

@iochromaland  
@dangates\_j

# Inferring the history of hybridization: A case study in *Lochrominae* (Solanaceae)

Stacey D. Smith<sup>1</sup> and Daniel J. Gates<sup>1,2,3</sup>

<sup>1</sup>University of Colorado-Boulder

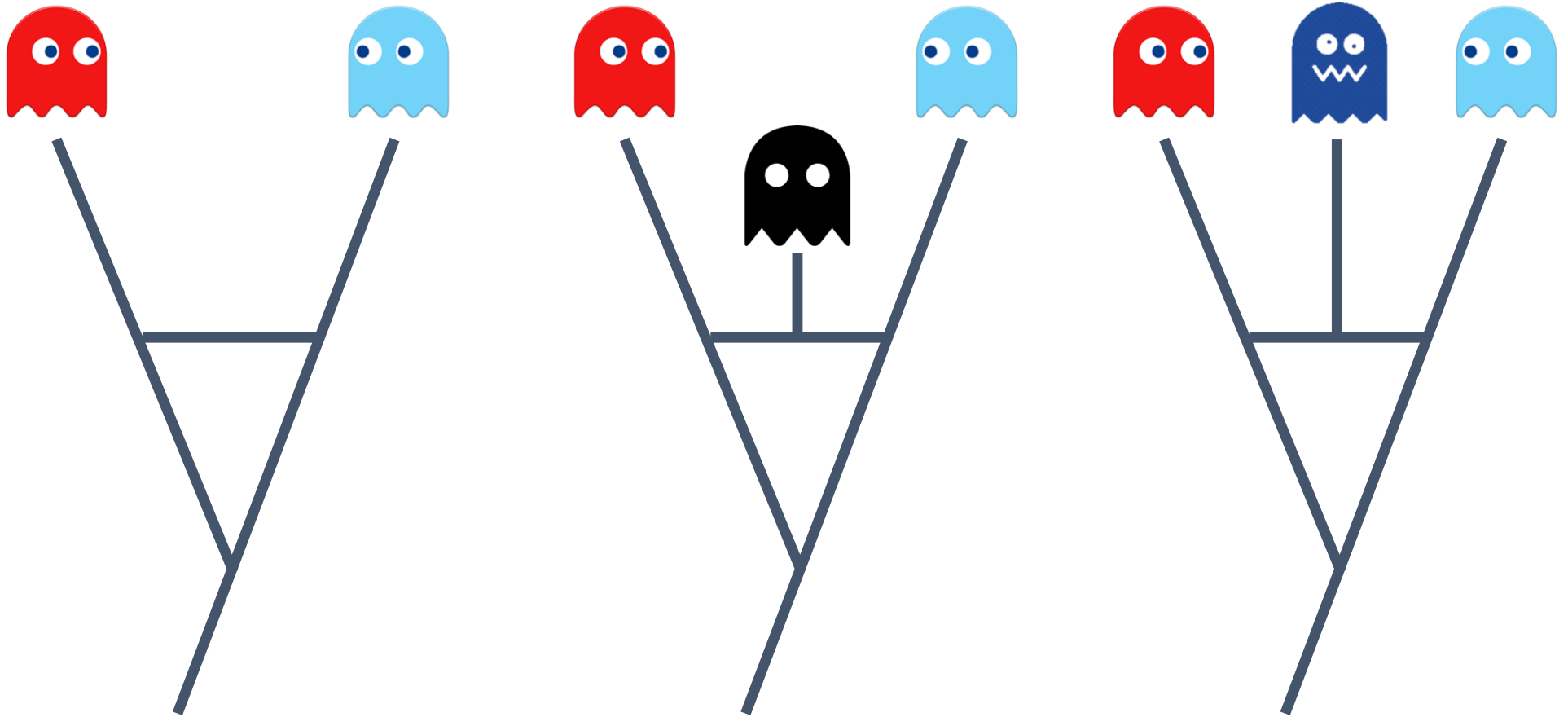
<sup>2</sup>University of Nebraska-Lincoln

<sup>3</sup>Currently at University of California Davis

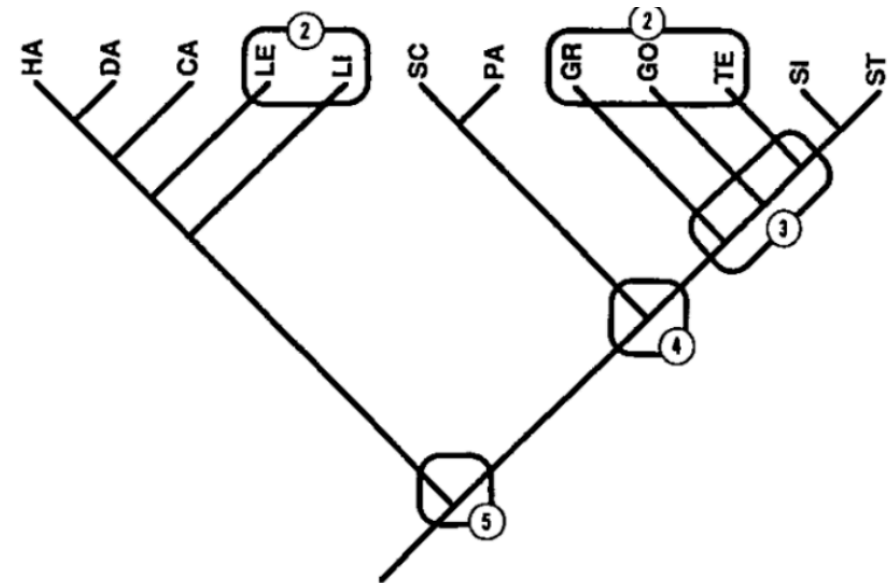




# Evolutionary outcomes



# Will hybrids 'stand out' during phylogenetic analysis?



Hybrids will not be 'readily identifiable' from indices like CI, N(trees), unless the parents are distantly related

McDade, 1990, 1992

# Study system: lochrominae (Solanaceae)

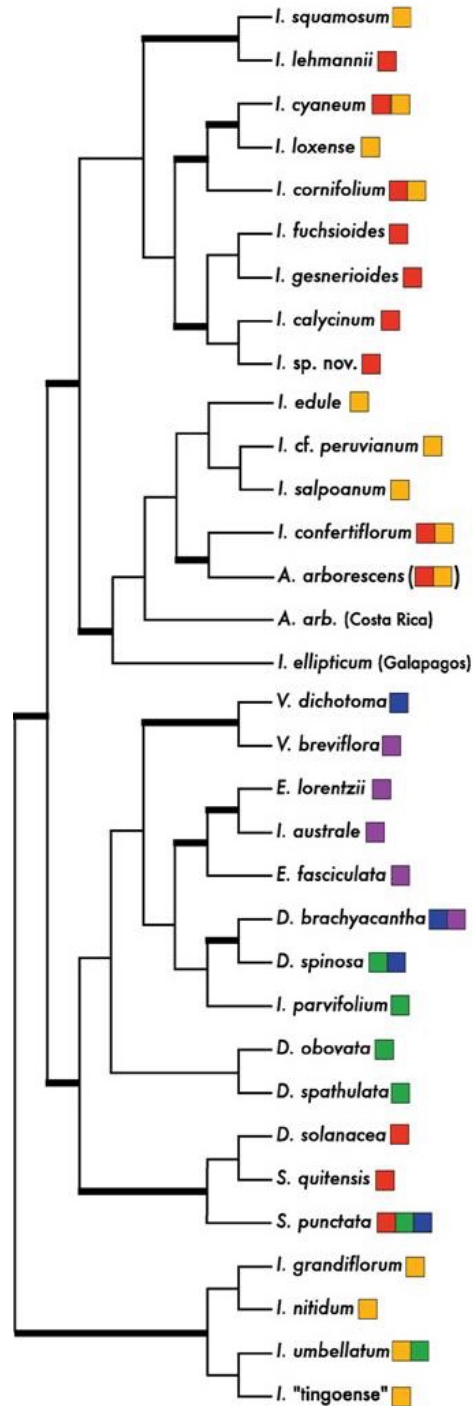
State of affairs before 2000

	<i>Acnistus</i>	1	Mexico - northern S. America
	<i>Dunalia</i>	5	Colombia - Argentina
	<i>Eriolarynx</i>	3	Bolivia - Argentina
	<i>Lochroma</i>	20 + five undescribed	Colombia - Peru, + Galapagos
	<i>Saracha</i>	2	Venezuela - Bolivia
	<i>Vassobia</i>	2	southern S. America

# Phylogeny of Lochrominae

Combined ML analysis  
of ITS, *LFY*, *waxy*  
(~4000bp)

