

Gene Flow and Admixture in *Clarkia xantiana* subspecies



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Introduction

When subspecies living sympatrically come into contact, gene flow can occur while populations remain distinct. Here, we used a computer model to study the extent of admixture, or incorporation of genetic material from one subspecies into another, in two subspecies of *Clarkia xantiana* flowers: *parviflora*, a largely selfing plant; and *xantiana*, an outcrosser.



Left: *Clarkia xantiana* ssp *xantiana*, an outcrosser.



Right: *Clarkia xantiana* ssp *parviflora*, a selfer.

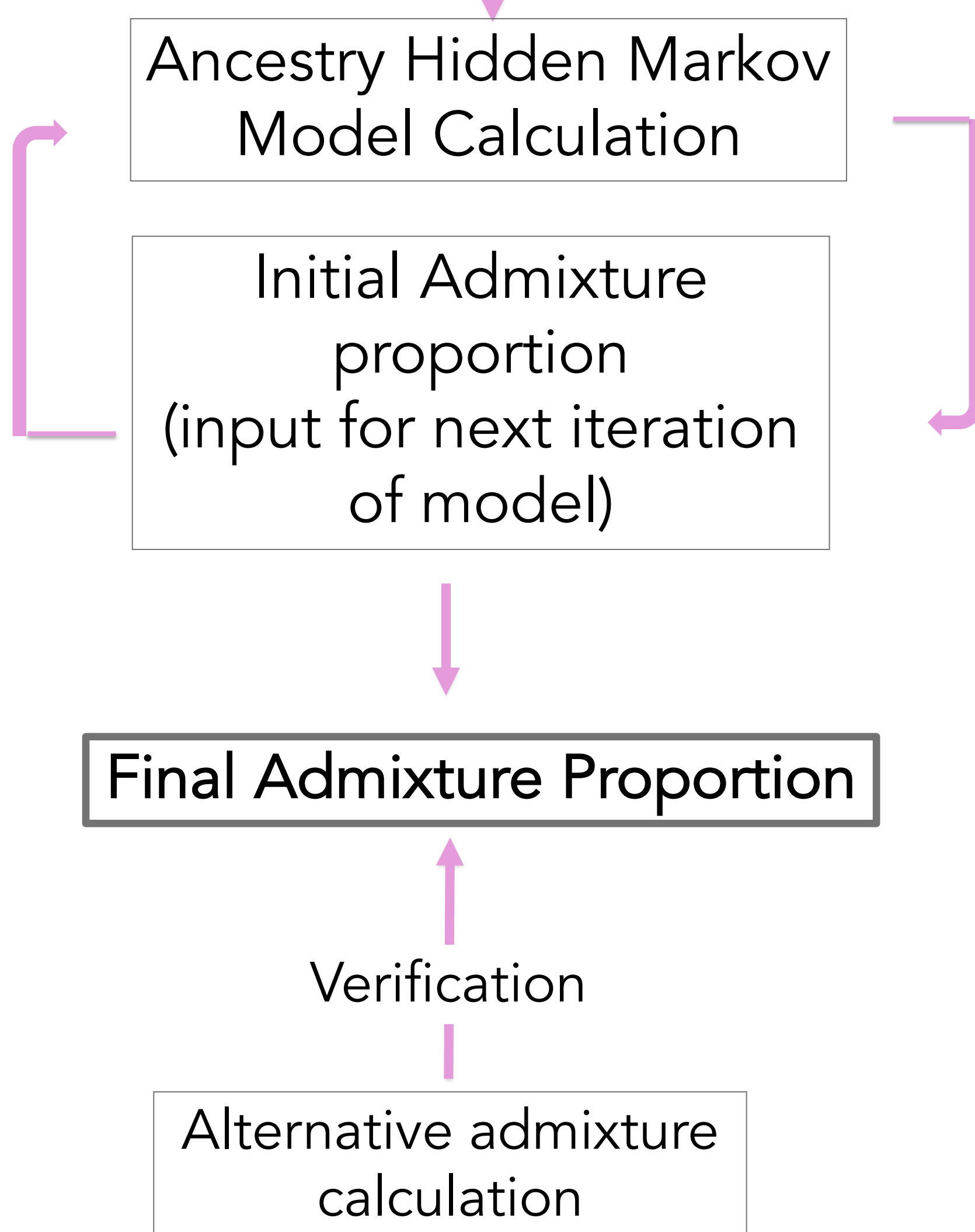
Conclusions

Admixture was significantly different between subspecies. *C.x.xantiana*, the outcrossing species, had higher admixture across all geographic sites than its selfing counterpart *parviflora*. Because outcrossing plants are physically structured to take up pollen from other plants, it's likely that these plants also took up more pollen from other species, in this case the selfing plants: but the reverse was not true, as the structure of selfers is geared mostly towards self-pollination.

