

Chelicerae Orientation and the Diversification of Spiders (Arachnida: Araneae)

Brianna Flynn^{1, 2}, Hannah Wood²

University of Texas at Austin, Department of Integrative Biology¹, Smithsonian Institution, National Museum of Natural History, Department of Entomology²

Introduction

Spider chelicerae, which are functionally equivalent to jaws, are a crucial component to spider biology and successful prey capture (Figure 1). Not much is known about the diversity of this trait in spiders, or how the chelicerae have evolved to adapt to different ecological pressures. In this study, we examine how the various shapes and orientations of the chelicerae have diversified across all major spider lineages.

Our hypothesis is that hunter spiders, because of their reliance on cheliceral performance compared to those that use a snare to capture their prey, have experienced an increased rate of cheliceral trait evolution.

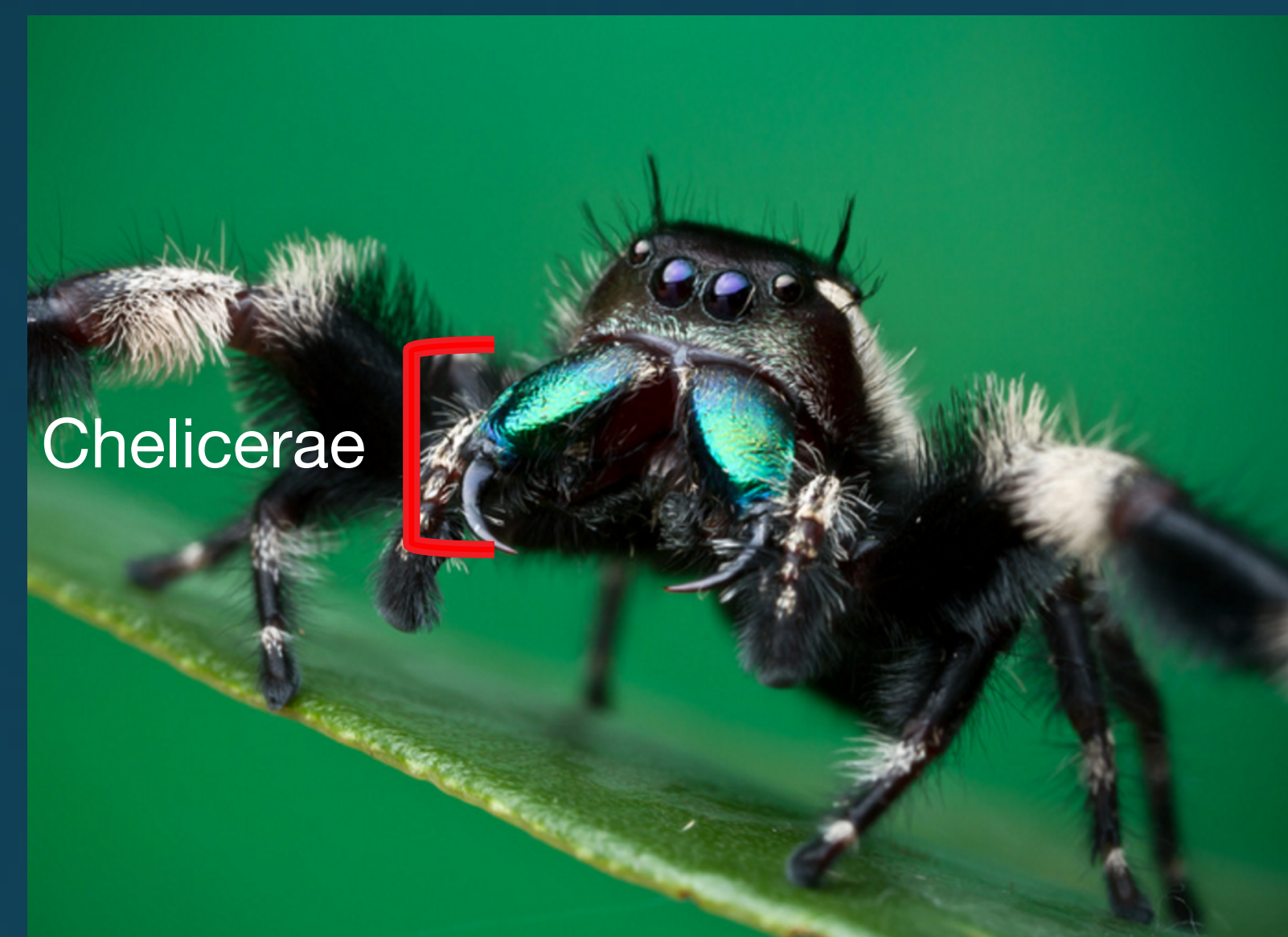
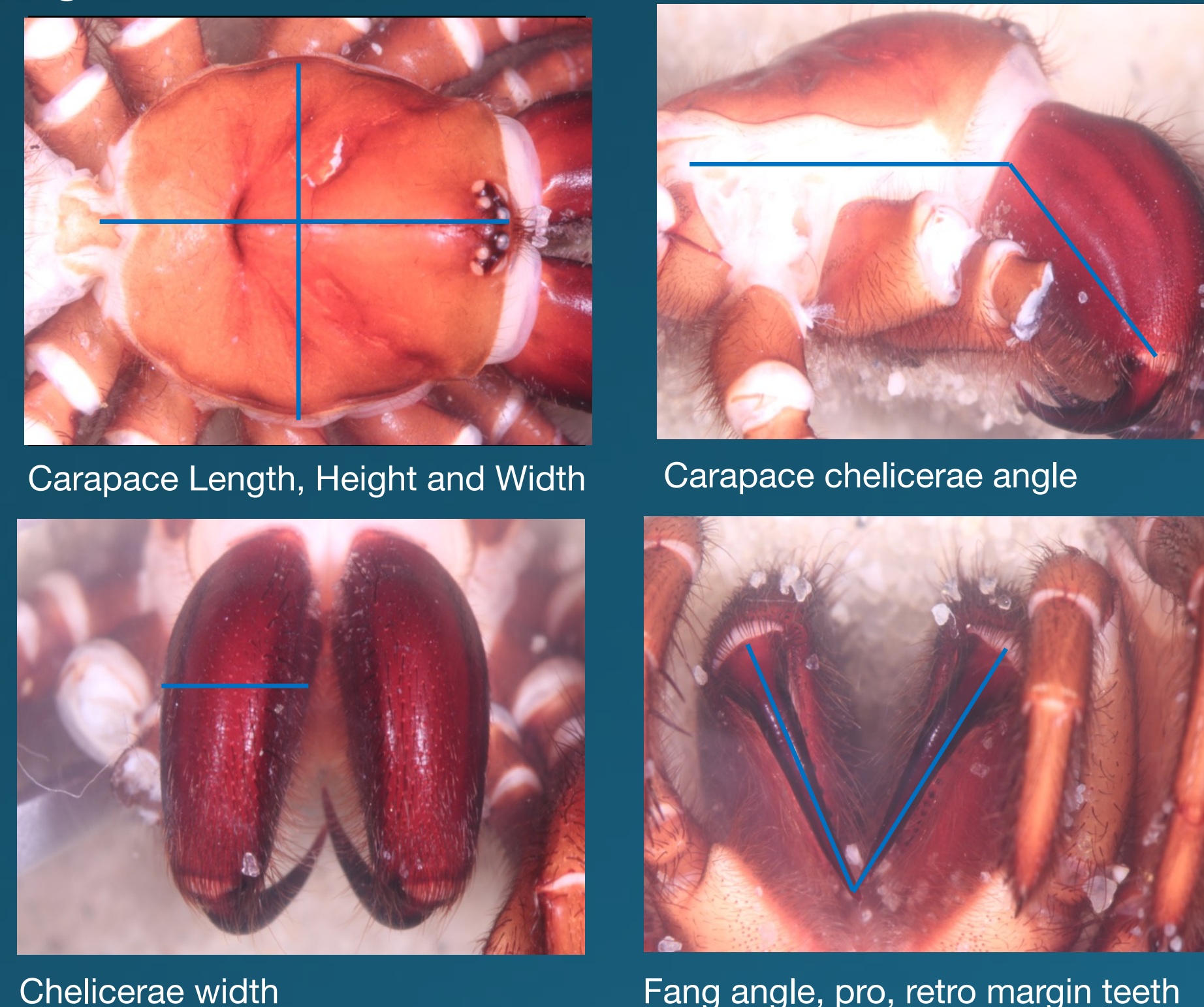


Figure 1. Chelicerae of a male canopy jumping spider *Phidippus otiosus*, image from Collin Powell Photography

Methods

Figure 2.