Bolded branches with  
>75% BS and >95% PP



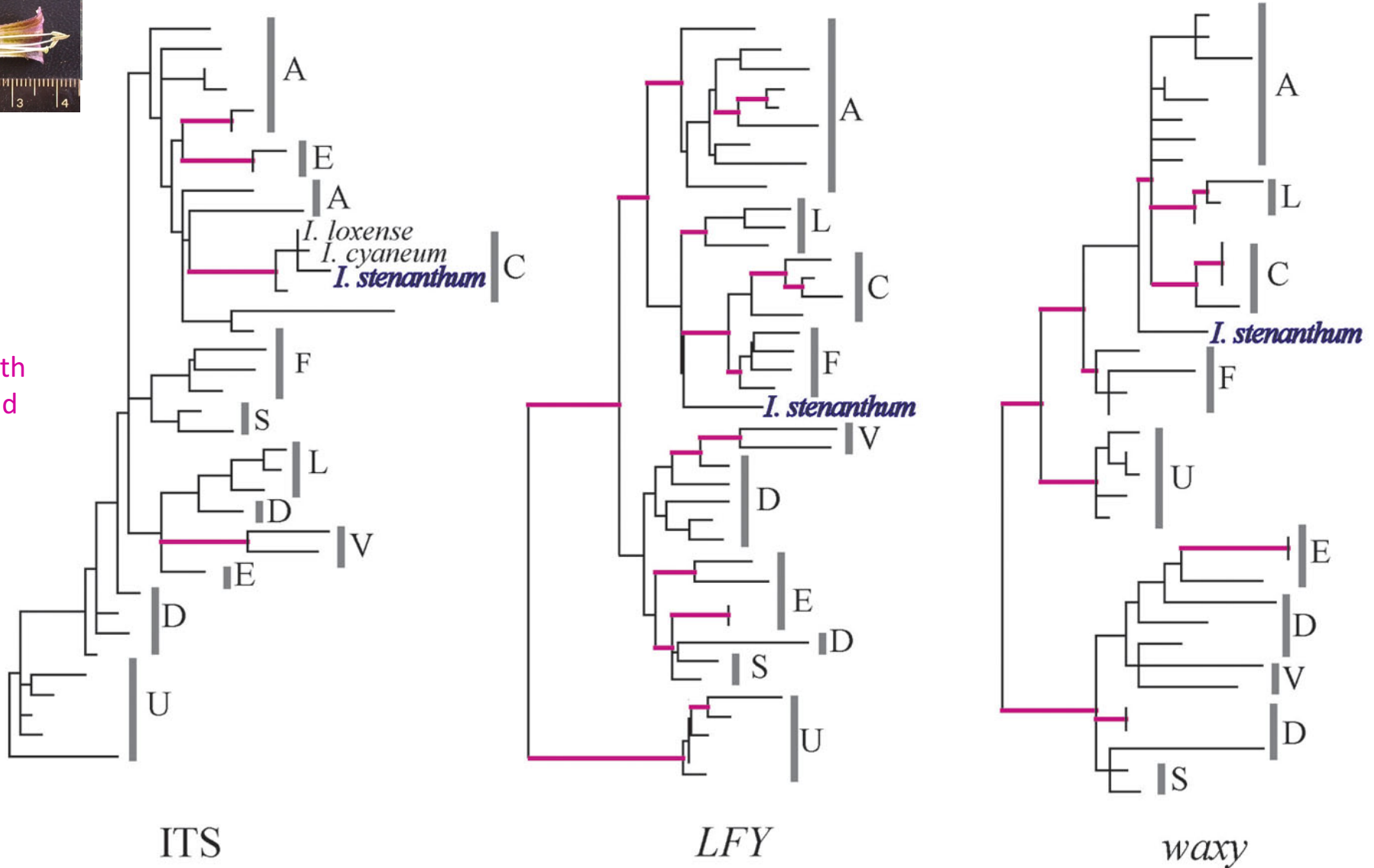
- Northern Andes
- Amotape-Huancabamba Zone
- Central Andes I
- Central Andes II
- Southern Andes

(Smith & Baum, 2006 AJB)



# Problematic taxa: *I. stenanthum*

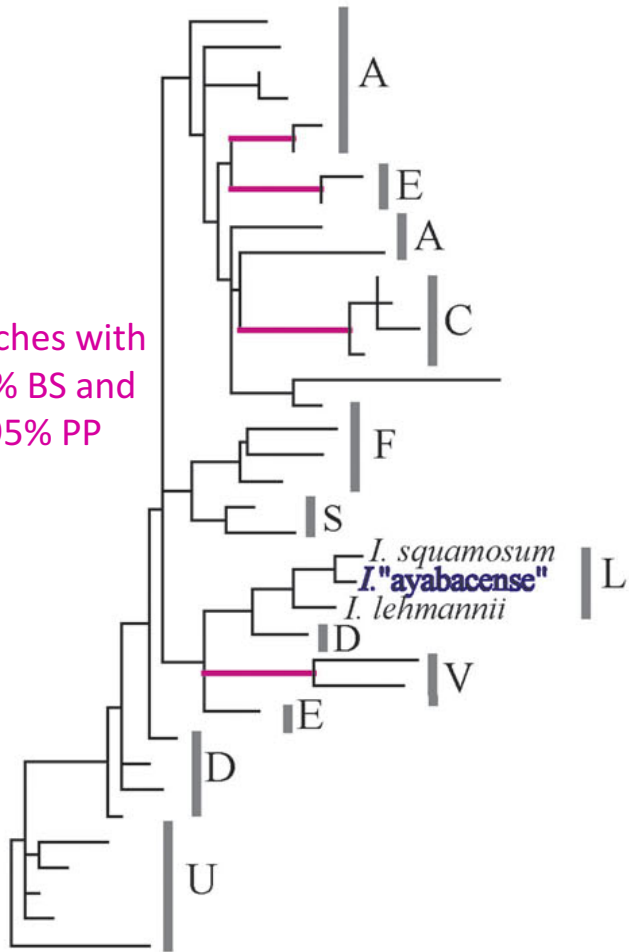
Branches with  
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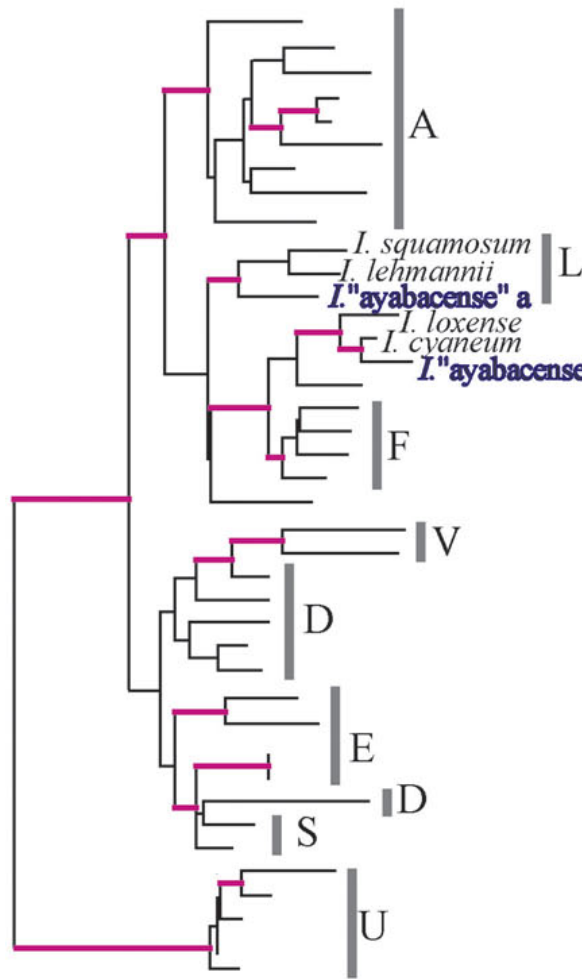


# Problematic taxa: *I. ayabacense*

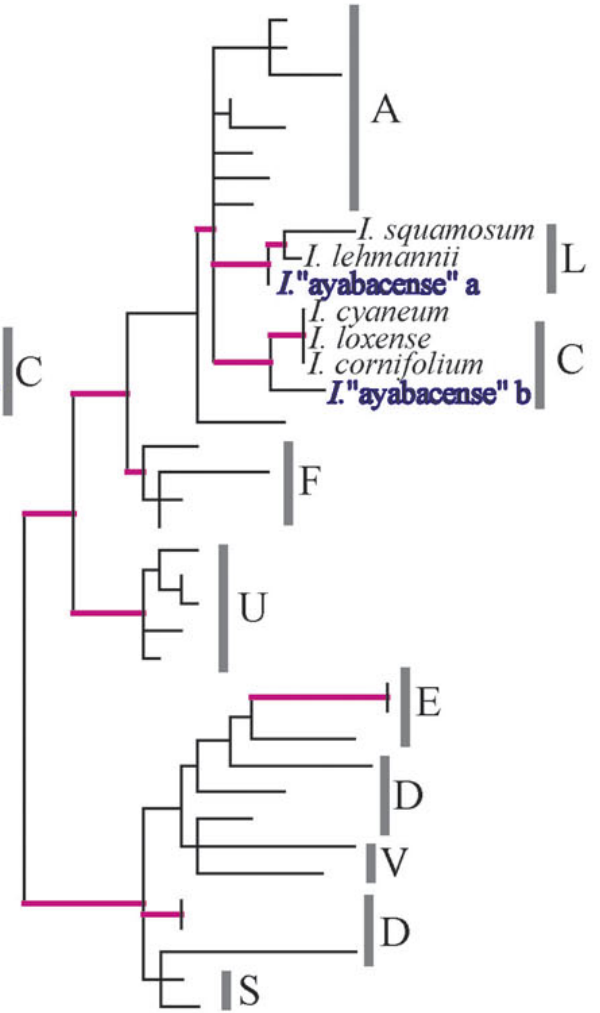
Branches with  
>75% BS and  
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ITS