Additionally, admixture varied among geographic site, with Site 22 consistently containing plants with higher admixture proportions. This indicates that spatial variation also plays a role in gene flow.

Materials and Methods

C. x. xantiana and *C. x. parviflora* sequencing data: 369 individuals, 3 locations, 77,748 sites



Results

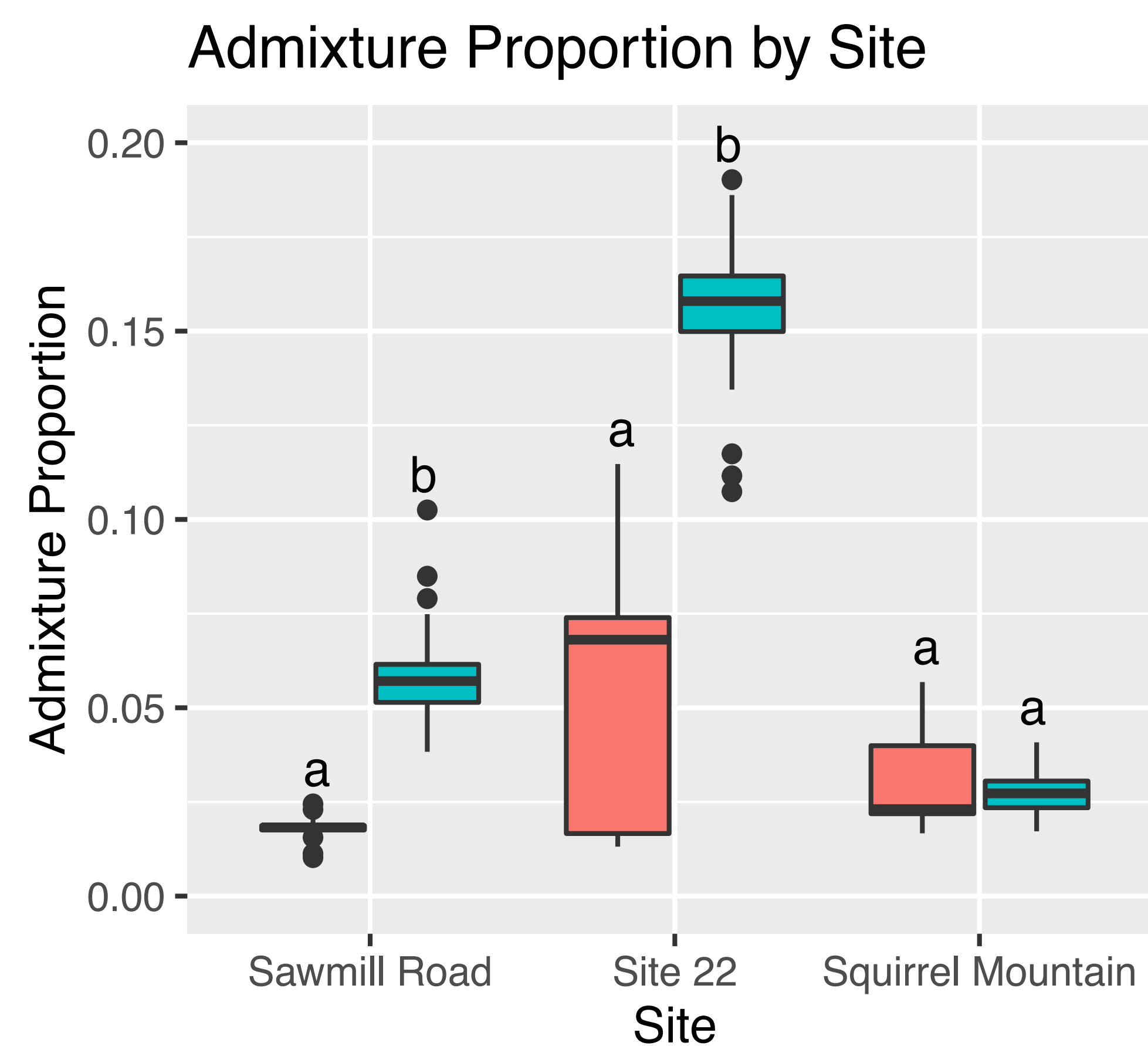


Figure 1: Admixture proportion by geographic site, subdivided by species. Different letters above box plots from the same geographic site indicate a significant difference in admixture proportion using a Tukey test with 5% significance level.

