

Methods

Genetic

Extract DNA

DNA library prep & HybSeq

Clean raw sequencing reads

Hybpiper assembly, gene alignment, trimming

Infer phylogeny

Morphological

Download digitized herbarium sheets of each species

Create model that identifies neotropical and paleotropical images

Model classifies temperate images as neotropical or paleotropical

Environmental

Use online databases to record 50-200 longitude and latitude points for each species

Quantify environment at each point based on bioclimatic variables

Analyze using PCA

Background

Prunus is an economically important genus that includes peaches, plums, and cherries. It has three distinct phylogenetic groups. The solitary and corymbose clades are found in the temperate northern hemisphere while the racemose group is separated into paleotropical, neotropical, and temperate groupings. We do not fully understand the biogeographic history of *Prunus*. While studies have identified the origin of *Prunus* in eastern Asia¹, it is unclear if temperate clades are more closely related to paleotropical or neotropical clades and how this tropical to temperate transition took place.

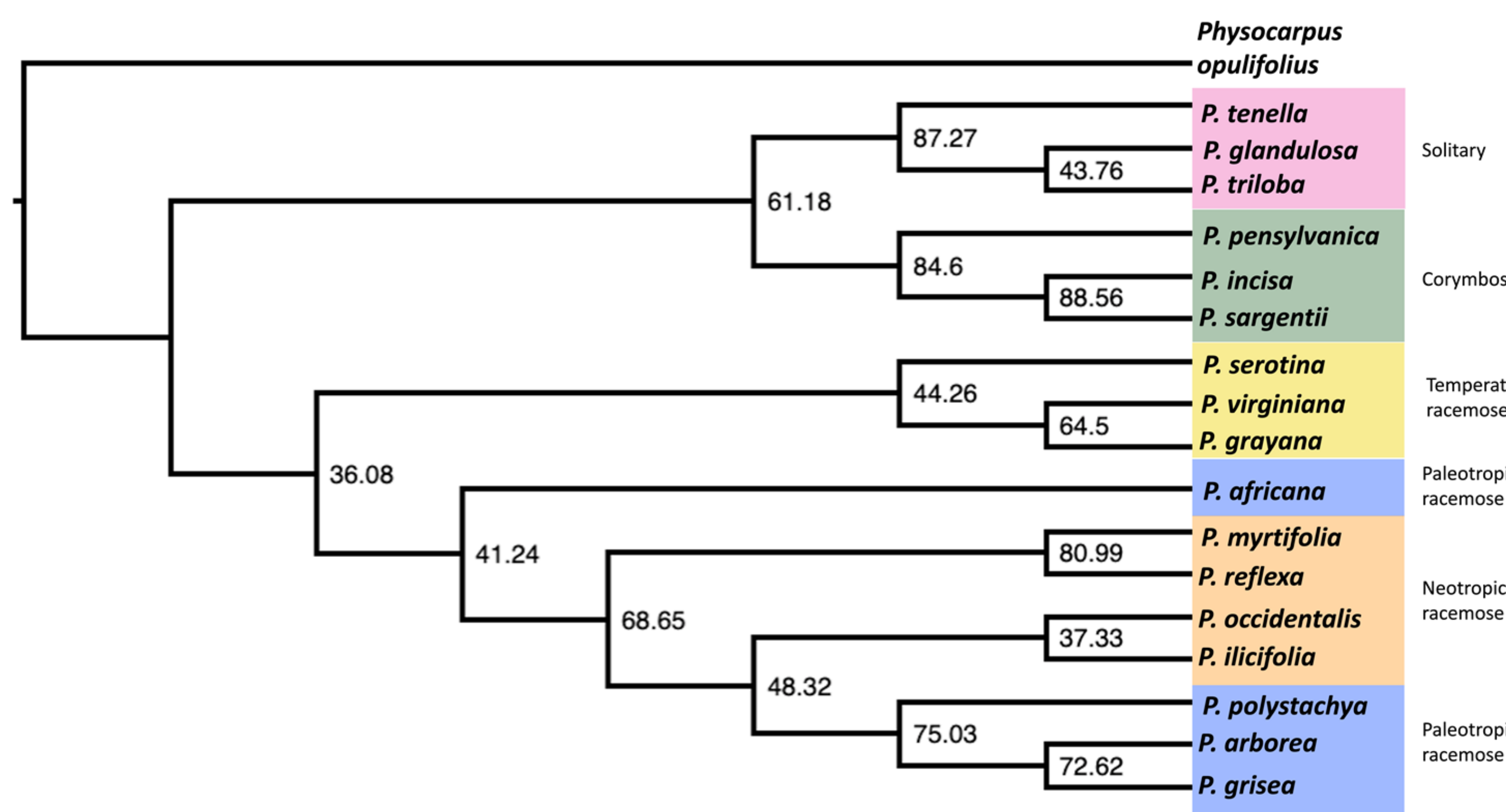


Figure 1: Phylogenetic tree of 18 species constructed from 606 gene trees. Each node is labeled with ASTRAL quartet support values. *Physocarpus opulifolius* is the outgroup.

