Nature Bites, BBC. https://www.youtube.com/watch?v=7n2M9TqbaM4

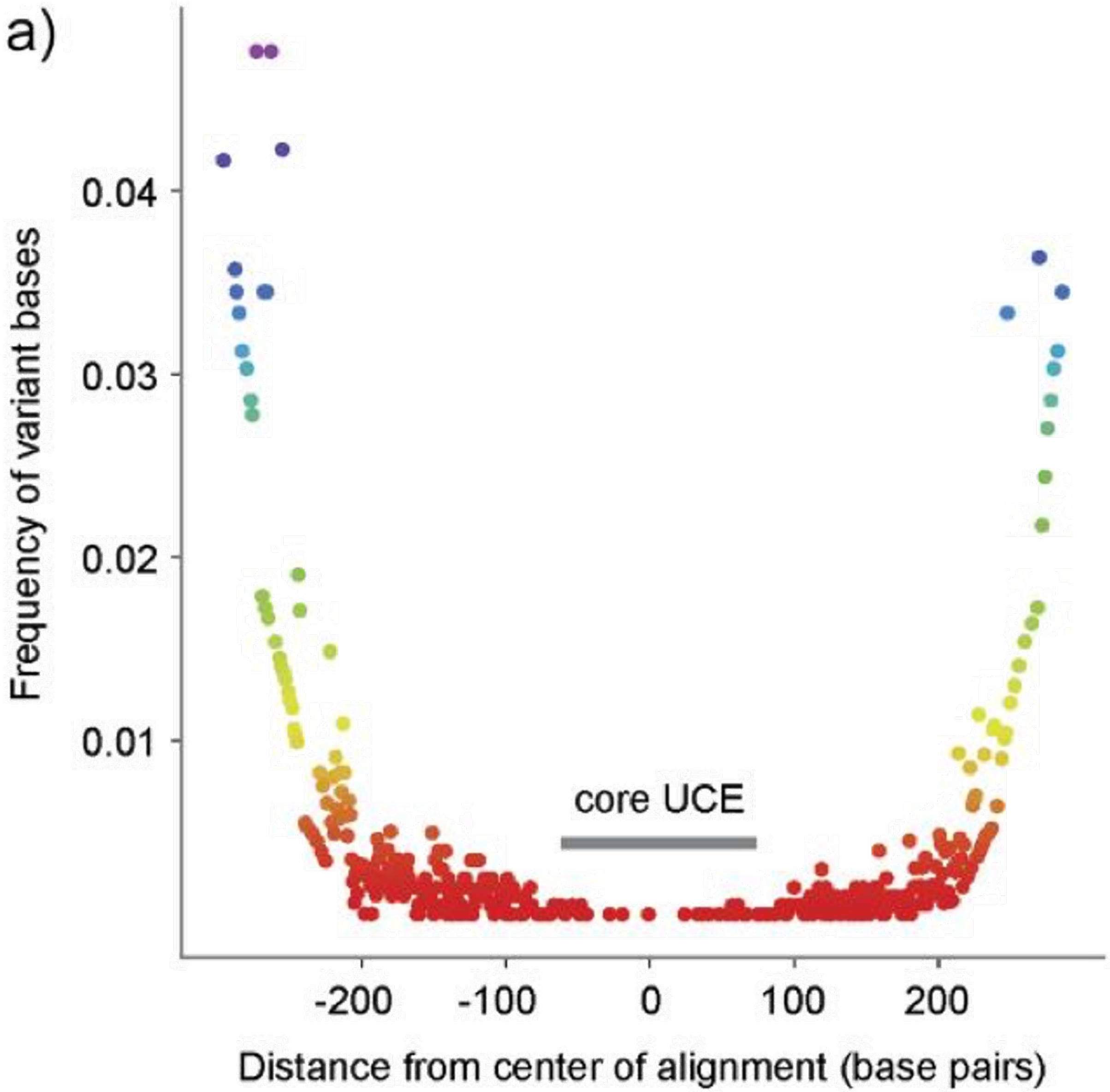
Emma E. Jochim, James Starrett, Hanna R. Briggs, Jason E. Bond. 2025. "Speciation Pattern and Process in the California Coastal Dune Endemic Trapdoor Spider Aptostichus simus (Mygalomorphae: Euctenizidae) and Description of a New Cryptic Species" *Ecology and Evolution* 15:e72346 <https://doi.org/10.1002/ece3.72346>.