LFY



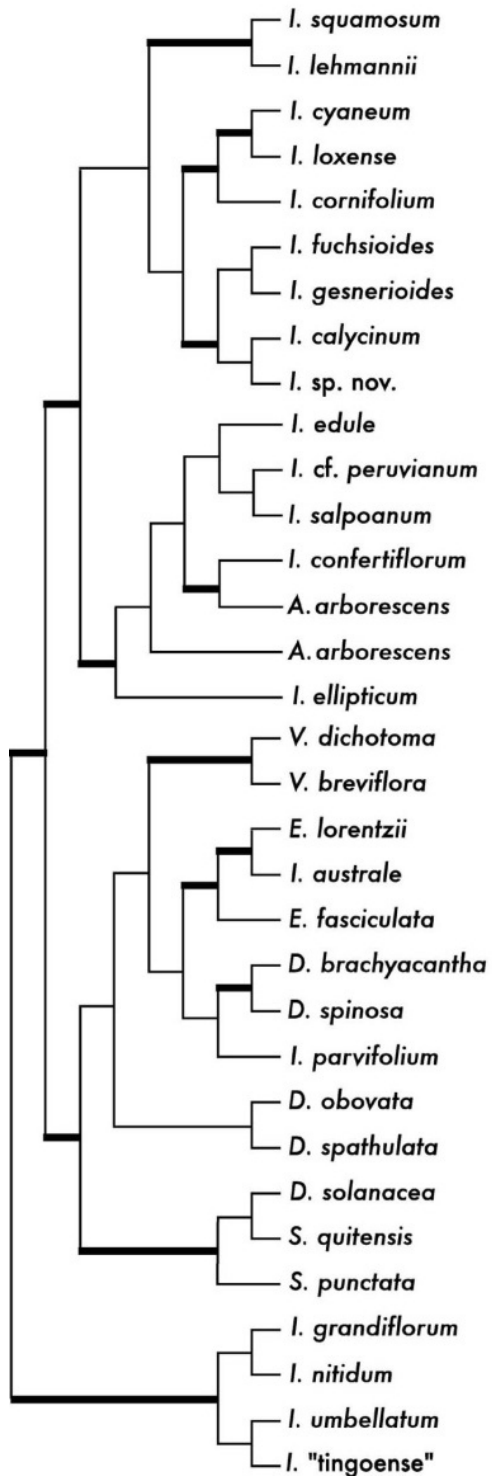
waxy



Maybe these are hybrids?!



# History of hybridization?



*I. ayabacense*



*I. stenanthum*



*I. "sagasteguii"*

(Smith & Baum, 2006 AJB)

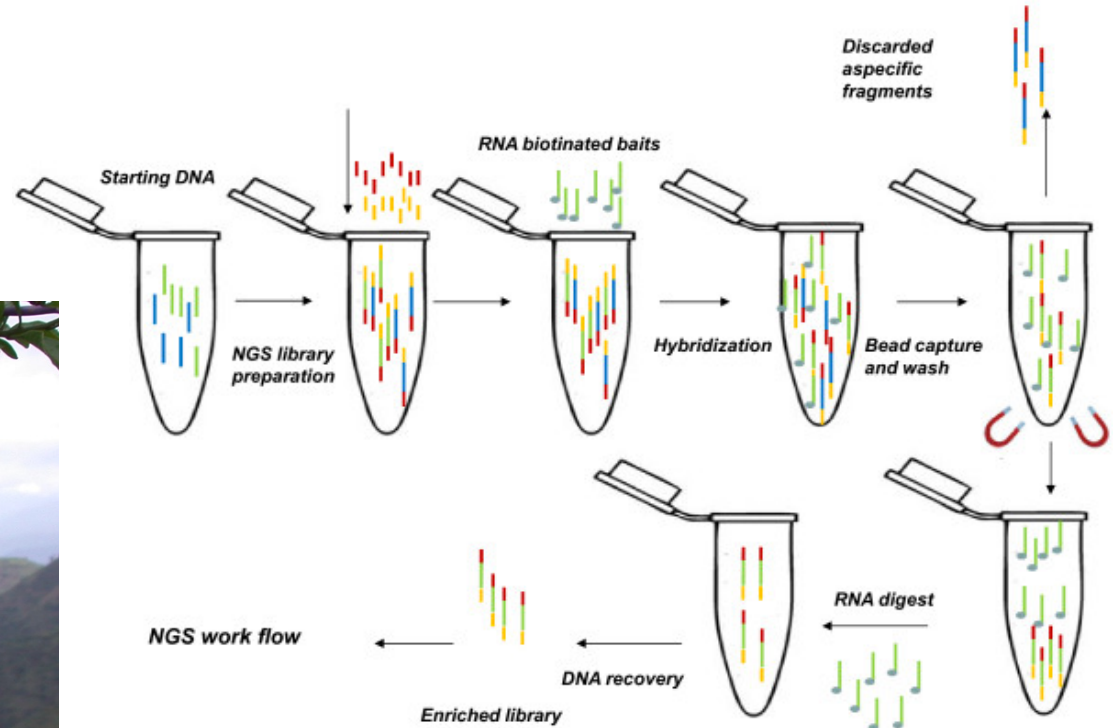
# A phylogenomic approaches to detecting hybridization



