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Comparing evolvabilities: common errors surrounding the use of coefficients of additive genetic variation

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Evolvability, the ability of populations to respond to natural selection, is contingent on the level of additive genetic variation underlying trait expression. Measures of additive genetic variation standardized by the trait mean, CV_A (the coefficient of additive genetic variation) and its square (I_A), are suitable measures of evolvability [1, 2].

CV_A has been used widely to compare patterns of genetic variation. However, the use of the CV_A (or I_A) relies on the correct calculation of this parameter.

We reviewed a sample of quantitative genetic studies to determine the extent to which mistakes in the calculation of CV_A occur in the literature, and their potential consequences.

$$CV_A = \frac{\sqrt{V_A}}{\bar{X}} \qquad \text{(Eq. 1)}$$

$$I_A = \frac{V_A}{\bar{X}^2} \qquad \text{(Eq. 2)}$$

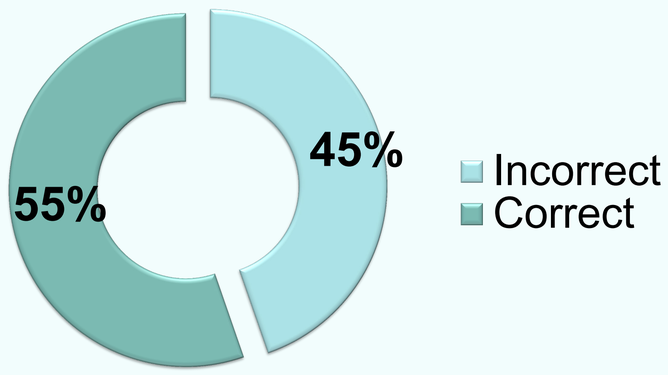
V_A, additive genetic variance
$\bar{X}$, phenotypic mean of the trait

Methods

Literature review. Step 1: Web of Science; articles citing Houle [1] and published in top journals within the Evolutionary Biology, Genetics and Heredity, Multidisciplinary Sciences, and Biology areas, between 2000 and 2010 (n=364 papers). Step 2: Focus on studies employing nested full-sib half-sib designs (n=49 papers). Step 3: Studies reporting CV_A (n=38 papers). Step 4: Recalculation of CV_A.

Results

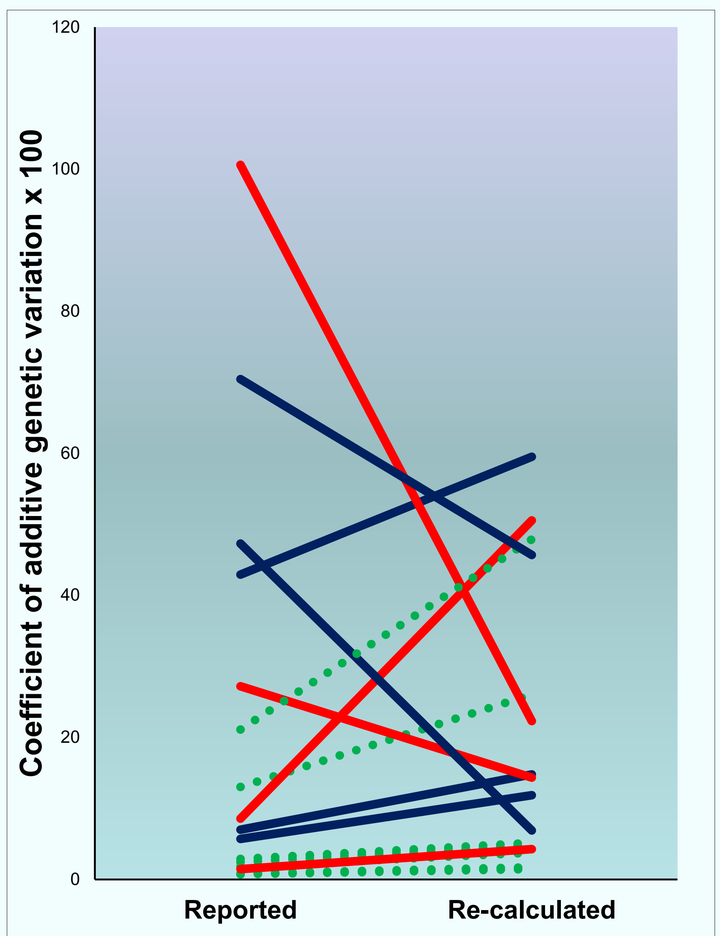
% Studies miscalculating CV_A in our sample



Distribution of most common errors (%)

Problems with scale transformation	29.40%
Undetermined errors	29.40%
23.50%	
Use of the sir variance component (V_{sire}) rather than V_A.	41.20%

Use of the square root of the ratio of additive genetic variance to the trait mean, instead of the square root of the additive genetic variance.



The magnitude of the errors vary to the extent that the actual CV_A value can be grossly over- or underestimated. Red lines: "square root" mistake. Blue lines: undetermined errors. Dotted green lines: use of V_{sire} instead of V_A problem.

Some issues to bear in mind when calculating and interpreting CV_A and I_A

Scaling effects

The interpretation of CV_A and I_A can be complicated by scaling effects [1] . For instance, where higher measurement errors are associated with small means (as one might expect), traits with smaller means will generally have comparatively higher CV_A / I_A.

Comparing traits with different dimensions

Correcting for the effects of dimensionality is not straightforward. In most cases dividing CV_As by their dimensionalities is not an adequate correction [3,5] .

Scale transformation

Only data on ratio and log-interval scales produce meaningful CV_A and I_A. CV_A and I_A have no meaning if they are calculated on transformed scales [2,4,5] .

Discussion

A high proportion of studies reporting CV_A use incorrect methods for calculating this derived statistic and practices that render these coefficients meaningless are frequent

→ Clearly this is likely to severely compromise studies that use such estimates for comparative purposes.

We advocate that researchers adopt the following practices when reporting quantitative genetic data:

1. Consistency in the calculation of CV_A, as in equation 1, and of I_A as in equation 2.
2. CV_A and I_A need to be calculated using the raw (untransformed) scale, and data need to be on ratio or log-interval scale.
3. Transparency in the reporting of methods and detailed reporting of summary statistics, sample sizes and genetic parameters.
4. Where possible, reporting the standard errors of CV_A and I_A. Standard errors of these derived statistics would allow researchers to carry out unbiased meta-analyses of data on evolvabilities.

The adoption of these practices will broaden the scope and value of future investigations on variability in evolvabilities.

References

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