Class focus area: Review of some of what we've learned

EEB603: Brian O'Meara

All quotes and images from the above paper unless otherwise noted

Goldilocks went into the kitchen and saw three bowls of porridge on the table. She scooped some from **the biggest bowl**, but it was too cold. She tried some from **the medium-sized bowl**, but it was too hot! Then she tried some from **the smallest bowl**, and it was just right—**so she ate it all!**



Faircloth et al. 2012

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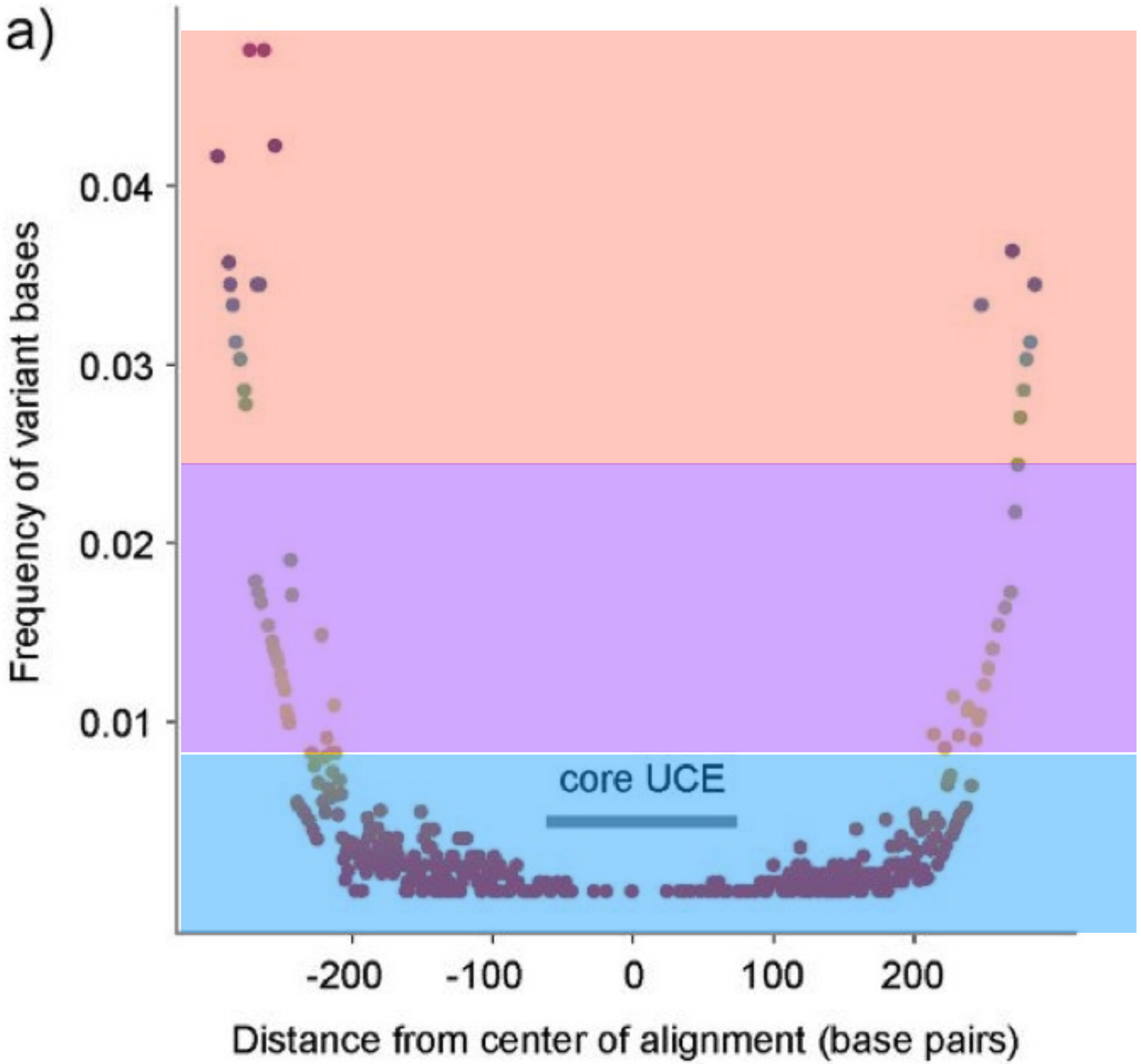

