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Summary Sheet
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The Impact of Gene Flow, Pollinators, and Mating System on *Aquilegia coerulea*

Flowers have long been studied in the context of population genetics. *Aquilegia coerulea,* better known as the Rocky Mountain Columbine, is becoming a model for understanding genetic structure and variation because of its evolutionary history. Reproductive isolation due to co-speciation within *Aquilegia* as a whole has led to demonstrated high diversification rates. In addition, the range of *Aquilegia* spreads across the northern hemisphere and there is a high level of morphological diversity among species within the genus. Brunet et al. (2012) investigate four unlinked microsatellite loci in two varieties of *A. coerulea* - var. *pinetorum* (in Utah and Arizona) and var. *coerulea* (in Colorado) - in order to see if the existence of two varieties can be explained by genetic structure. The study utilizes at least three populations of *A. coerulea* from each of four regions: Arizona, Utah, Northwest Colorado, and Central Colorado. After sequencing the four microsatellite loci, Brunet et al. calculates traditional population genetics values such as AMOVA, FST, FIS (inbreeding coefficient), and Dest in addition to using newer methods such as Genetic Clusters using the program Structure, and Population Graphs. If the two varieties of *A. coerulea* truly exist, the values they find in this study should reflect that.

However, most of the values returned by Brunet et al. imply that there is no genetic structure that reflects the existence of two varieties. Average pairwise FST values, migration rates, and Dest are all relatively high between populations of different regions compared to those between populations of the same region. However, all of those values are low for all populations and do not represent significant differentiation between any two regions. Structure and Population Graphs also show similar results. Structure uses bayesian inference to identify genetic clusters in a given dataset. While the program did return distinct genetic clusters, the clusters did not reflect the existence of two varieties; however, the clusters did represent regions relatively well. Finally, Population Graphs showed that there is significant isolation by distance and that similarities in the genetic structure of this species between regions is due not to recent colonization events, but rather due to long distance dispersal, most likely by hawkmoths. Similarly, Population Graphs showed that there is restricted gene flow between some populations in the same region, most likely due to differences in flowering time (based on altitude) and also frequency of fires in these regions. In summary, this shows that variation in *A. coerulea* is likely not represented by genetic structure.

References

Brunet, J., Larson-Rabin, Z. and Stewart, C.M. (2012) ‘The distribution of genetic diversity within and among populations of the Rocky Mountain Columbine: The impact of Gene Flow, Pollinators, and mating system’, International Journal of Plant Sciences, 173(5), pp. 484–494.

Hodges, S.A. (1997) ‘Floral nectar spurs and diversification’, International Journal of Plant Sciences, 158(S6), pp. S81–S88.