Dan Gates

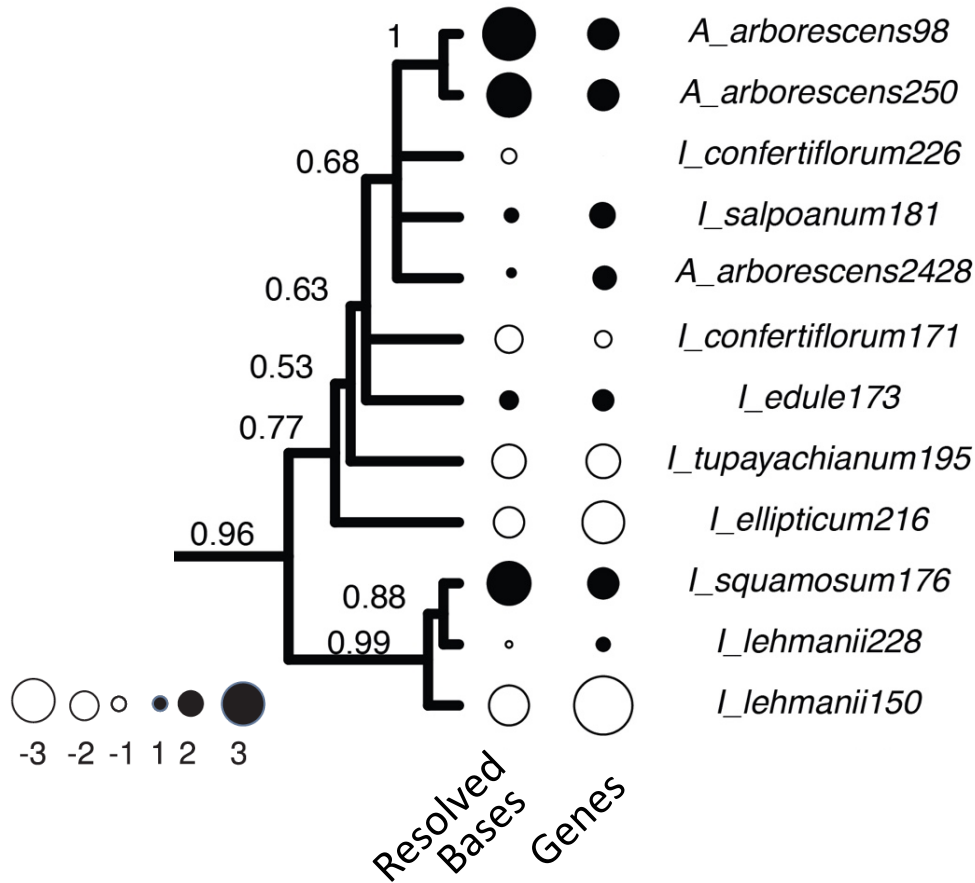


*Lochroma cyaneum*  
Genome size ~ 3Gb

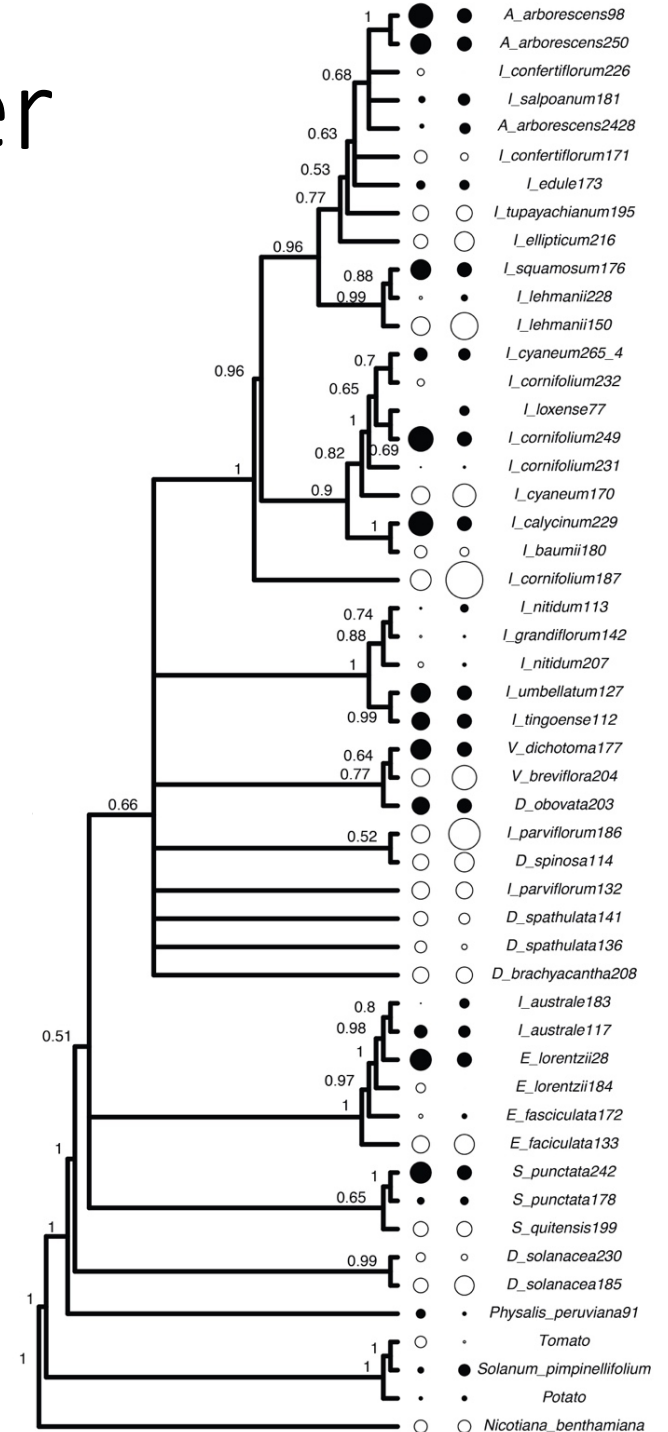


Target capture based on *I. cyaneum* probes

# Data quality vs. power



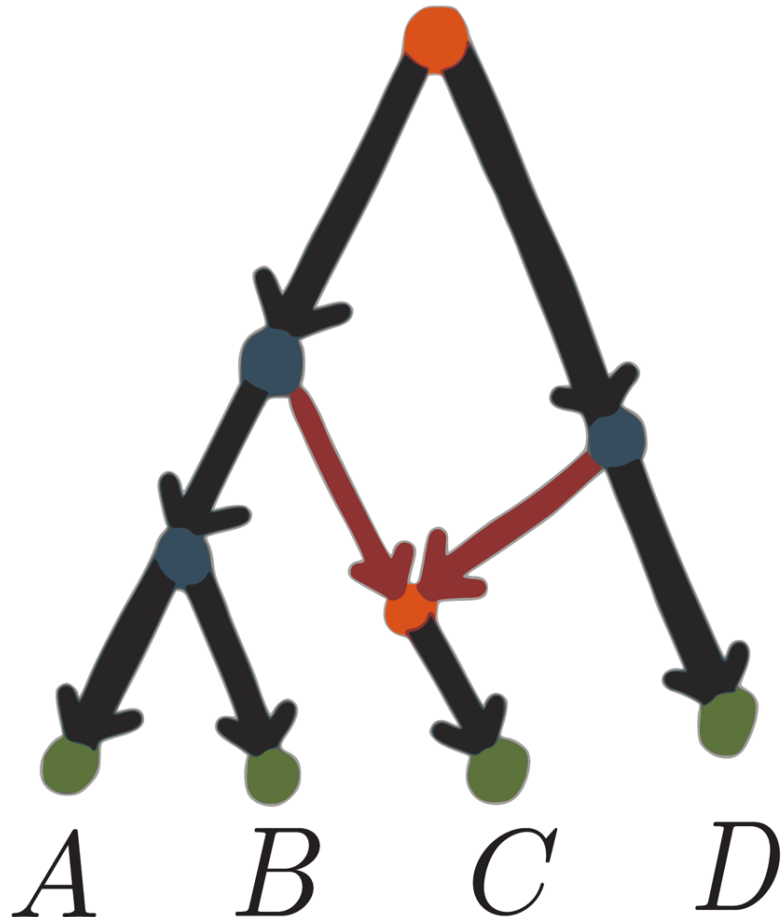
Consensus species tree inferred from ca. 240 loci with STAR (Liu et al., 2008) from Gates et al. (2018)





Gates et al. 2018

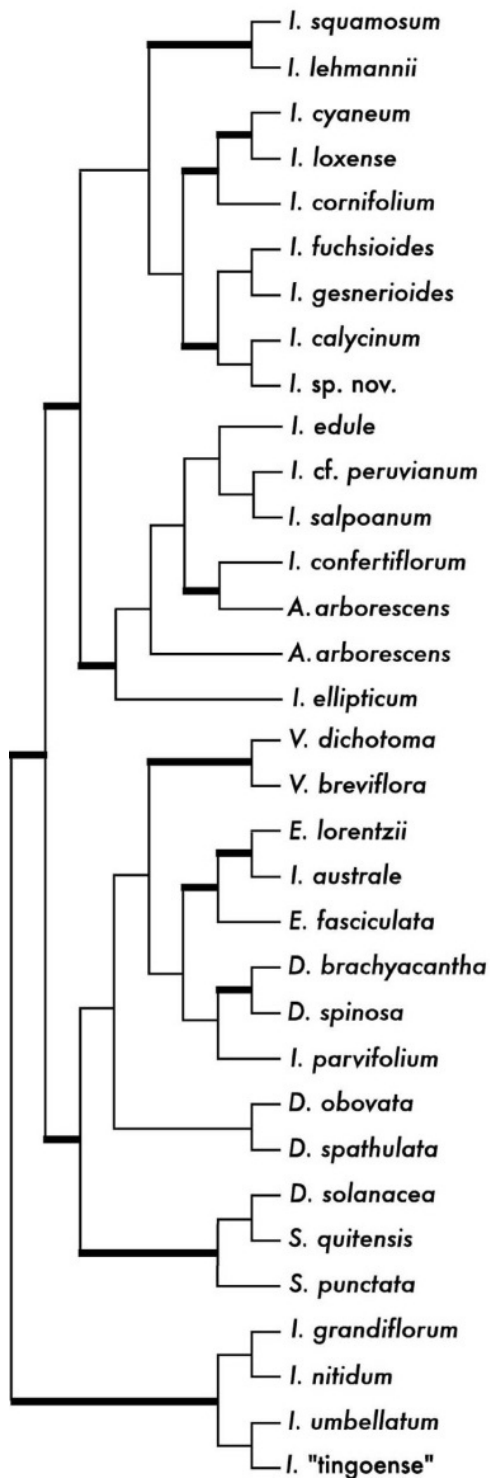
In the best of all possible worlds..