Too hot

Just right

Too cold

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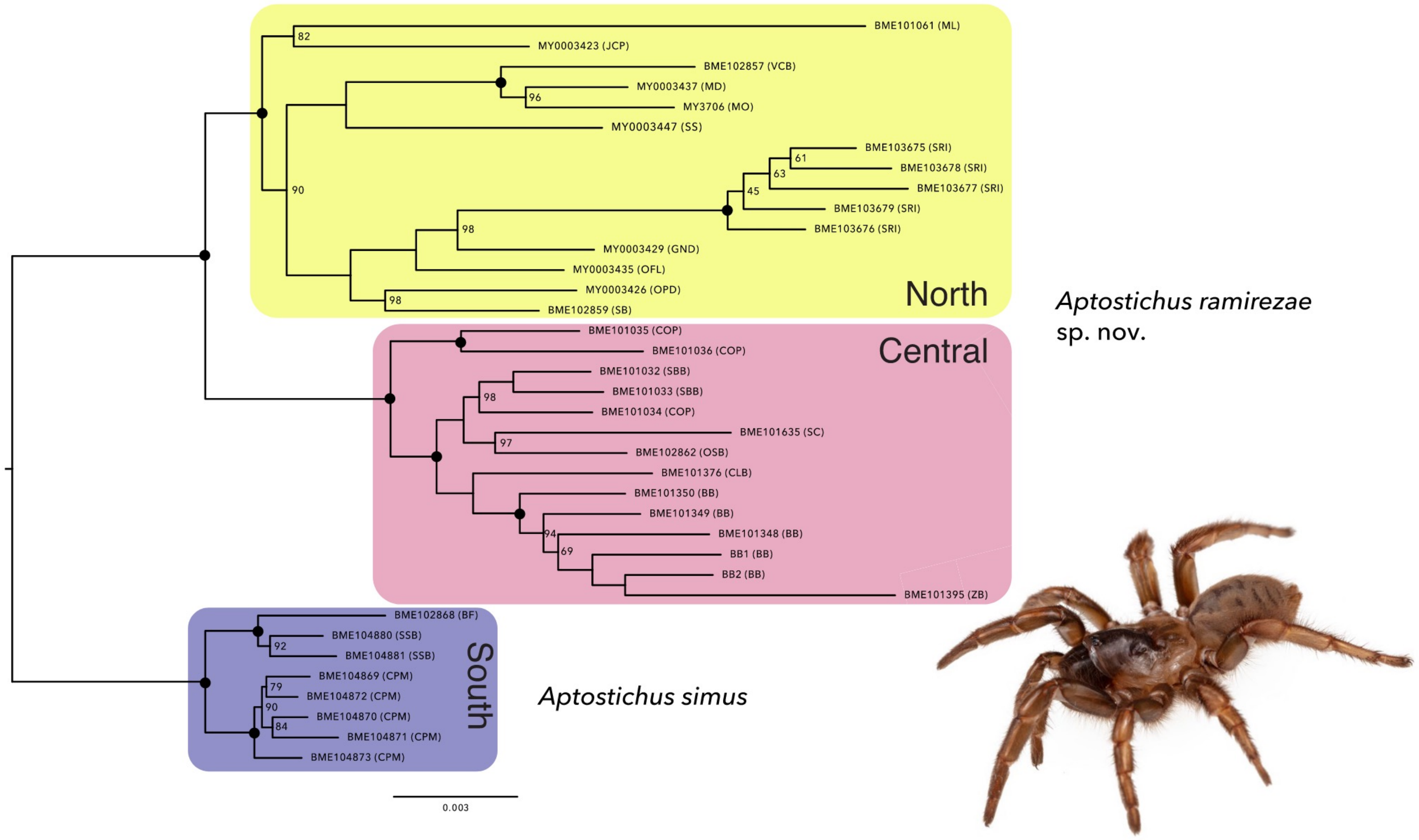
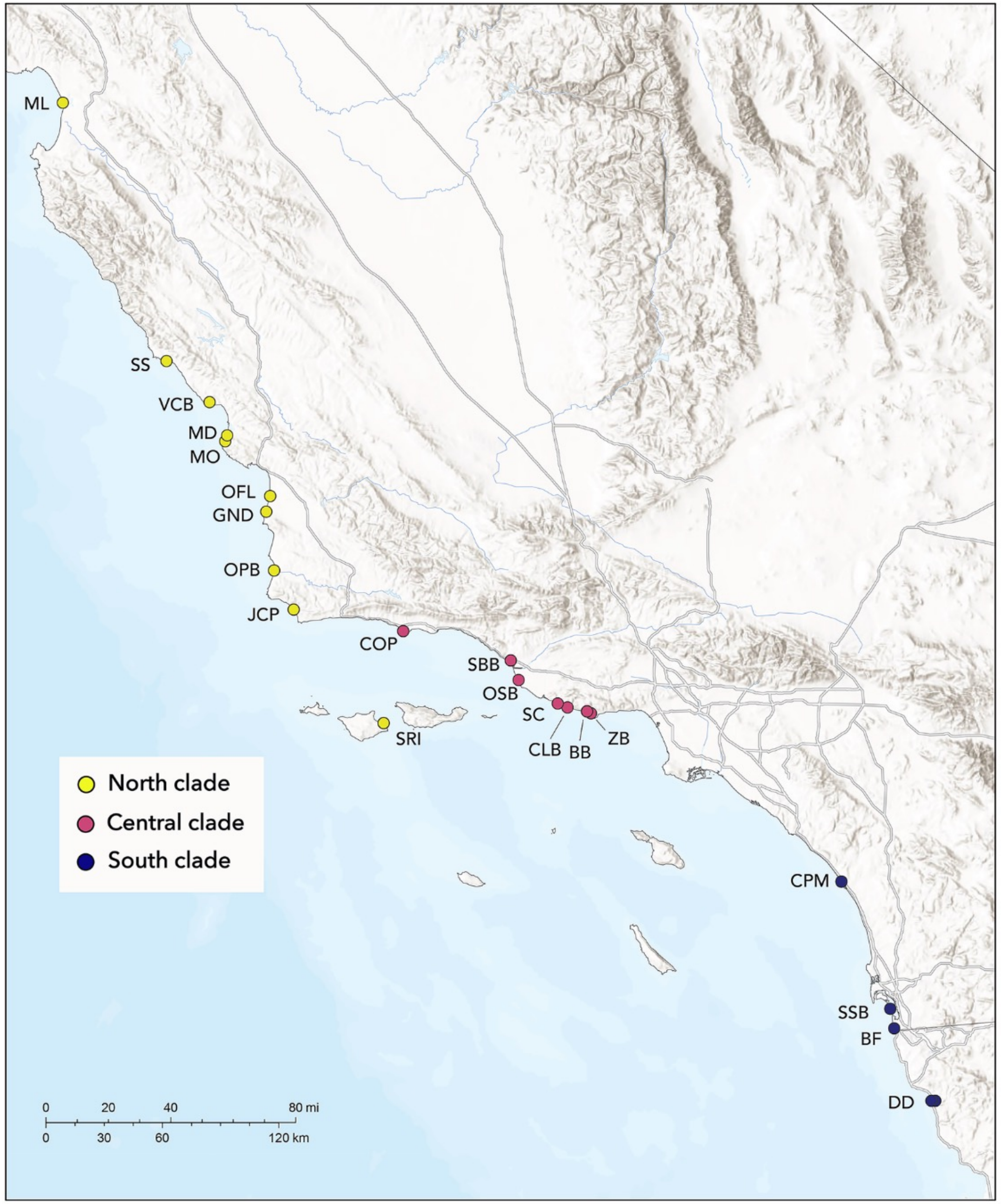


