File S2: analysis of flowering traits of [3]

Our broad-sense heritability estimates differ from those reported in Supplementary table 7 of [3], for the following three reasons. First, the broad-sense heritability estimates in [3] were calculated using the formula

$$\frac{MS(G)}{MS(G)+MS(E)}. \tag{1}$$

Although this quantity may be an adequate criterion to compare heritabilities of traits within the same experiment (as long as they have the same number of replicates), this is a biased estimator of broad-sense-heritability. Since the expectation of $MS(G)$ is $r\sigma_G^2 + \sigma_E^2$, $MS(G)/(MS(G)+MS(E))$ will tend to overestimate heritability. The usual estimator defined in the materials and methods section is also biased, but this bias is usually small, and (in contrast to (1)) tends to zero when the number of genotypes increases ([4], [2]).

Second, broad-sense heritability estimates in [3] were based on more accessions: 189 for LDV and 186 for LD. To allow a direct comparison with mixed model analysis we restricted our analysis to genotyped accessions, excluding 21 accessions for LDV and for 19 LD. This had little impact on heritability estimates.

Third, the analysis of variance in [3] did not include a replicate effect. In our analysis, the mean sums of squares for replicates removes some environmental variance, therefore giving higher estimates than in an analysis without a replicate effect. This however did not compensate for the use of (1); hence our heritability estimates are lower than those reported in [3].