

# "Ant you cold?": How cuticular hydrocarbon (CHC) genes in ants vary across climate zones

Banyan Brewer<sup>1</sup>, Bradon Coy<sup>1</sup>, Ingrid Groose<sup>1</sup>, Polina Sokolova<sup>1</sup>, M. Fiorta<sup>1</sup>, A. Conde<sup>1</sup>, R. Antalek<sup>1</sup>, A. Auletta<sup>1</sup>, E. Cash<sup>1,2</sup>

1. University of Florida, Entomology & Nematology Dept.

2. University of Florida, Engineering School of Sustainable Infrastructure & Environment (ESSIE)

## Introduction

Ants, among other social insects, utilize cuticular hydrocarbons (CHCs) in intercolonial pheromone communication and kin recognition [1]. CHCs also protect ants from desiccation by creating a hydrophobic barrier around the cuticle [2]. There have been targeted studies investigating how temperature affects genes in other insects, but there is a gap in the research regarding more widespread climatic variation across several ant species [3]. Current literature suggests that both **desaturase (Desat)** and **fatty acid synthase (FAS)** gene families are involved in desiccation resistance and temperature regulation in insects [4, 5]. In a rapidly changing global climate that threatens biodiversity, it is more important than ever to understand how ants survive in their respective environments.