FIGURE 1 | Maximum likelihood phylogram based on minimum 75% locus occupancy concatenated dataset. Shaded boxes correspond to major phylogenetic clades. Bootstrap support values < 100% are labeled, otherwise node support is 100%. Black circles indicate nodes with 100% support from consensus species trees generated with ASTRAL-III with bootstrap resampling run with 100 pseudoreplicates in ASTRAL v5.7.8 Outgroup not shown for display purposes. Acronyms in parentheses next to specimen codes correspond to localities (see Figures 2 and S1). Subset image shows live *Aptostichus ramirezae* sp. nov. (BME101034).



California State Parks, Esri, TomTom, Garmin, FAO, NOAA, USGS, Bureau of Land Management, EPA, NPS, USFWS, Esri, USGS

FIGURE 2 | Distribution map of California and Baja California (partial) with localities (and their acronyms) included in genetic analyses. Colors correspond to major phylogenetic clades (see Figure 1). Map made with ArcGIS Online (Esri 2025).

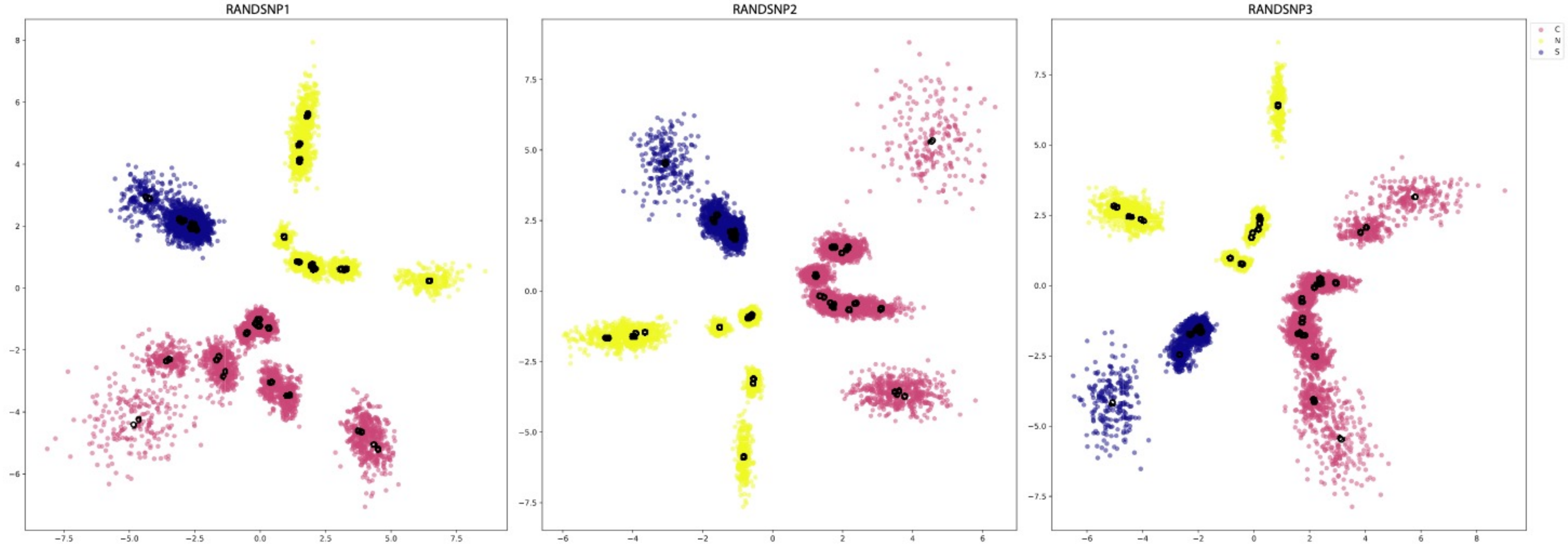


FIGURE 3 | Variational AutoEncoder cluster analyses of three random unlinked SNP datasets. All datasets are based on the minimum 75% locus occupancy. Black open circles represent the mean of phased SNP data for an individual and color clouds represent the standard deviation for the latent distribution. Colors are based on assignment to the major clades (see Figure 1).