- Detect signature of hybridization in phylogeny
- Identify tips with hybrid ancestry and their parents
- Estimate timing of event
- Scale to sizeable clades

Solís-Lemus and Ané 2016

# Revisit our putative hybrids



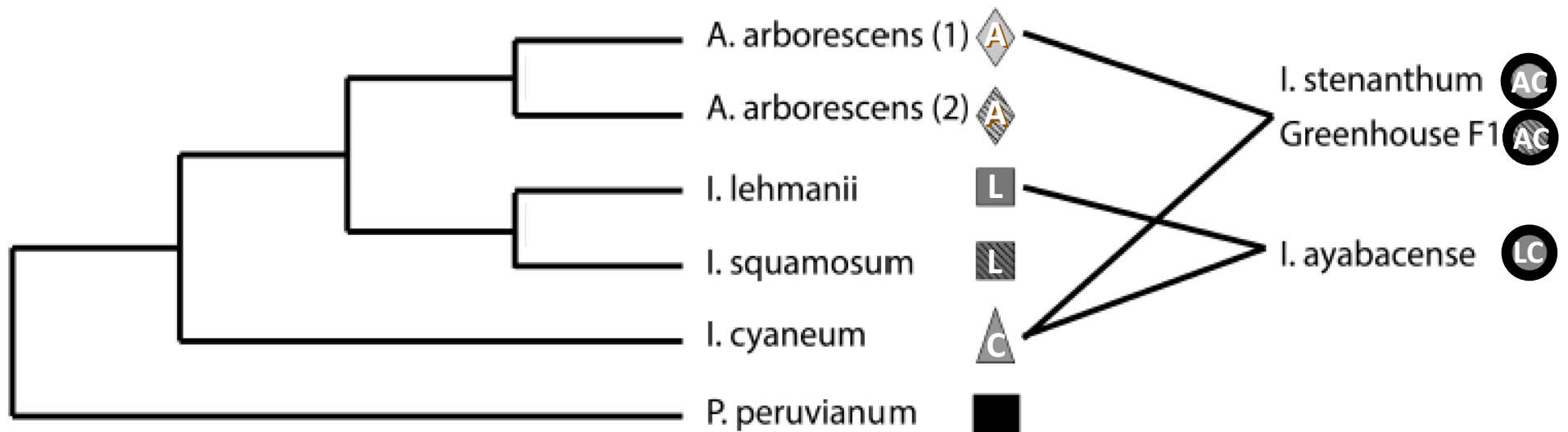
*I. ayabacense*



*I. stenanthum*

Can we identify them *and* their parents with phylogenomic data?

# A McDade-style experiment

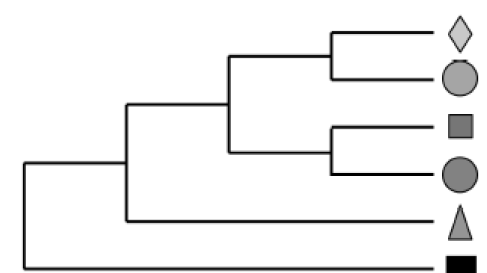
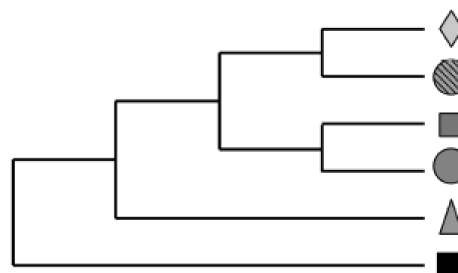
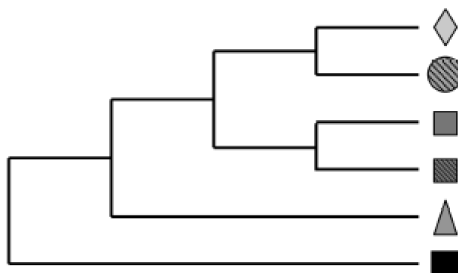
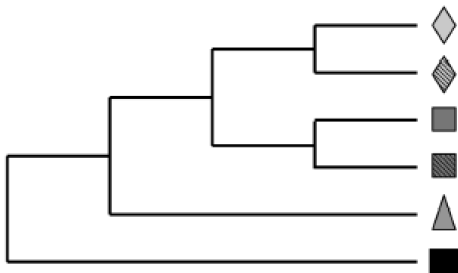


No Putative Hybrids

One F1

F1 + ayabacense

Two Putative Hybrids

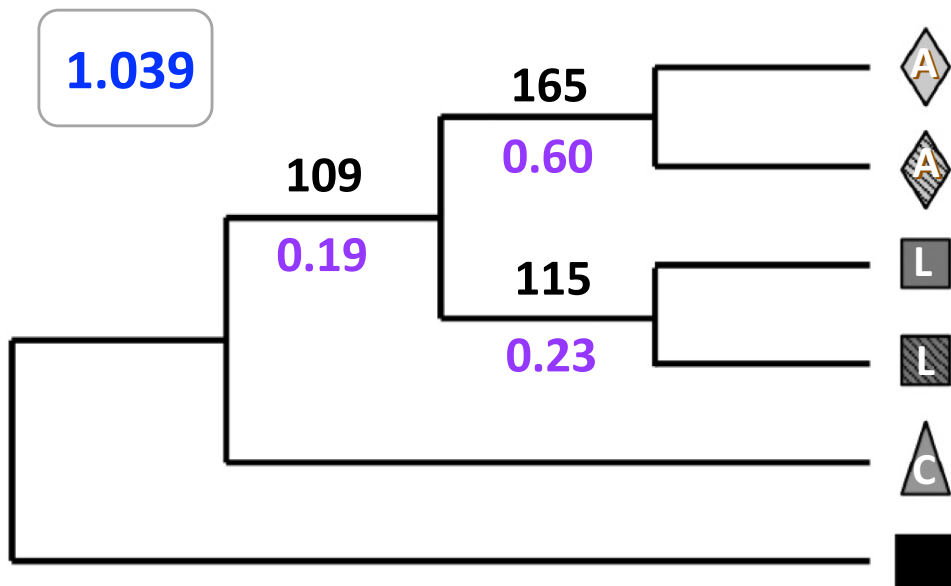




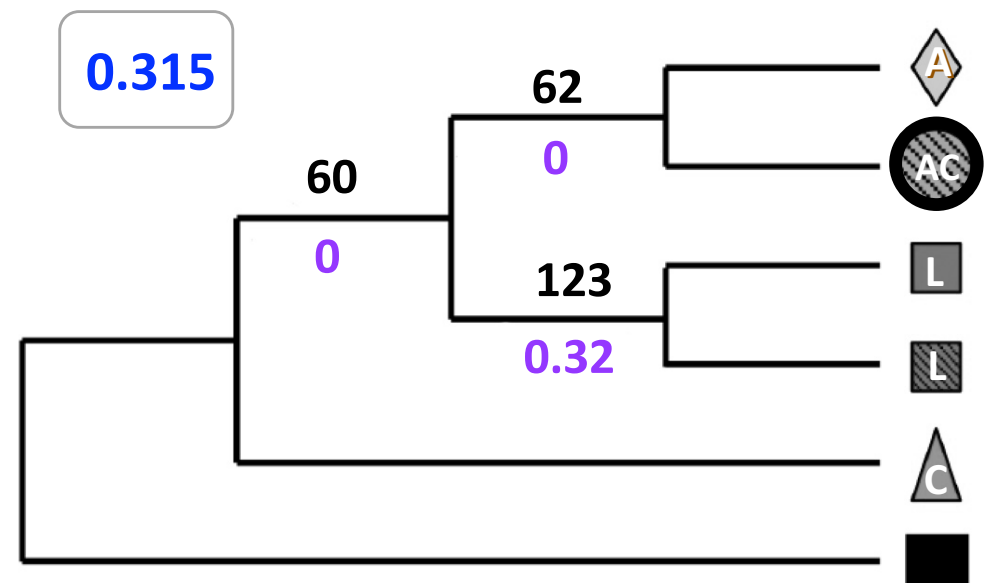
# Phylogenetic signature of hybridization

Prediction: Addition of hybrids will increase conflict, reducing the concordance among genes and certainty of relationships

Approach: Quantify **concordance** and internode certainty (**IC**) for each branch and across the tree (**TC**) (Salichos et al. 2014)