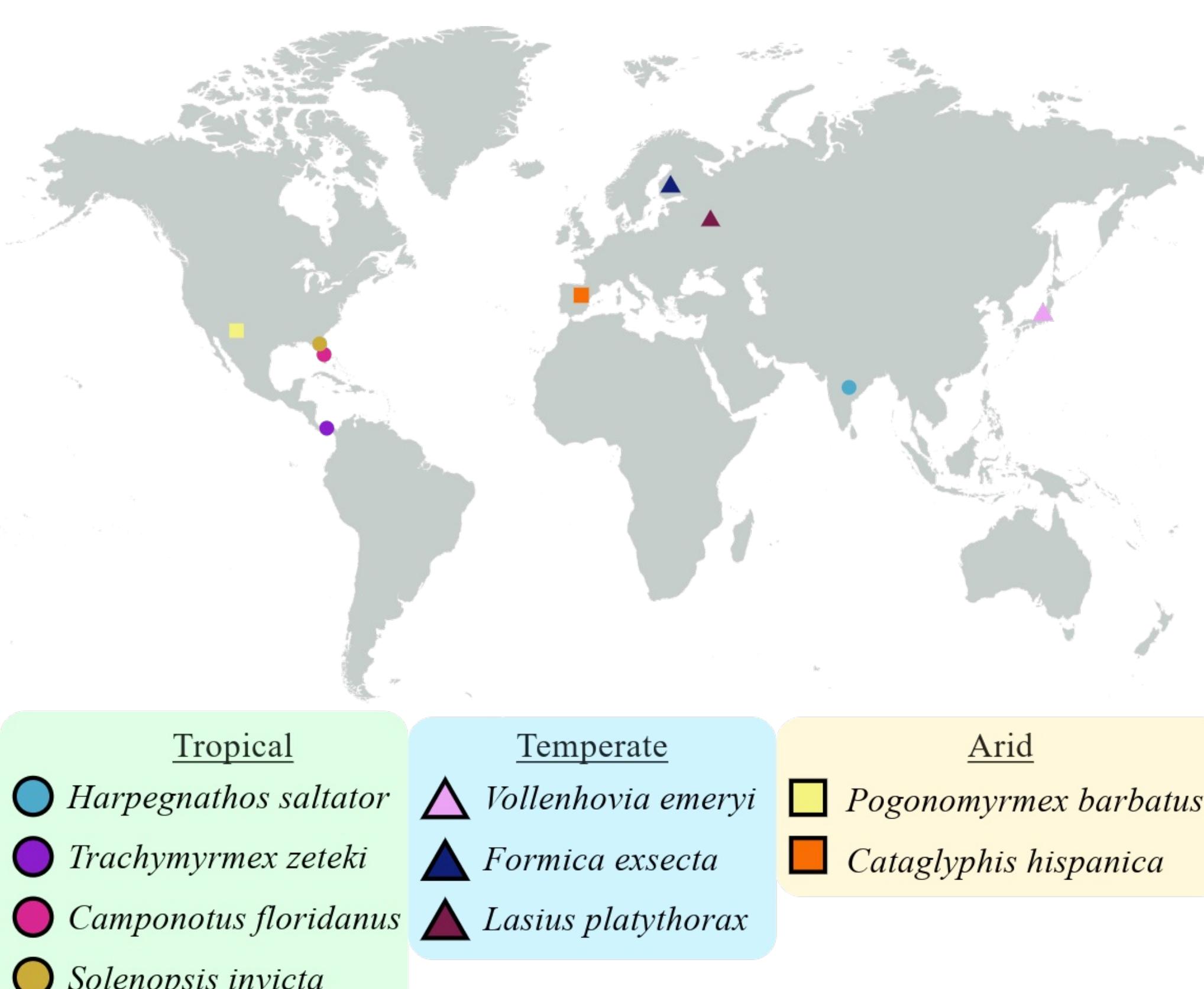


Figure 1: Map of ant genome collection locations

## Objectives & Hypothesis

- Understand how **Desat** and **FAS** genes phylogenetically vary amongst ant species living in temperate, tropical, and arid zones
- We hypothesize that there is a significant effect of **climate** on the quantity of **Desat** and **FAS** genes present in ant species

## Methods

- AntWiki & NCBI Database:** Species ID'd by considering available genomes and geographic distributions
- BLASTp in HiPerGator:** Protein sequences ID'd by comparison to *Drosophila melanogaster* Desat1 and FASN3
- MAFFT:** Conducted multiple sequence alignment and created phylogenetic trees to prune out replicates
- iQTree:** Final trees constructed to visualize results
- Phylogenetic analysis:** Conducted to find conserved gene sequences between species
- R Studio:** ANOVA statistical test used to determine the significance of differing climate groups on gene counts

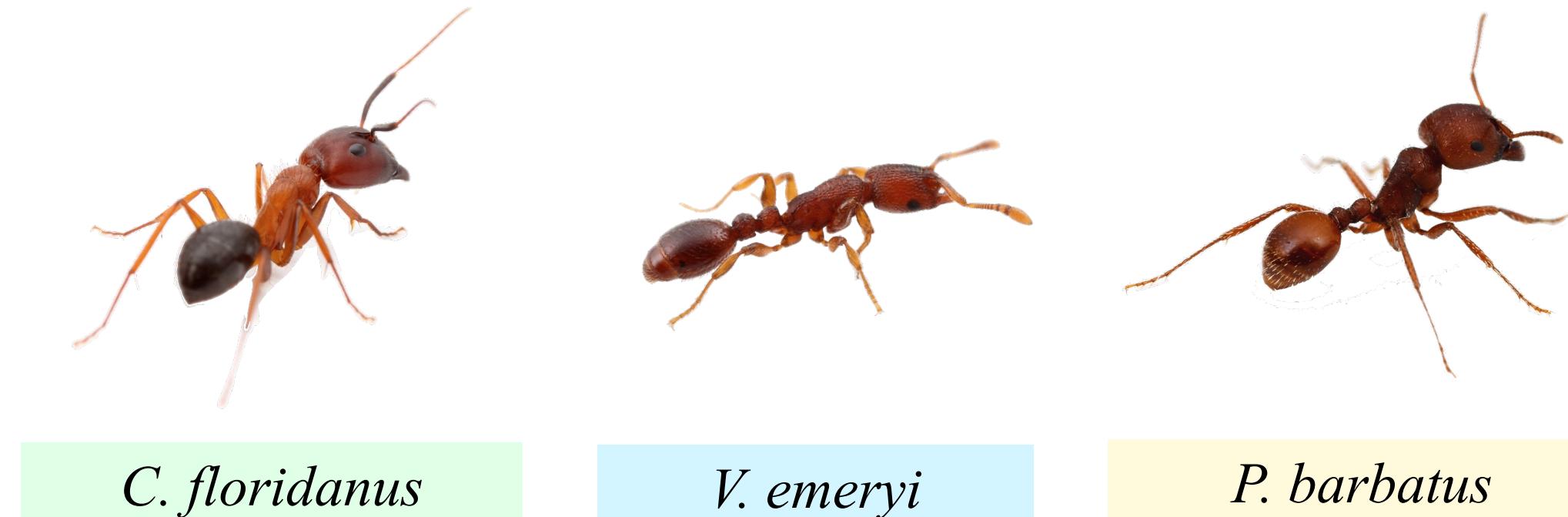


Figure 5: Representative ant species from each climate zone [6, 7, 8]

## Discussion & Future Directions

**Desat:** Gene clades were found to be directly parallel with those described in Helmkampf et al. 2014 [9]. Small expansions in species, namely *H. saltator* and *C. floridanus* coincide with the analogous expansions found in **FAS**.