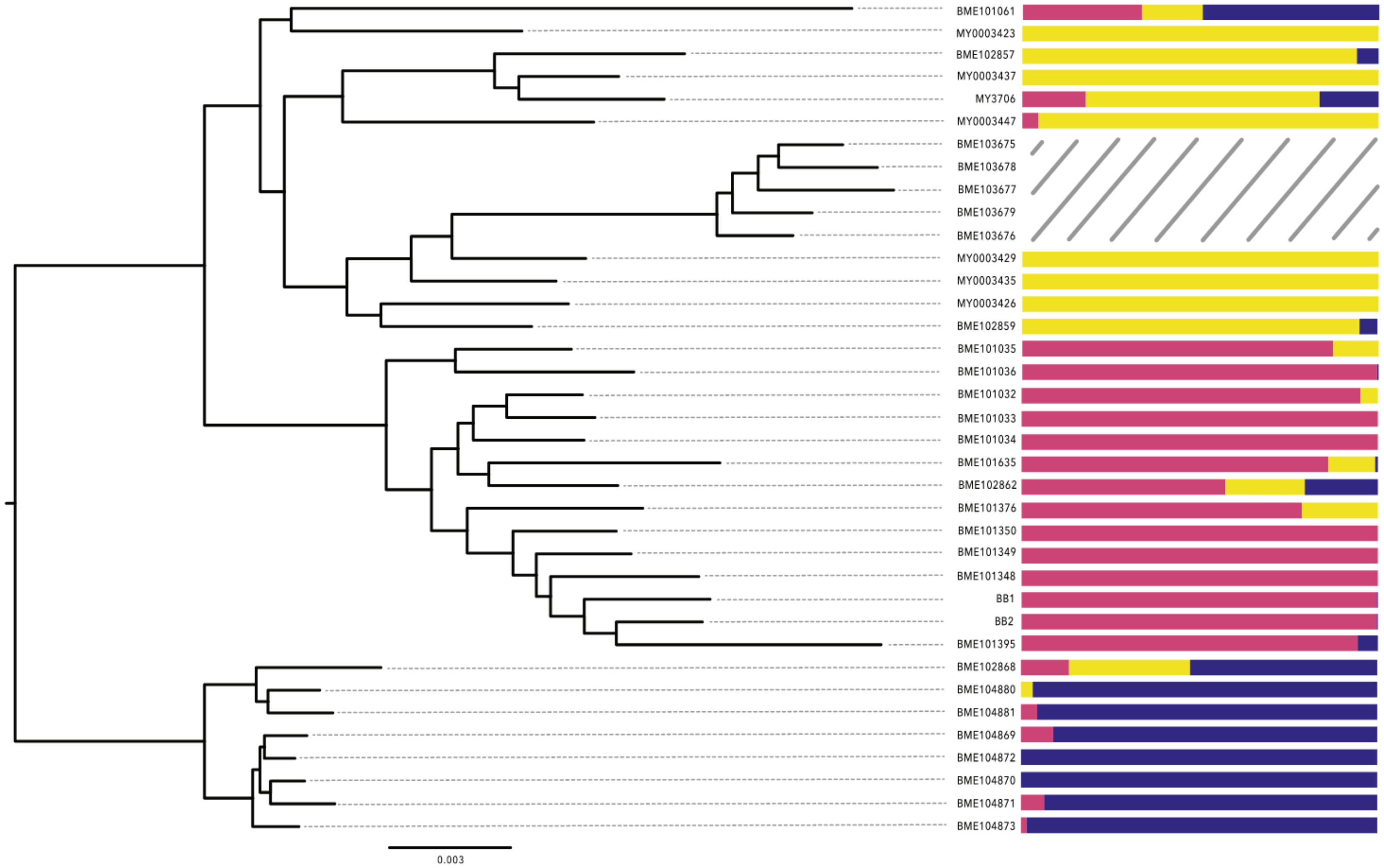


FIGURE 4 | Results of maximum likelihood phylogeny with 75% locus occupancy (see S4a for exact bootstrap values). Ancestry proportions based on RANDSNP1 dataset generated using sNMF are plotted next to individuals. Individuals from Santa Rosa Island (indicated by hatch marks) were not included in this analysis due to higher levels of divergence and missing data.

TABLE 1 | Results of ANOVA of morphological characters for 38 adult males.

Character	*F*	Pr(>*F*)	North	Central	South
Palpal tibia length	22.6	4.99e-07***	a	a	b
Palpal tibia width	6.016	0.00568**	a	a	b
Carapace width	3.125	0.0564	—	—	—
Sternum length	4.311	0.0212*	ab	a	b
Sternum width	0.907	0.413	—	—	—
Labium length	2.551	0.0924	—	—	—
Labium width	1.763	0.186	—	—	—
Femur I length	8.589	0.000923***	a	ab	b
Patella I length	8.341	0.00109**	a	ab	b
Tibia I length	28.87	3.93e-08***	a	a	b
Metatarsus I length	15.39	1.6e-05***	a	a	b
Tarsus I length	1.516	0.234	—	—	—
Femur IV length	1.224	0.306	—	—	—
Patella IV length	4.06	0.026*	a	ab	b
Tibia IV length	2.636	0.0858	—	—	—
Metatarsus IV length	5.919	0.00611**	a	ab	b
Tarsus IV length	1.506	0.236	—	—	—

Note: Measurements for all characters were standardized by carapace length. *F* and *p* value results are shown. *F* value is calculated as the ratio of between-group variance to within-group variance. *p* value represents the probability that a difference between group means (*F* value) is observed by chance. Asterisks in column 3 represent the level of significance as determined by ANOVA. Letters in North, Central, and South columns represent group assignments from Tukey HSD post hoc tests for significant results. Bolded characters represent secondary sexual characters, and nonbolded are somatic characters. See Methods for character definitions.

TABLE 2 | Results of ANOVA of morphological characters for 84 adult females.

Character	*F*	Pr(>*F*)	North	Central	South
Carapace width	1.475	0.235	—	—	—
Sternum length	2.665	0.0757	—	—	—
Sternum width	13.11	1.17e-05***	a	a	b
Labium length	0.594	0.554	—	—	—
Labium width	8.681	0.000384***	a	ab	b
Femur I length	7.98	0.000686***	a	a	b
Patella I length	16.97	6.98e-07***	a	a	b
Tibia I length	24.01	6.47e-09***	a	a	b
Metatarsus I length	0.54	0.585	—	—	—
Tarsus I length	1.579	0.212	—	—	—
Femur IV length	5.994	0.00374**	a	a	b
Patella IV length	5.348	0.00658**	a	ab	b
Tibia IV length	0.151	0.86	—	—	—
Metatarsus IV length	1.704	0.188	—	—	—
Tarsus IV length	3.114	0.0498*	a	ab	b

Note: Measurements for all characters were standardized by carapace length. *F* and *p* value results are shown. *F* value is calculated as the ratio of between-group variance to within-group variance. *p* value represents the probability that a difference between group means (*F* value) is observed by chance. Asterisks in column 3 represent the level of significance as determined by ANOVA. Letters in the North, Central, and South columns represent group assignments from Tukey HSD post hoc tests for significant results. See Methods for character definitions.

