

Online Appendix: Numerical Examples to Reinforce the Argument Against Plausibility of Genetic Explanations of Differences Between Group Means

Despite the logical and methodological points made in Section 2, I can anticipate requests to be shown a realistic case in which, in the absence of an unrealistic environmental factors, the variances of the cultivar and location effects from an AOV (and heritability estimates based on them) are disparate from the variances of measurable genetic and environmental factors. Let me provide two numerical examples that reinforce the critical review of the second line of thinking (section 2.2).

1) Consider Table 3 in Taylor (2006, Online Appendix 1), in which Data Set 1c is divided into two arbitrary groups. The within-cultivar-group by location interaction variance component ($\sigma^2_{c:c,l}$) is comparable to the location variance component (σ^2_l) at the same time as key features for IQ test scores are found, namely, within-cultivar-groups, within-location heritabilities are high and the difference between the means across cultivar groups and locations is substantial in relation to the standard deviation (SD) for the data set as a whole. For data set 1c, the difference between means of 1.0 is 65% of the SD for the data set as a whole; for data set 2 the difference between means is 91% of the SD.

(The values can be rescaled to match the mean and SD of IQ test scores if that helps any readers visualize the results. Subtract 3.0 from each data point, multiply by $15/SD_y$, i.e., 9.84, and add 100—the resulting values for the genetic types or cultivars will look very much like values for IQ test scores.)

2) The first example does not refer to measurable environmental factors for which variances could be calculated. Consider then following variant of model 17 from Taylor (2006; Online Appendix 1, #6):

$$y'_{ijk} = \Pi_r (g_{ir} \epsilon_{jrk}) \quad (2)$$

where g , and e denote genetic and environmental factors (with random noise built into the latter),

$$\gamma_{ir} = 1 \text{ or } 1+\gamma,$$

$$\epsilon_{jrk} = \pm\beta * (1+\text{random number in interval}(-\delta,\delta)) \text{ with } \pm\beta \text{ having equal probability}$$

Table 1 gives an AOV using linear model 3 from Taylor (2006) of one data set generated with $\gamma = .8$, $\beta = .5$, $\delta = 1.25$, $r=1, \dots, 5$, scaled using equation 16a (Taylor 2006, Online Appendix 1, #6) so the data the same mean and SD as data set 1c ($\text{constant}_1 = -2.19$, and $\text{constant}_2 = 3.87$). Table 2 presents the variances of the genetic and environmental factors. The square root of the average within-group or within-location variances is given to allow comparison to the corresponding gap between cultivar-group and location means.

This example may not be typical—there is considerable variation among data sets generated by model 2 even with the same values of the parameters. Yet, there is nothing about model 2 that renders the example unrealistic. This case shows that it is possible to produce high within-cultivar group, within-location heritability values without any systematic difference between the two cultivar groups in the values of the genetic factors (see bottom two rows on the left in table 2). Moreover, the between-location gap for the environmental factors is comparable to the within-location (between replicates) standard deviation (top right two columns in table 2).

Table 1

Data Set 5 divided into two arbitrary groups. (Data sets 1-4 are included in Taylor 2006 and online appendices.)

				Estimates of effects		Variance components & heritability estimates	
Cultivar Group	location	1	2	m	3.0	σ^2_C	0.01 (1%)
	cultivar			l_1	0.78	$\sigma^2_{c:C}$	1.12 (48%)
	A	1	2.1, 1.6 0.8, 2.2	l_2	-0.78	$\sigma^2_{l_1}$	0.61 (26%)
	A			2	6.3, 5.9 2.7, 3.4	C_A	0.12
	B	3	5.3, 3.4 1.8, 2.6	C_B	-0.12	$\sigma^2_{c:C,l}$	0.29 (13%)
	B			4	2.2, 3.6 2.1, 2.1	$c_{1:A}, c_{2:A},$	± 0.37
				$c_{4:B}, c_{3:B}$	± 1.45	h^2 within cultivar group	
				Cl_{A1}, Cl_{B2}	-0.07	within location	0.84
				Cl_{A2}, Cl_{B1}	0.07	h^2 within cultivar group	
				$cl_{i:A,j}$	± 0.34	across both locations	0.49
				$cl_{i:B,j}$	-/+0.69		
				$\epsilon_{k:ij}$	varied		

Table 2

Variances of the genetic and environmental factors underlying Data Set 5.

	envtl factors	Location, replication				square root of mean b/w replication var.	difference b/w location means		
		1,1	1,2	2,1	2,2				
		1	0.03	0.77	0.00			0.01	0.26
2	-0.28	-0.89	-0.61	-0.37	0.23	-0.09			
3	-0.73	-0.44	-0.92	-0.55	0.17	0.15			
4	0.91	0.45	0.64	-0.12	0.29	0.38			
5	0.97	0.91	0.30	0.95	0.23	0.32			
genetic factors									
	1	2	3	4	5				
cultivars	1	1.8	1.8	1	1.8	2.1	1.6	0.8	2.2
	2	1.8	1	1.8	1.8	6.3	5.9	2.7	3.4
	3	1.8	1.8	1	1.8	5.3	3.4	1.8	2.6
	4	1.8	1	1	1	2.2	3.6	2.1	2.1
square root of mean b/w cultivar var.		0.28	0.40	0.28	0.40	0.28			
difference b/w cultivar group means		-0.40	0.00	0.40	0.00	0.40			

References

Taylor PJ (2006) Heritability and Heterogeneity: On the limited relevance of heritability in investigating genetic and environmental factors. *Biological Theory* 1: 150–164.