**FAS:** Expansions in the genes from tropical species could indicate a need for higher amounts of each gene type in high heat, high humidity environments. This is consistent with data supporting the role of **FAS** in synthesizing precursors to CHCs that contribute to desiccation resistance, as described in Moriconi et al. 2019 [4].

Although our results are not statistically significant, the patterns in gene expansion indicate that climate may influence gene expression across species, castes, and developmental stages.

Further research could:

- Conduct analysis with a wider variety of arid species once annotations become available
- Utilize signature of selection analysis to analyze how natural selection is shaping the evolution of **Desat** and **FAS** gene families based on temperature variation
- Analyze gene expression patterns within **Desat** and **FAS** gene families across these species using RPKM/FPKM & differential expression
- Look for other ways climate may serve as an evolutionary selective force on genes

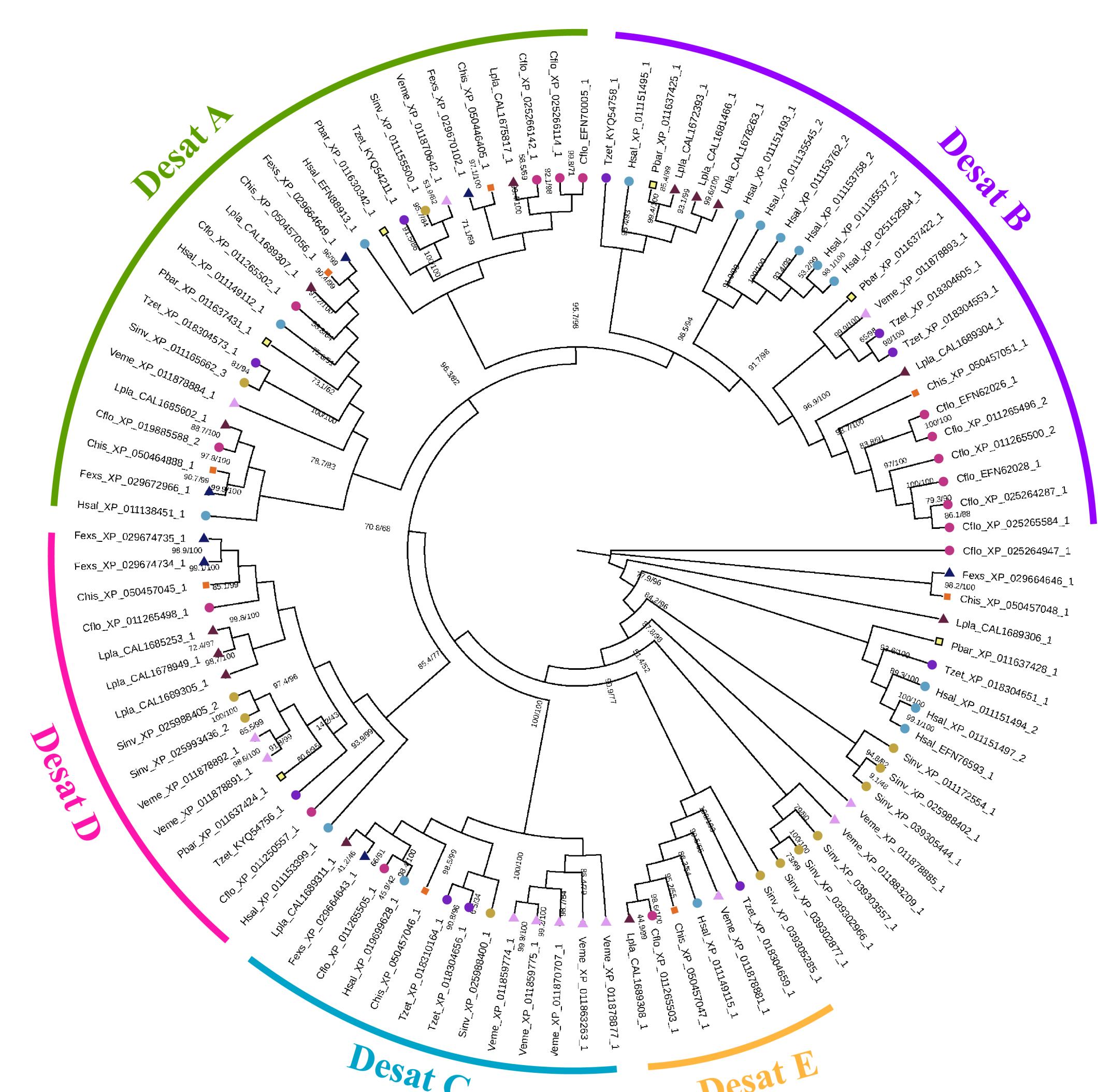


Figure 2: Desat phylogenetic tree with BS support values

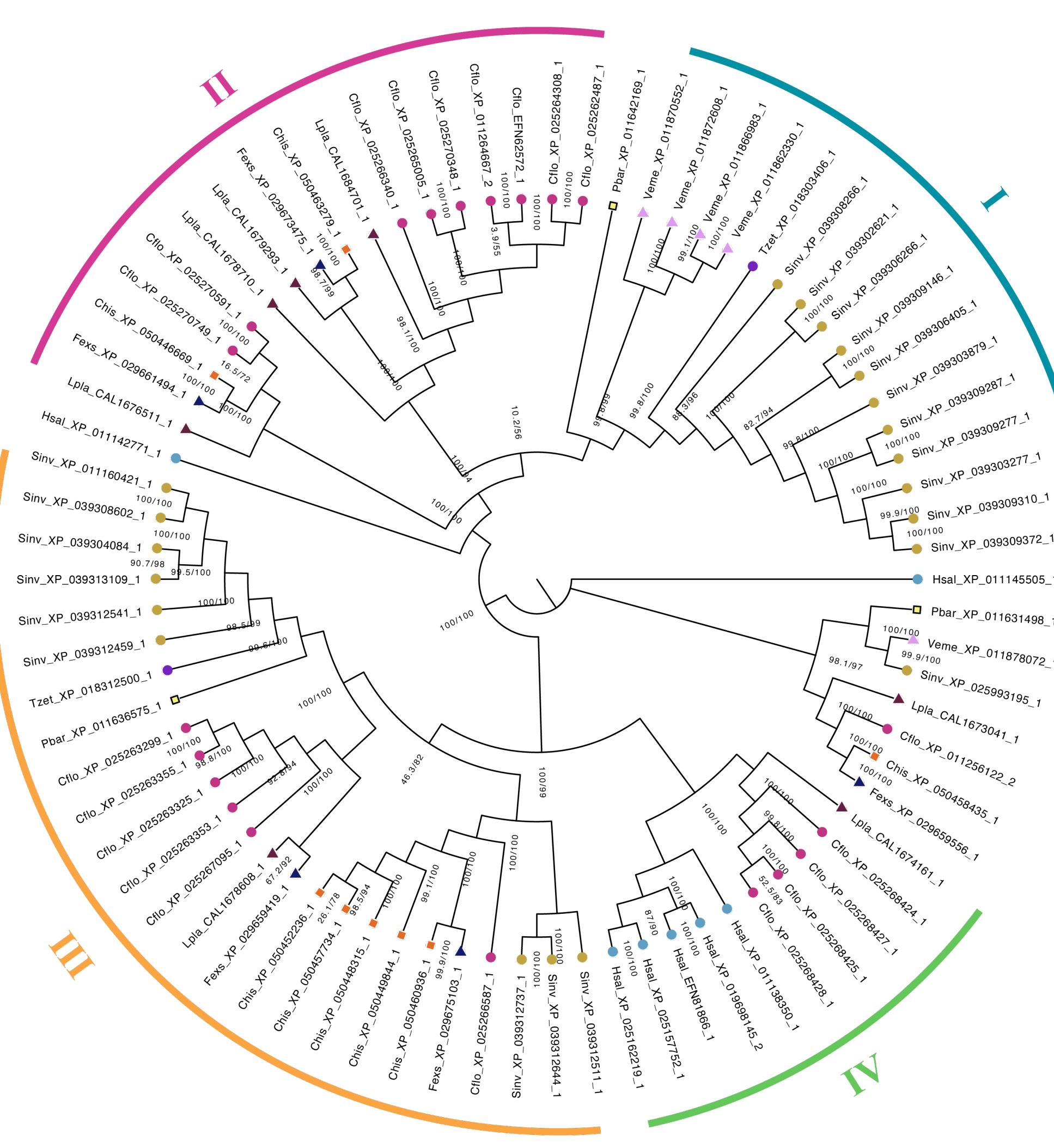


Figure 3: FAS phylogenetic tree with BS support values