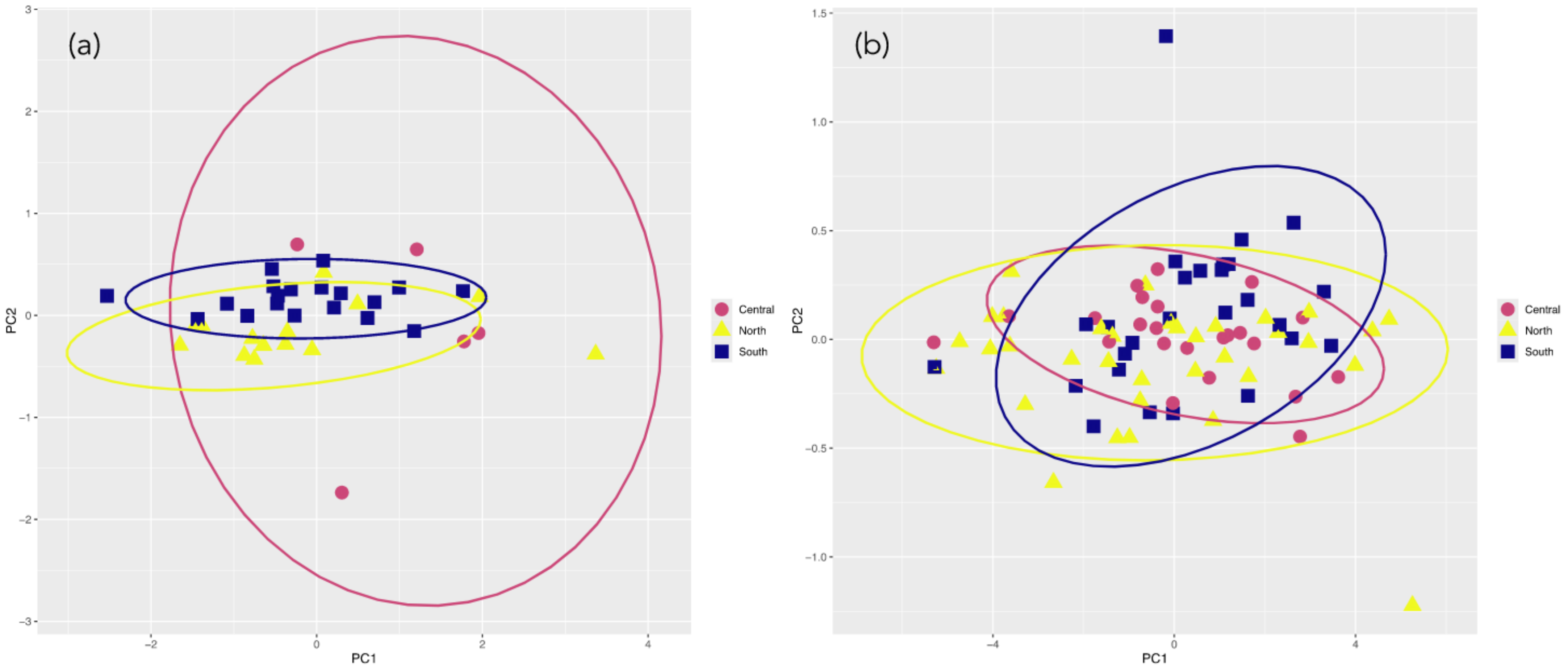


FIGURE 5 | Visualization of principal components 1 and 2 for morphological measurements. (a) males (b) females. Ellipses are based on the multivariate *t*-distribution at the 95% confidence level.

