

Supplementary Material

Embracing biodiversity: multispecies population genomics of leafless *Bossiaea* species shows novel taxa, population dynamics and conservation strategies

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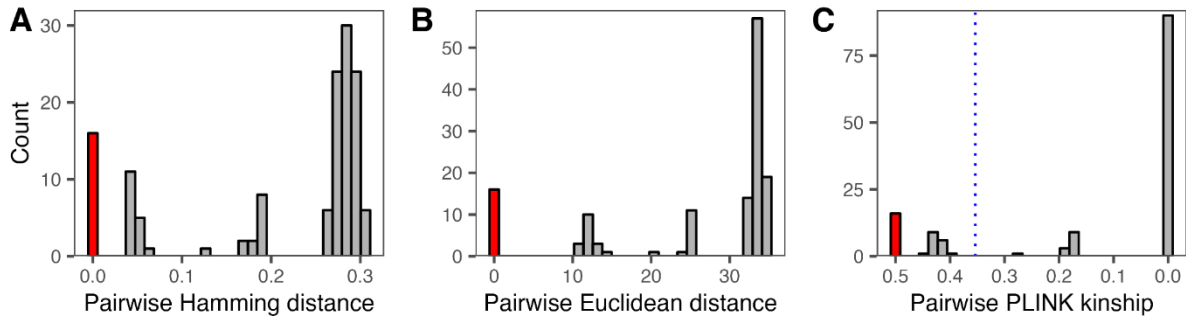


Figure S1. Histograms of (A) Hamming pairwise distance between *B. vombata* individuals as implemented by Amor *et al.* (2020), (B) Euclidean pairwise distance between *B. vombata* individuals, and (C) PLINK pairwise kinship between *B. vombata* individuals. Red bins indicate self-comparison values for each method. All methods used 1359 loci that have MAF>5% and missingness <30% in the *B. vombata* samples. In (C), the blue dotted line indicates our chosen clonality threshold $k > 1 \div (2^{3-2})$. In (A), which corresponds to the Amor *et al.* (2020) method, we observed a distinct difference in the distribution of distance values compared to their results. Specifically, we noticed a clear separation between self-comparison pairwise values and the next highest values. This separation is also evident in both Euclidean distances and the PLINK IBD method. As a result, we have identified a significant degree of clonality within the sites, consistent with the findings of Amor *et al.* However, it's important to note that we have also detected first-degree relationships within the sites, suggesting that not all sites exhibit complete clonality.

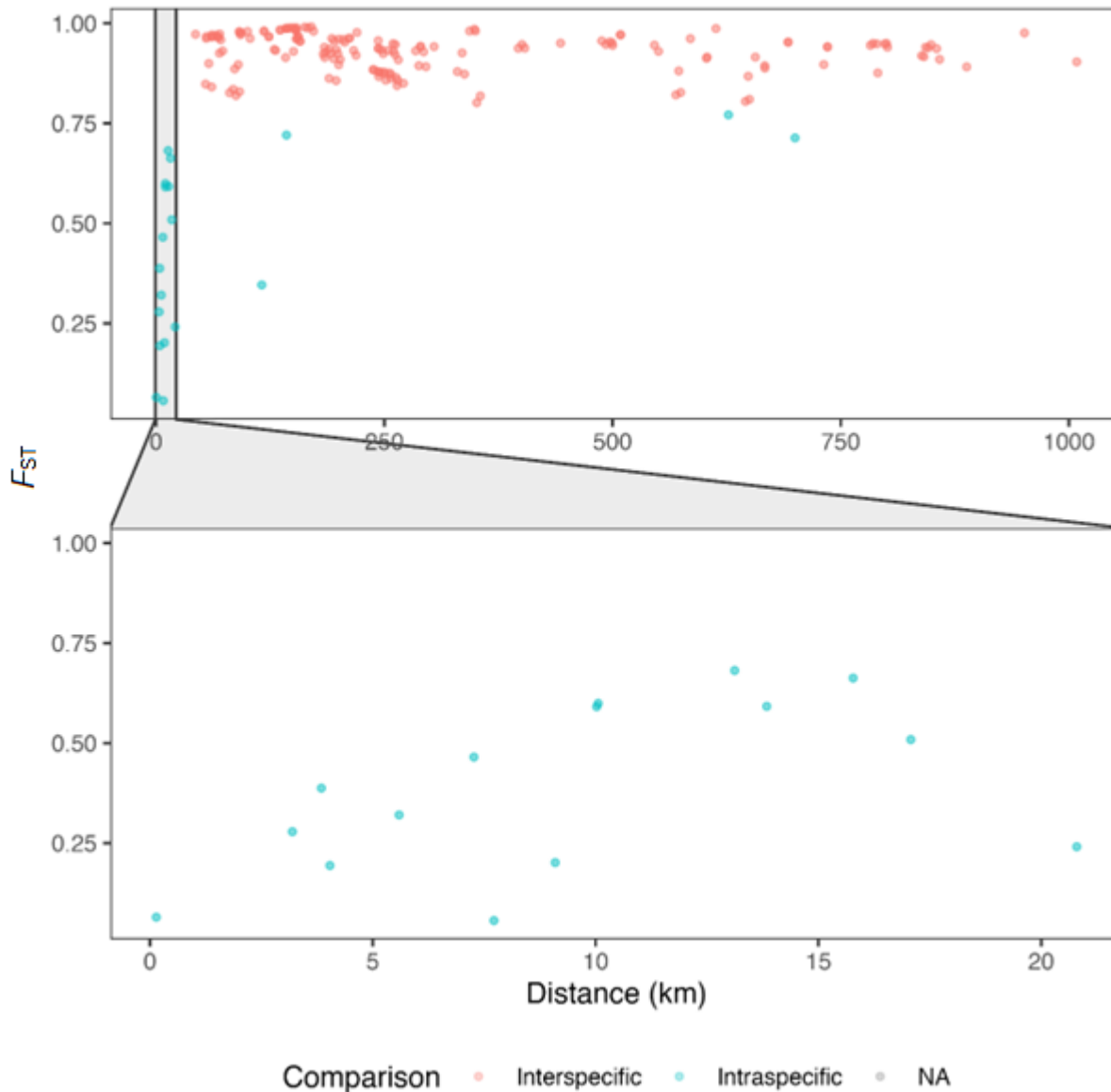


Figure S2. Pairwise F_{ST} across site distances (km). The colouration of pairwise values distinguishes between comparisons of sites belonging to the same species (intraspecific, indicated in blue) and different species (interspecific, indicated in pink). In the initial panel, geographically proximate sites (<25 km) primarily exhibit intraspecific comparisons with some degree of gene flow ($F_{ST} < 0.5$). However, pairwise comparisons between sites separated by over 50 km display diminished gene flow ($F_{ST} > 0.5$), irrespective of species similarity. This suggests that genetic exchange between species becomes limited as geographical distance increases. The second panel provides an expanded view of site distances within the range of 0–25 km. It reveals that F_{ST} occasionally shows lower values at very short distances (<1 km), while generally remaining below 0.5 across the 0–25-km range. This suggests that species within this distance range are still exchanging genetic material to some extent. Mantel statistic using Pearson correlation r is 0.2601, $P = 0.001$.

Reference

Amor MD, Johnson JC, James EA (2020) Identification of clonemates and genetic lineages using next-generation sequencing (ddRADseq) guides conservation of a rare species, *Bossiaea vombata* (Fabaceae). *Perspectives in Plant Ecology, Evolution and Systematics* **45**, 125544. doi:[10.1016/j.ppees.2020.125544](https://doi.org/10.1016/j.ppees.2020.125544)