No hybrids

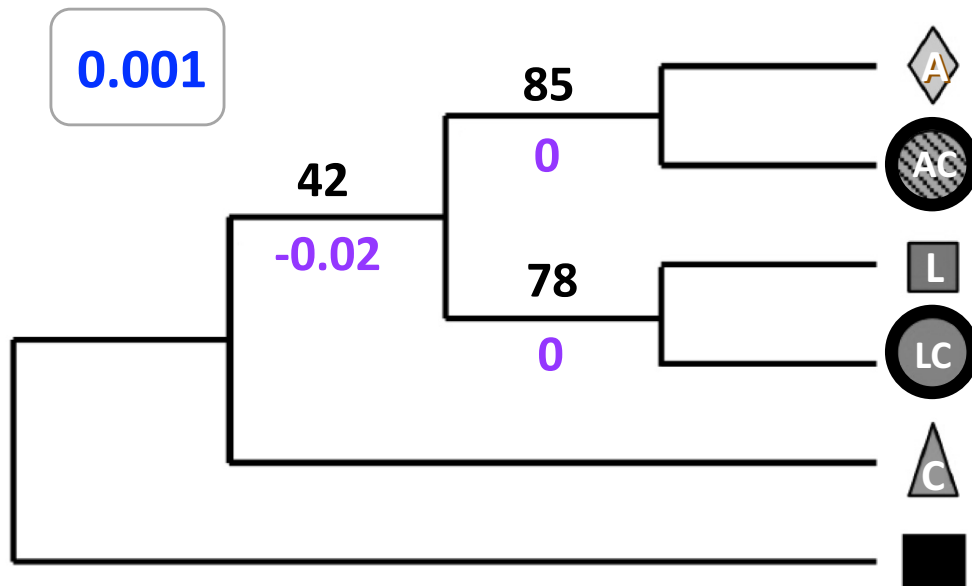


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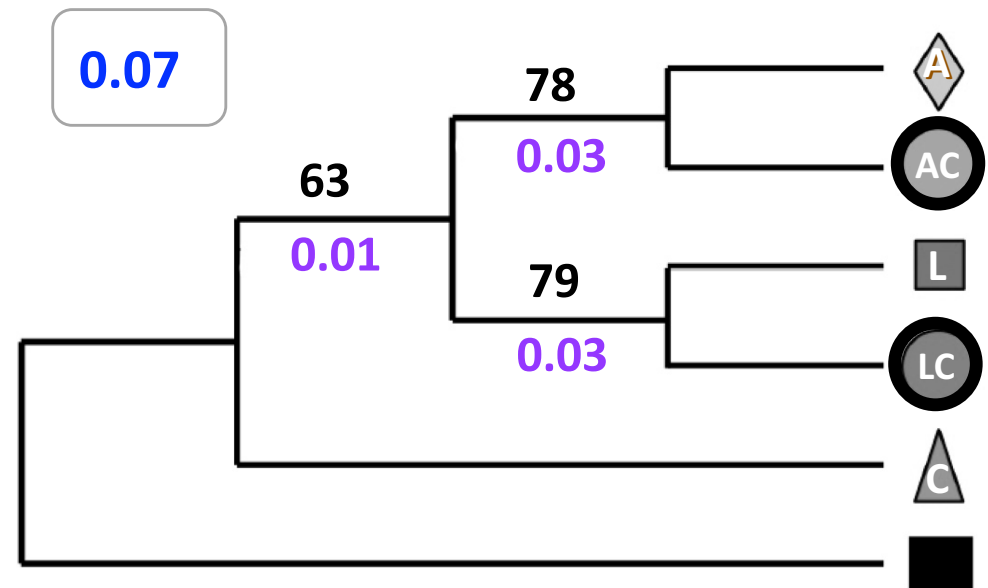
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F1 + *I. ayabacense*

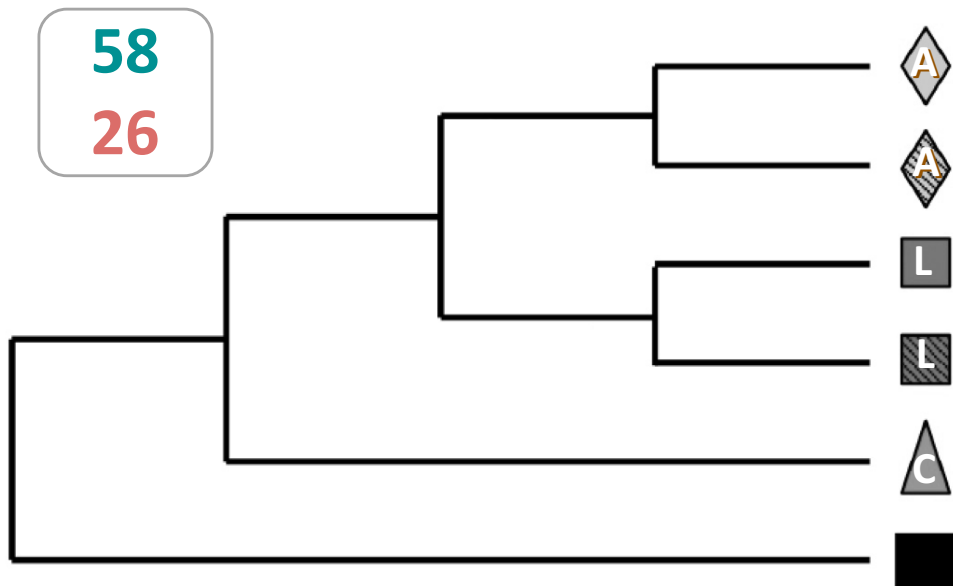


*I. ayabacense* + *I. stenanthum*

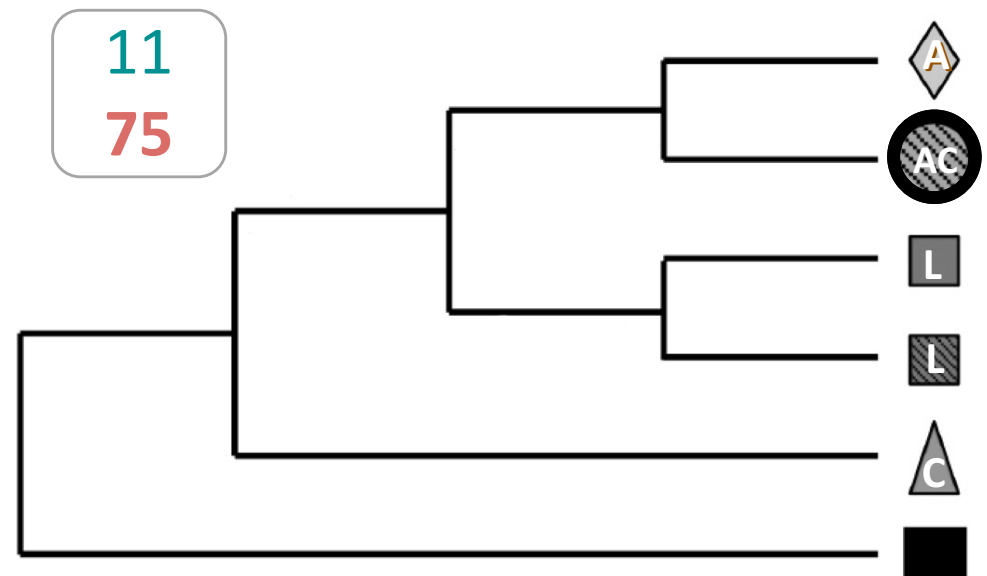
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Prediction: Addition of hybrids will reduce tree-like structure of species relationships

Approach: Test ability to reject **panmixia** or fully **bifurcating** model ( $\chi^2$  statistics) with TICR (Stenz et al. 2015)



