**Appendix 1 – Phylogenetic reconstruction**

We generated a phylogenetic tree for the six milkweed species tested in the experiment by using sequence data from three noncoding chloroplast regions (Agrawal and Fishbein 2008). These sequences were aligned and concatenated in MAFFT v7.427 (Katoh and Standley 2013). We used BEAST v1.10.4 (Suchard *et al.* 2018) to run Bayesian MCMC for 100,000,000 iterations, using a GTR+I+G substituiton model and default priors and with sampling over every 1,000 trees. We used FigTree v 1.4 (Rambaut 2012) to visualize summary trees. We discarded the first 10,000 trees as a burnin and sampled from the remainder to generate a consensus tree using ape v 5.0 (Paradis and Schliep 2019). The resulting consensus tree reflects general patterns of relatedness among sampled taxa and recapitulates the phylogeny in Agrawal and Fishbein (2008) but does not include branch lengths.

**References**

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