

CORRIGENDUM

Corrigendum to “Coherent synthesis of genomic associations with phenotypes and home environments”

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We discovered an error in our analyses (Lasky, Forester, & Reimherr, 2018). The specific error was in the analysis of enrichment of (a) SNPs associated with G×E for fitness with (b) SNPs associated with G×E for flowering time under experimental warming (Li, Cheng, Spokas, Palmer, & Borevitz, 2014). The error resulted from a failure to convert SNPs from two different versions of the Arabidopsis reference genome assembly: from TAIR8 (used in Li et al., 2014 supplemental materials, which we reanalyzed in our paper) to TAIR9 (used in our analyses of G×E for fitness, Lasky et al., 2018).

We fixed the error, converting the Li et al. (2014) SNPs from TAIR8 to TAIR9 and reanalyzing the enrichments. This reanalysis showed (as in Lasky et al., 2018) that SNPs associated with flowering time response to experimental warming (G×E, Li et al., 2014) were significantly and most strongly enriched in SNPs associated with change in fitness across gradients of growing season minimum

temperatures (Table 1 here, which supersedes the relevant row from Table 2 in Lasky et al., 2018). Additionally, reanalysis showed a weaker, but significant enrichment of flowering time G×E SNPs in SNPs associated with change in fitness across gradients of growing season variability in precipitation. As in Lasky et al. (2018), SNPs associated with change in fitness across gradients of annual aridity or winter cold were not enriched in flowering time G×E SNPs.

In summary, our conclusion that “variants causing flowering time plasticity drive changes in fitness across growing season temperature gradients” (Lasky et al., 2018) is supported by this reanalysis and corrigendum.

DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

TABLE 1 *p*-Values for permutation tests of enrichment for SNPs having significant ($\alpha = .05$) associations with change in flowering time (G × E) in response to warming during growth for Arabidopsis (experiments in Li et al., 2014). We tested for enrichment of signal in the SNPs in the .01 lower tail of *p*-values for SNP × climate associations with relative fitness (four climate variables representing columns here)

	Aridity enrichment	CV grow. seas. prec. enrichment	Min. temp. enrichment	Min. temp. grow. seas. enrichment
Flowering time under warming G×E	0.1026	0.0068	0.1202	0.0030

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REFERENCES

- Lasky, J. R., Forester, B. R., & Reimherr, M. (2018). Coherent synthesis of genomic associations with phenotypes and home environments. *Molecular Ecology Resources*, 18(1), 91–106. <https://doi.org/10.1101/051110>
- Li, Y., Cheng, R., Spokas, K. A., Palmer, A. A., & Borevitz, J. O. (2014). Genetic variation for life history sensitivity to seasonal warming in *Arabidopsis thaliana*. *Genetics*, 196(2), 569–577. <https://doi.org/10.1534/genetics.113.157628>