores of parents (and even sibs) was included in the calculations. From the mid-parent score P (arithmetical mean of the parents) the genotypic value G of a child can be estimated as follows:

$$G = \frac{h_{f1}}{(P - S)} + S,$$

where S is the mean of the sub-population or type, to which the parents belong, and h_{f1} is the heritability calculated from parent-offspring correlations (or the heritability of sib pairs). Also such results can be included in an overall index for personnel selection.

With the breakdown of East bloc countries and their highly sophisticated sports research (Kovár, 1981; Wolanski & Siniarska, 1984), the spirit went back into the bottle and was replaced again by the purely theoretical and quite unfruitful debate (see the citations by Stelzl) about the sense and nonsense of heritability, a debate that has already lasted half of a century.

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