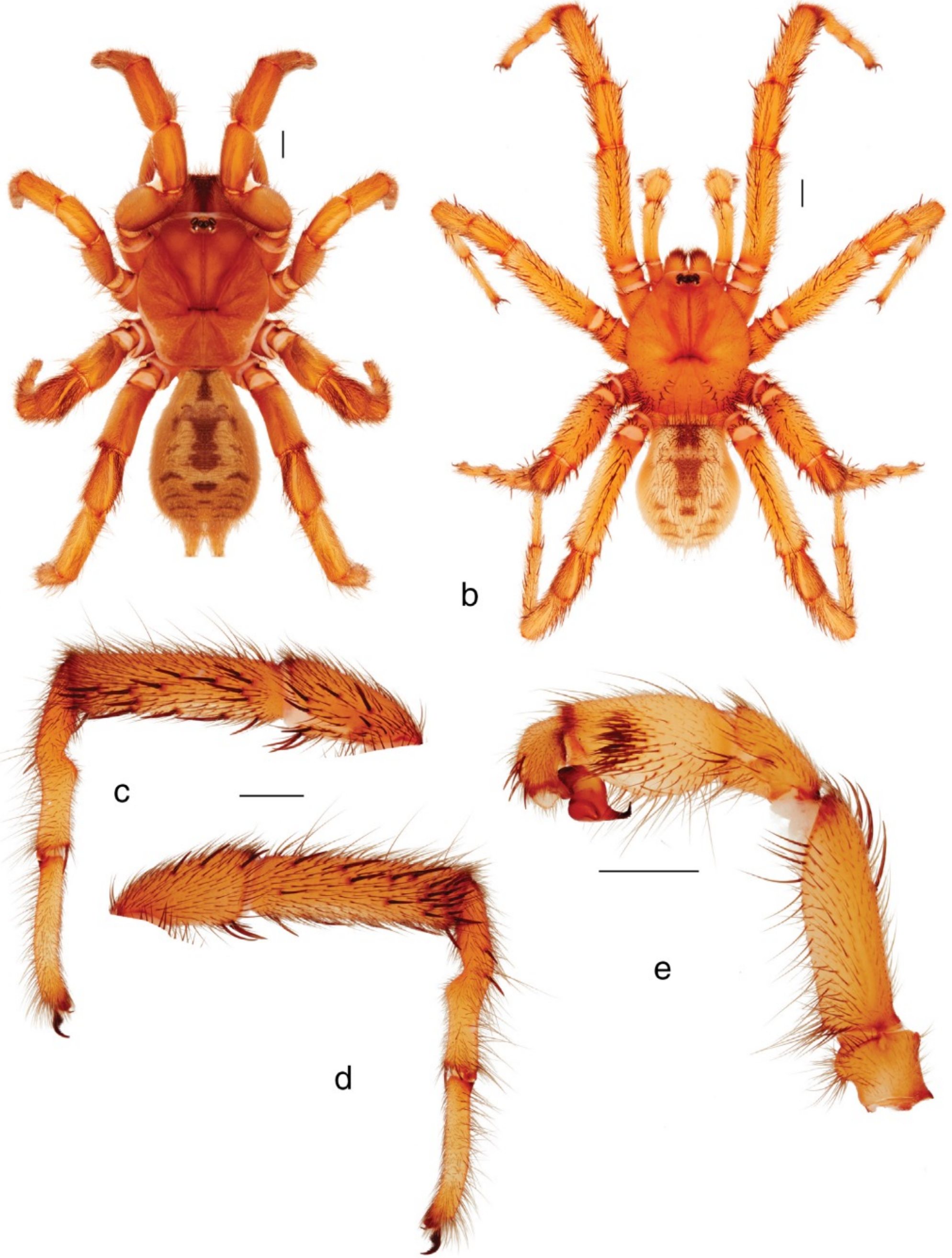


FIGURE 6 | *Aptostichus ramirezae* sp. nov. (a) PARATYPE female (MY3749) habitus. (b–e) HOLOTYPE male (BME101067). (b) habitus, (c) retrolateral view of leg I, (d) prolateral view of leg I, (e) retrolateral view of pedipalp. Scale bars = 1 mm.

- Cohesion species concept?
- What does the new species mean, ethically and legally?
- What caused the speciation event?
- What is an ultraconserved element?
- How important is sample size?
- How do we know the morphological differences aren’t plastic?
- What does locus occupancy mean?
- This may be just a me issue, but whenever I see PCA's I feel weird. Like I understand what is going on and why people do them (they are pretty and fun to look at), but I get a bit concerned when people start to make bold claims about them (e.g. the circles don't overlap so the two groups are different) without running some type of stats on them (like an RDA). Or just treating PC axes as the most biologically meaningful. Is it just a thing with morphology (or other fields of high dimensionality) to do a PCA and not worry about the stats behind it?
- Why do trapdoor spiders bring me so much joy?
- What was the purpose of RANDSNP? What is ABBA-BABA? VAE analyses? Hardy-Weinberg?
- When do you need an outgroup?
- The only thing I find a bit complex is naming a new taxon when you don't have enough morphological characteristics to recognize it in the field. It doesn't seem entirely viable or practical. But one thing I like about this approach is the idea that we should conserve genetic diversity (not the diversity of species as such).
- Naming species after people? After living people?
- I am not an animal person, but I am interested in how they get the DNA sample from the specimens. Like they get the DNA from the legs, but do they have to kill the spider to do that?