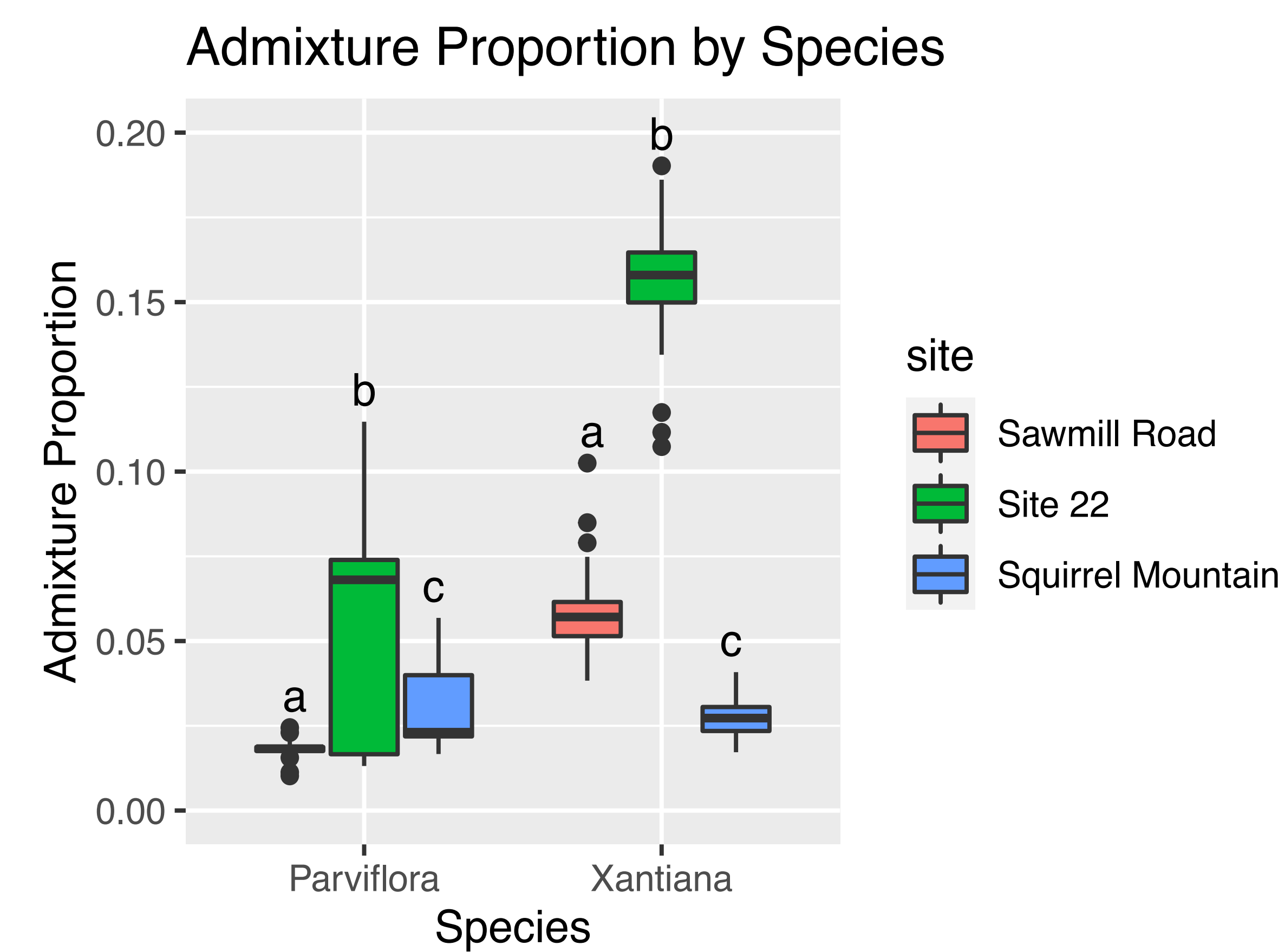


Figure 2: Admixture proportion by species, subdivided by geographic site. Different letters above box plots from the same species indicate a significant difference in admixture proportion using a Tukey test with 5% significance level.

Literature cited

Corbett-Detig, R. and Nielsen, R., 2017. A hidden Markov model approach for simultaneously estimating local ancestry and admixture time using next generation sequence data in samples of arbitrary ploidy. *PLoS genetics*, 13(1), p.e1006529.

Pettengill JB, Moeller DA. Tempo and mode of mating system evolution between incipient *Clarkia* species. *Evolution*. 2012;66(4):1210-1225.

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Future Directions

After finding evidence of admixture between *Clarkia* living in the same area, we are working on making a genetic map of the *Clarkia* genome in order to explore linkage among different genes, as well as investigating association between genes and quantitative traits.