No hybrids

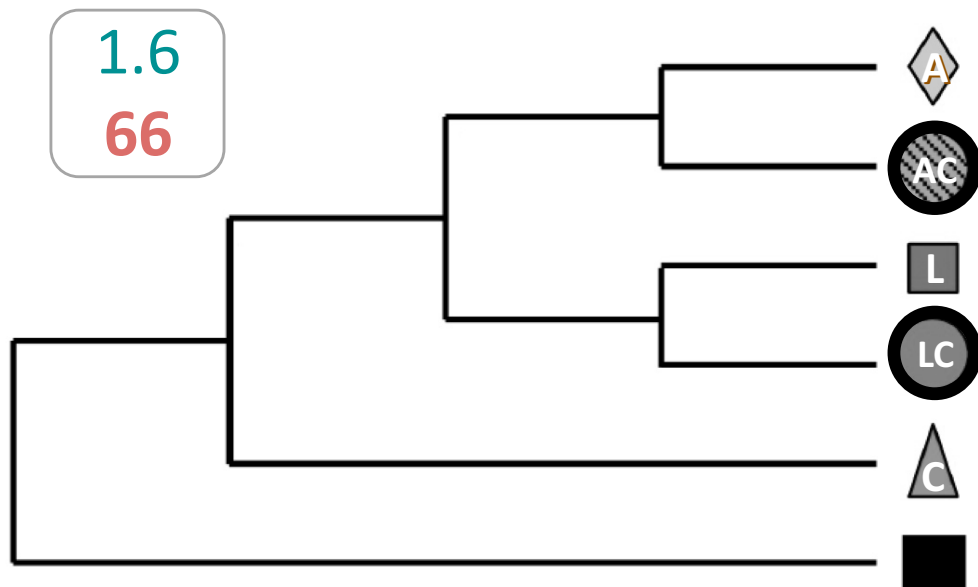


One F1

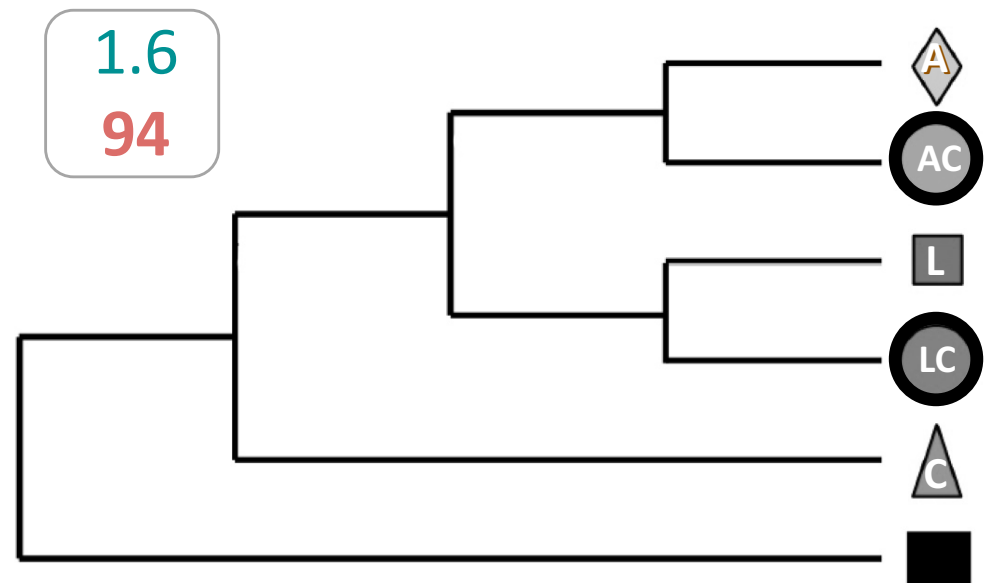
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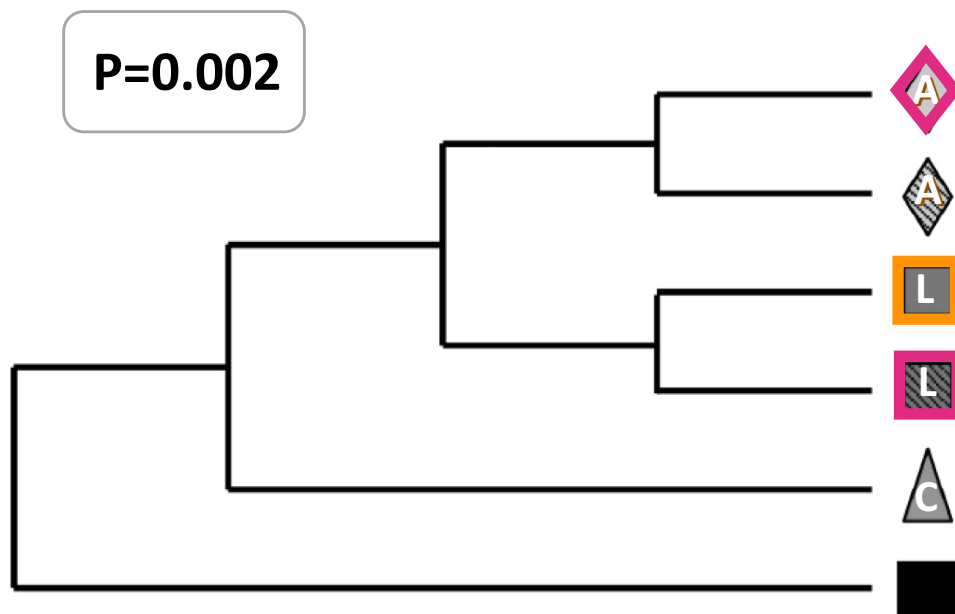


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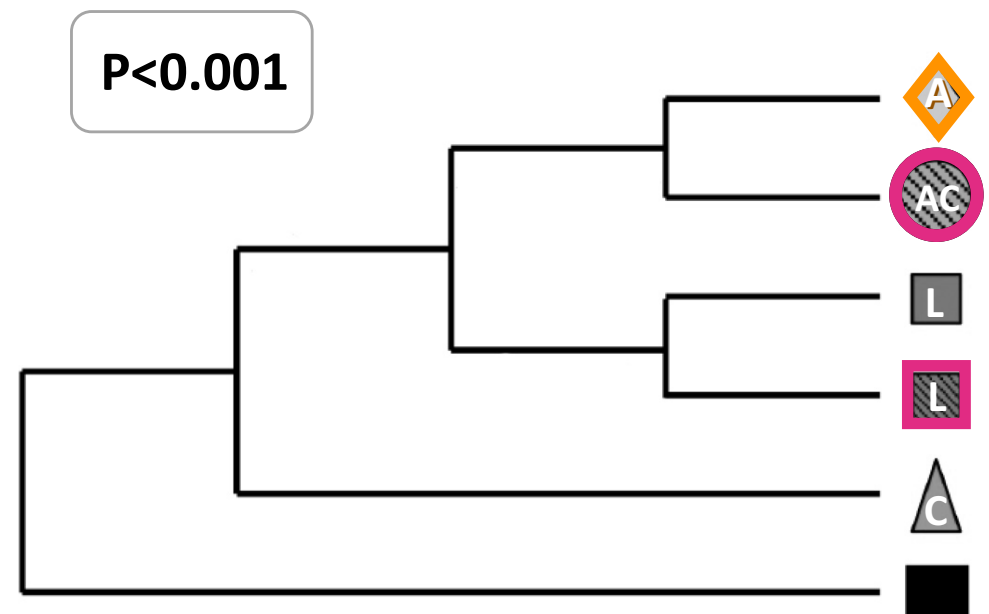
# Identification of hybrid taxa and parents

Prediction: Putative hybrids will reflect inferred ancestry based on morphology and geography

Approach: Use HyDe (Kubatko and Chifman, 2015) to detect **hybrid taxa** and **parents**; similar results with D-statistic analysis



No hybrids

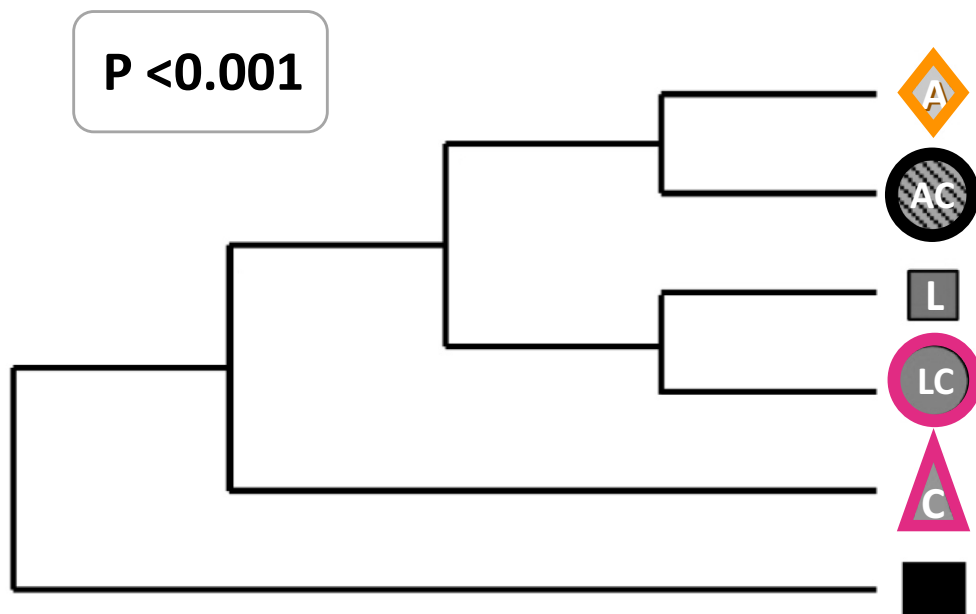


One F1

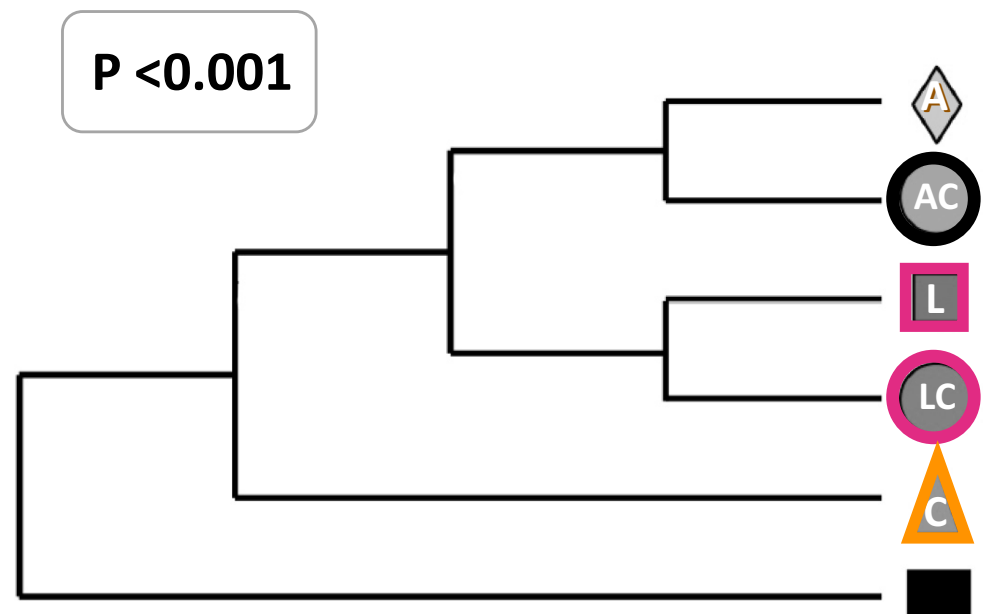
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# The known-knowns

- Adding hybrid taxa to the phylogeny decreases concordance, certainty in relationships, and tree-like structure
- Inferring which taxa are hybrids or parents of hybrids is hard



# Future directions

- Expand sampling within and across species of *Lochrominae*
- Combine existing (and new) statistics in an ABC approach to localize events
- Test power in relationship to parental distance, evolutionary rate, etc.