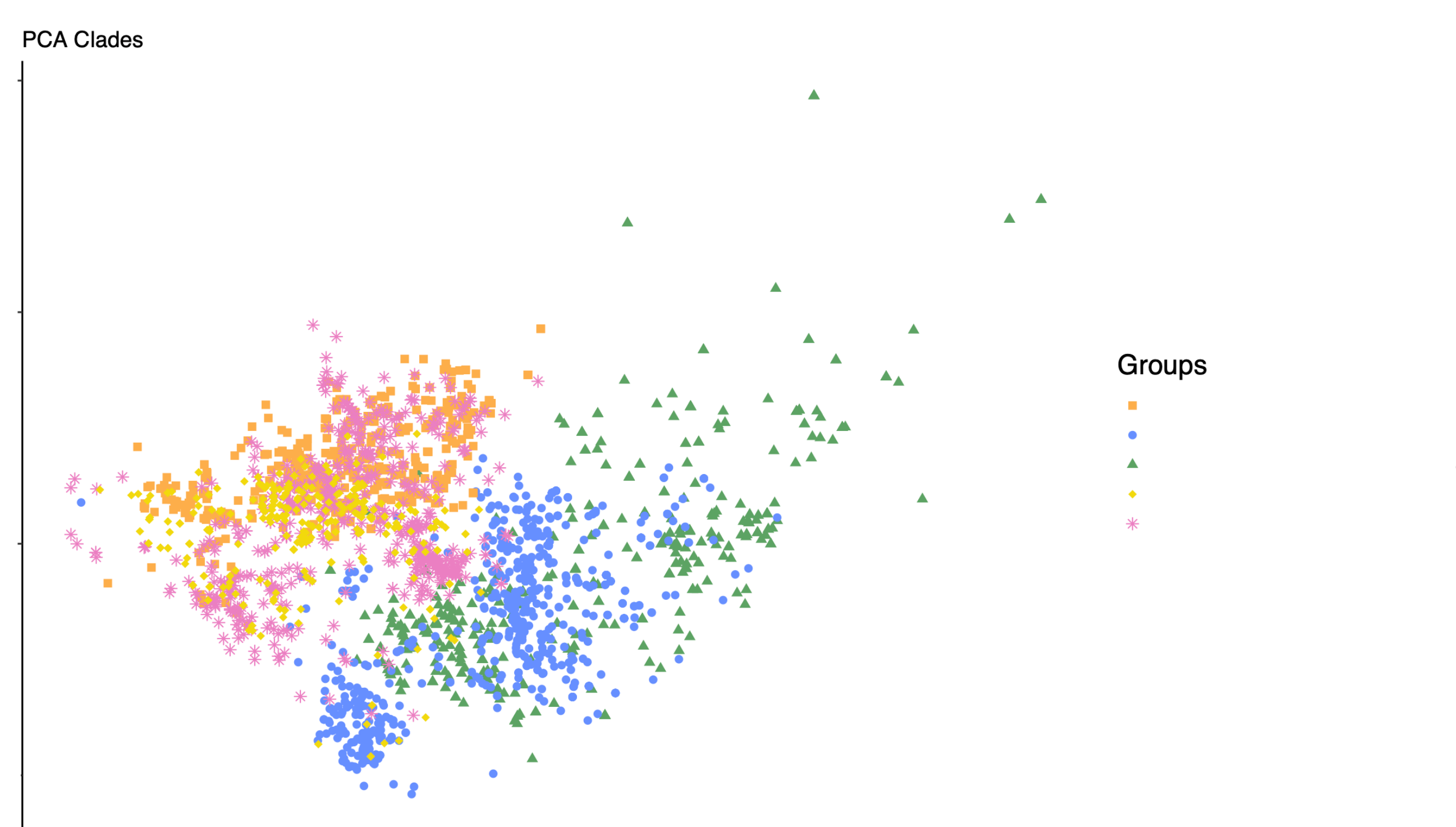


Figure 3: Environmental range of each of the five clades based on principal component analysis (PCA).

Purpose

This study will examine the tropical to temperate transition in the genus *Prunus* through three main objectives:

1. Phylogeny: Construct a phylogenetic tree inferring genetic relationships among seventeen *Prunus* species.
2. Morphology: Use machine learning to determine if nine temperate species are more morphologically similar to paleotropical or neotropical species.
3. Environmental: Compare environmental conditions associated with these nine temperate species to those experienced by paleotropical and neotropical species