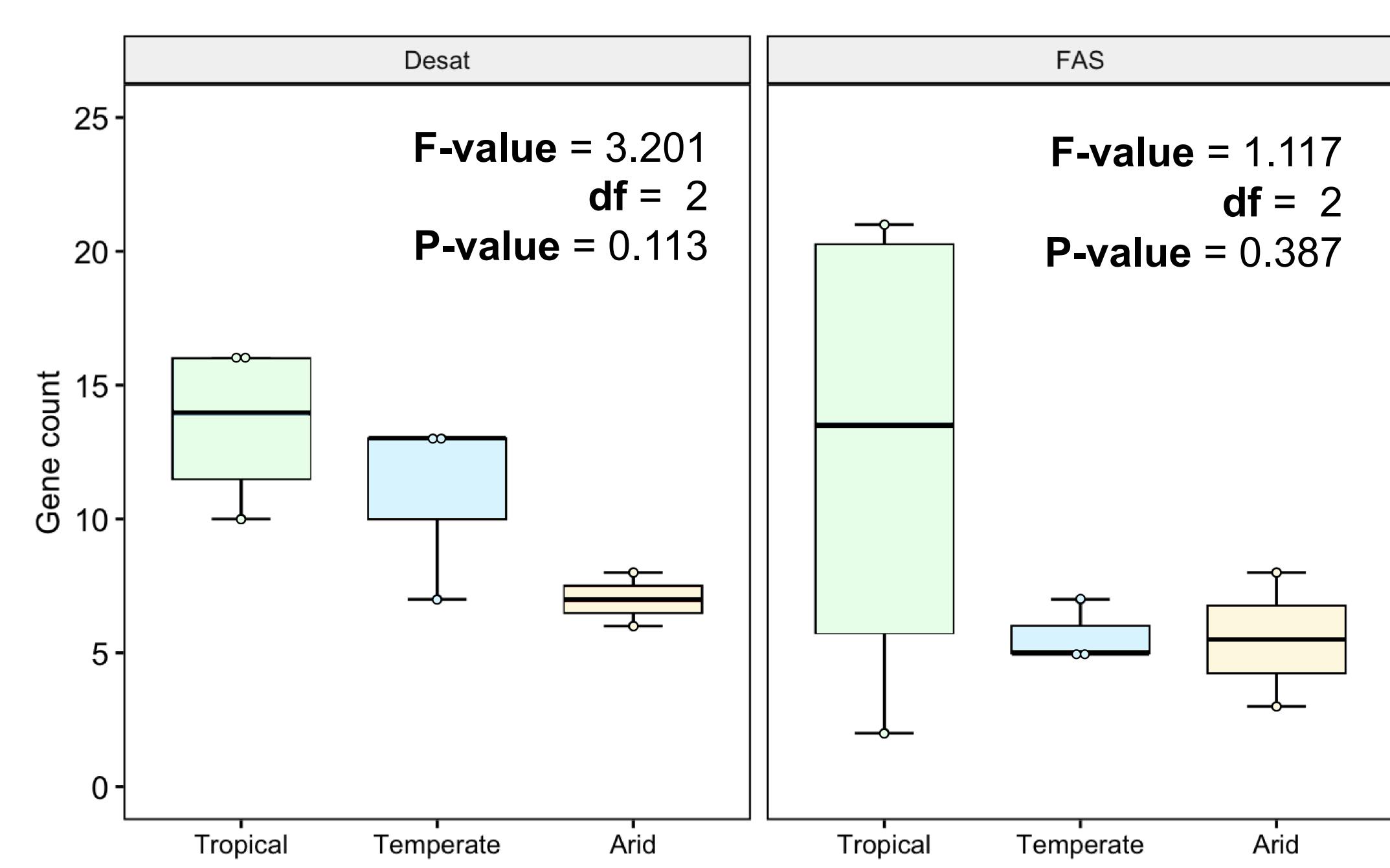


Figure 4: Gene count distributions by climate zone ( $P > 0.05$ )

- Differences in **Desat** and **FAS** gene counts between **climate** groups are NOT statistically significant (Fig. 4)

**Desat** (Fig. 2):

- Clades generally had most species present
- Large outgroup of genes that did not fit into clades

**FAS** (Fig. 3):

- Clade I primarily comprised of expansions in *S. invicta*
- Clade II mostly comprised of *C. floridanus* expansions
- There are primarily expansions in the genes from tropical species

References & Acknowledgements



Bradon.coy@ufl.edu