# Acknowledgements

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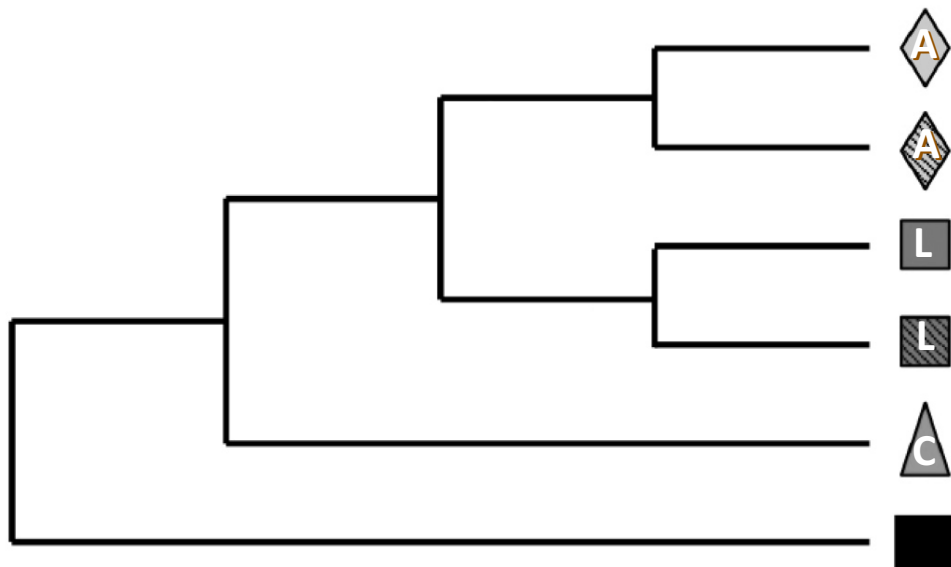
[for-the-love-of-trees.blogspot.com](http://for-the-love-of-trees.blogspot.com)



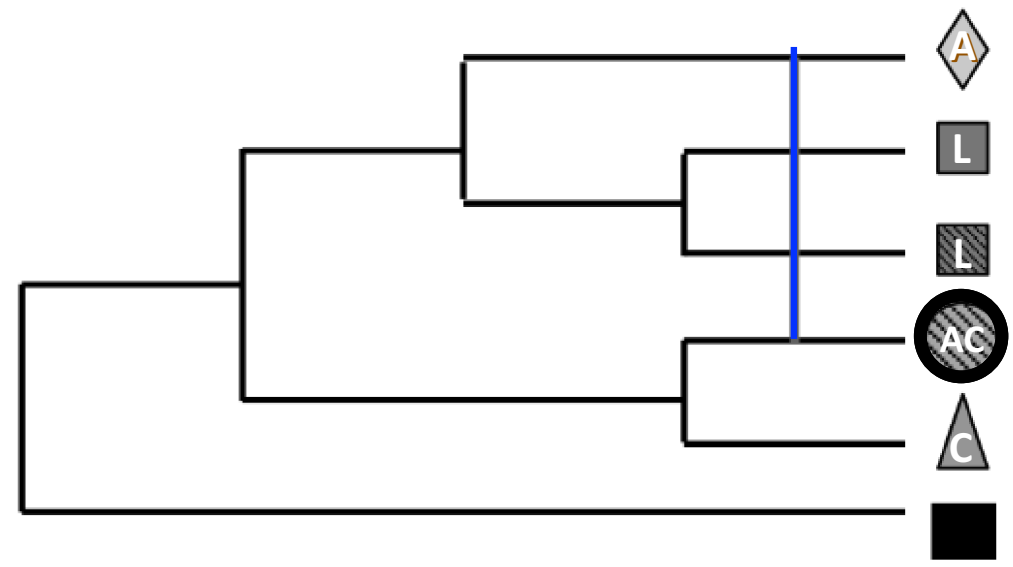
# Localization of hybridization

Prediction: Reticulate events will be inferred in datasets with hybrids; among hybrids and/or their parental lineages

Approach: Fit significant **reticulation events** with SNaQ (Solís-Lemus and Ané 2016)



No hybrids

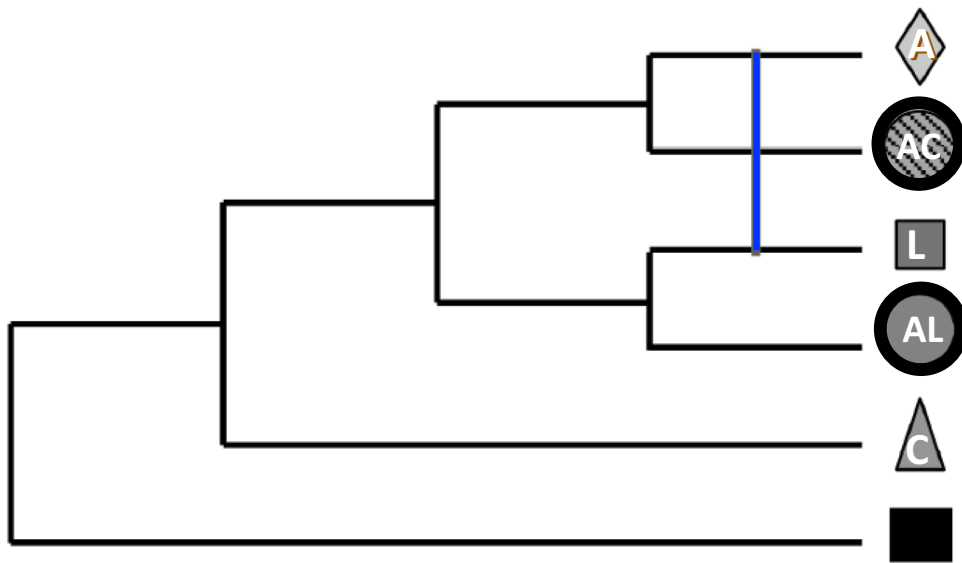


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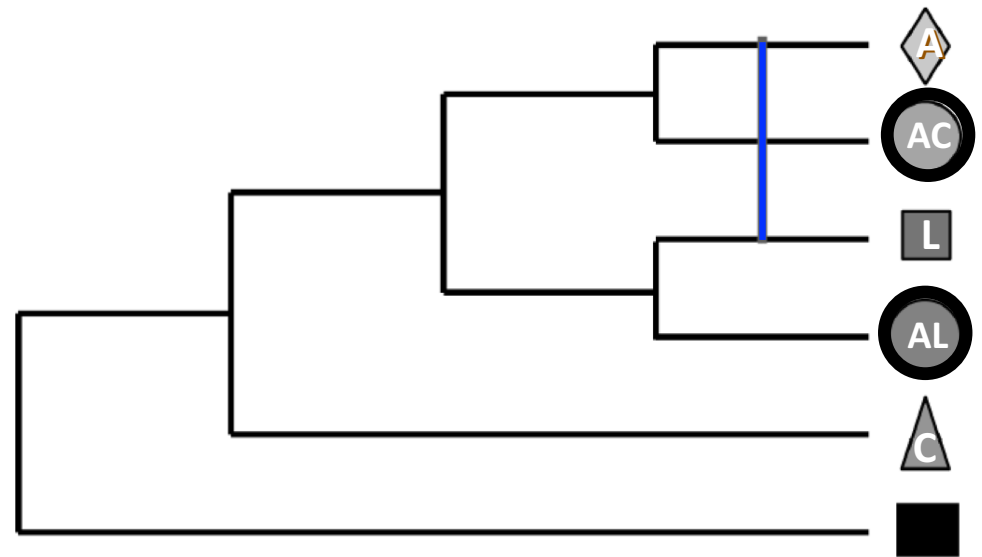
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