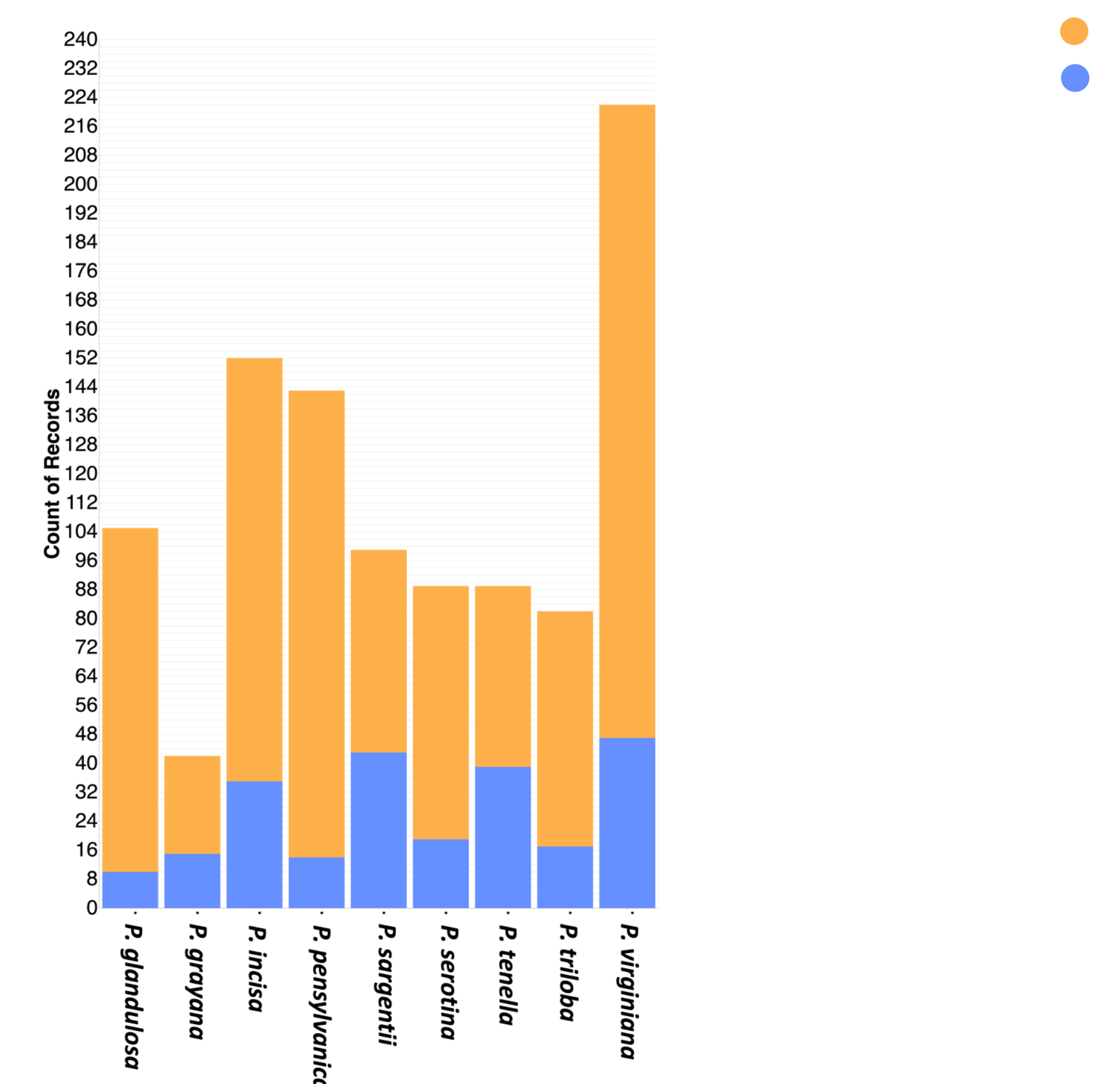


Figure 2: Number of digitized herbarium sheets for each of the temperate species which were classified as paleotropical or neotropical by a convolutional neural network classifier model.

Results and Conclusions

Phylogeny

Nuclear data implies the temperate racemose clade has a more recent common ancestor with the tropical racemose clades than with the corymbose or solitary clades. This node has a low support value of 36.08 (Figure 1). Other studies suggest the temperate racemose clade may group with the solitary and corymbose clade in nuclear phylogenetic trees while grouping with the tropical racemose clades in chloroplast trees⁴. This incongruence is likely due to an ancient hybridization or allopolyploid event.

Morphology

Most herbarium images from temperate species were classified as neotropical by our machine learning model with a 3:1 neotropical to paleotropical prediction ratio. Many of our temperate species are found in North America which could imply these species have a closer relationship to the neotropical clade.

Environment

While there is some overlap in the temperate and tropical environments, broadly the temperate clades form a cluster separate from the tropical cluster. This implies that the temperate species' morphological similarity to neotropical species is not due to shared environmental conditions.

Prunus serotina and plums.
Photo courtesy J. Wen



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Case Study And Future Directions

Figure 4, 5, and 6: PCA graph comparing *P. virginiana*, *P. serotina*, and *P. pennsylvanica* to neotropical and paleotropical species.

- *P. serotina* and *P. virginiana* are morphologically and phylogenetically similar but occupy different environments. Their morphology may be impacted by phylogeny more than environment.
- *P. virginiana* is more closely related to the tropical racemose group than *P. pennsylvanica*, but both occur in similar environmental space. Perhaps *P. virginiana*'s phylogenetic similarity to the tropical racemose group explains its larger geographic range.
- Both comparisons suggest a need for a larger phylogeographic study of *P. virginiana* that investigates its morphological and genetic diversity.

References

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