

CORRIGENDUM

Here, we correct several analytical and clerical errors in our paper titled “Phylogeography of a widespread eastern North American shrub, *Viburnum lantanoides*”.

An error in our sequence handling pipeline caused the SNP dataset used in our population genetic and demographic analyses to retain a non-negligible number of sites that did not conform to the SNP filtering procedure described in our paper (i.e., bi-allelic SNPs with >50% sample coverage and MAF > 0.01). To address this, we generated a new, properly filtered SNP dataset and repeated these analyses. The revised population genetic analyses agree with those reported previously and do not change the conclusions of our study. We have updated Figure 1, Figure 2, Figure 3 [see note below], Appendix S4, Appendix S5, and the relevant text accordingly. The revised demographic analyses do, however, differ from those reported previously. These differences are primarily due to a conversion error, in which our previous estimates of the reference population sizes (N_{ref}) were incorrectly converted from θ by a factor of 4. The revised population sizes are slightly

smaller than our previous estimates, but continue to support much larger population sizes in the southern cluster compared to the northern lineage. However, revised divergence times are shifted forward from ~40,000 to 20,000 ybp. As divergence time estimates were not critical to our conclusions, the updated results do not alter our interpretation of the demographic history of *V. lantanoides*. We have updated Table 1 and the affected text accordingly.

Finally, we have taken this opportunity to correct two clerical errors. In Figure 1A, the correlation coefficient (r) was incorrectly reported as a coefficient of determination (R^2). In Appendix S1, the number of sampled populations was incorrectly reported as 69 rather than the correct number of 70. We have updated Figure 1A, Appendix S1, and the relevant text accordingly.

[Note: Figure 3 (the population phylogeny which is not affected by any of the SNP filtering issues) is also revised to reflect the changes to Appendix S1 (locality data for the populations sampled) and the updated ancestry inferences from the new SNP dataset.