Results

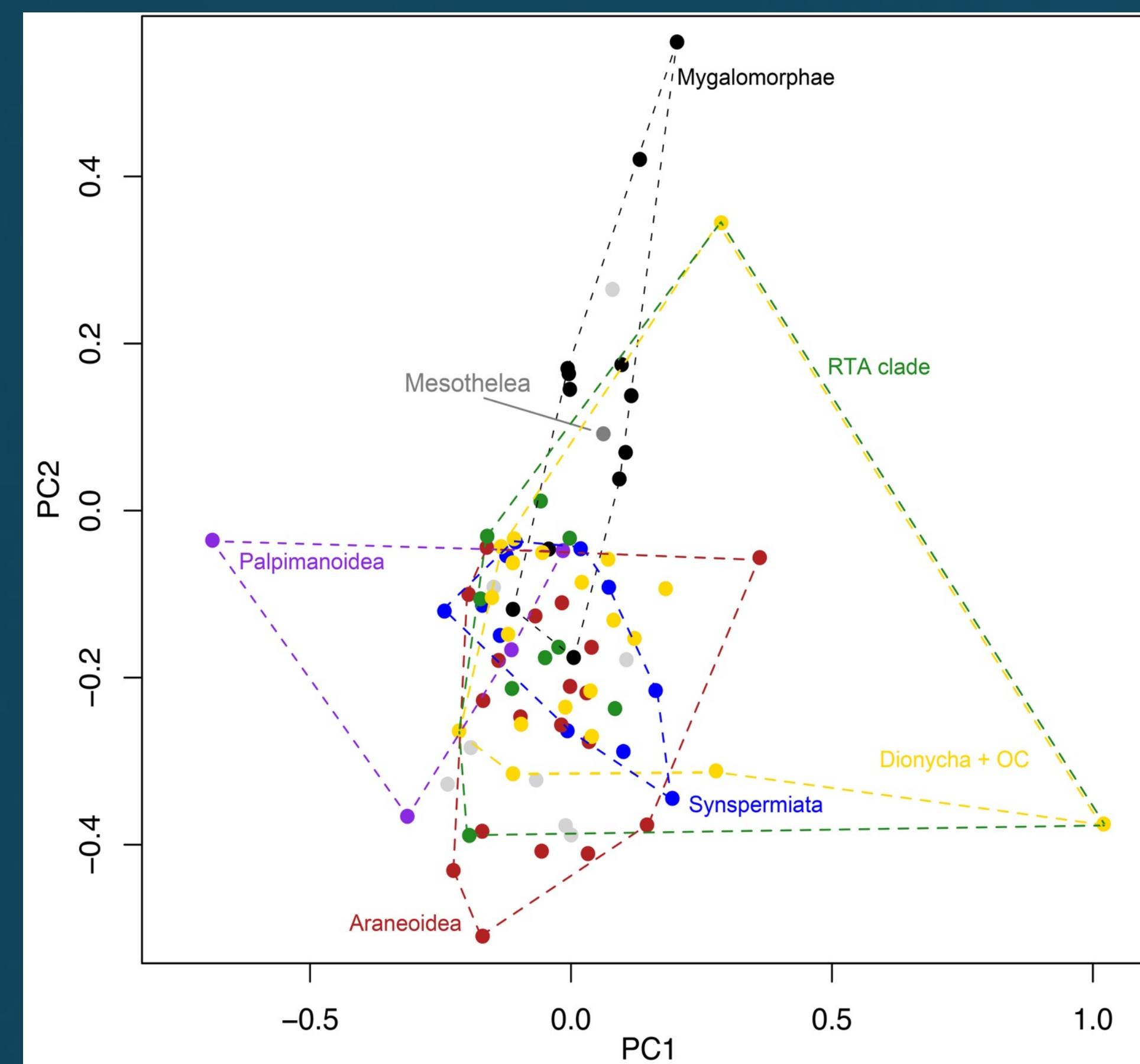


Figure 3. Morphospace plot of the first two PC axes showing cheliceral morphospace across spiders.

The first three PC axes, which were retained based on having eigenvalues greater than 1, explain 33.8%, 18.3% and 13.8% of the variation, and combined 65.9%.

PC1 describes the height of the carapace and length of the chelicerae. PC2 describes the number of teeth, and PC3 describes the orientation of the chelicerae (fang angle).

Trait evolution: For each trait BAMM analyses found 2-3 rate shifts across spiders. For PC1, the rate shift occurred at the Palpimanoidea + Entelegynae, with a slowdown occurring in the Araneoidea; for PC2 (Figure 4) a small increase occurred in a Mygalomorphae lineage, and just preceding the Entelegynae, with a large increase at the RTA clade (including Dionycha and OC clade); for PC3, an increase occurred that preceded the Entelegynae.

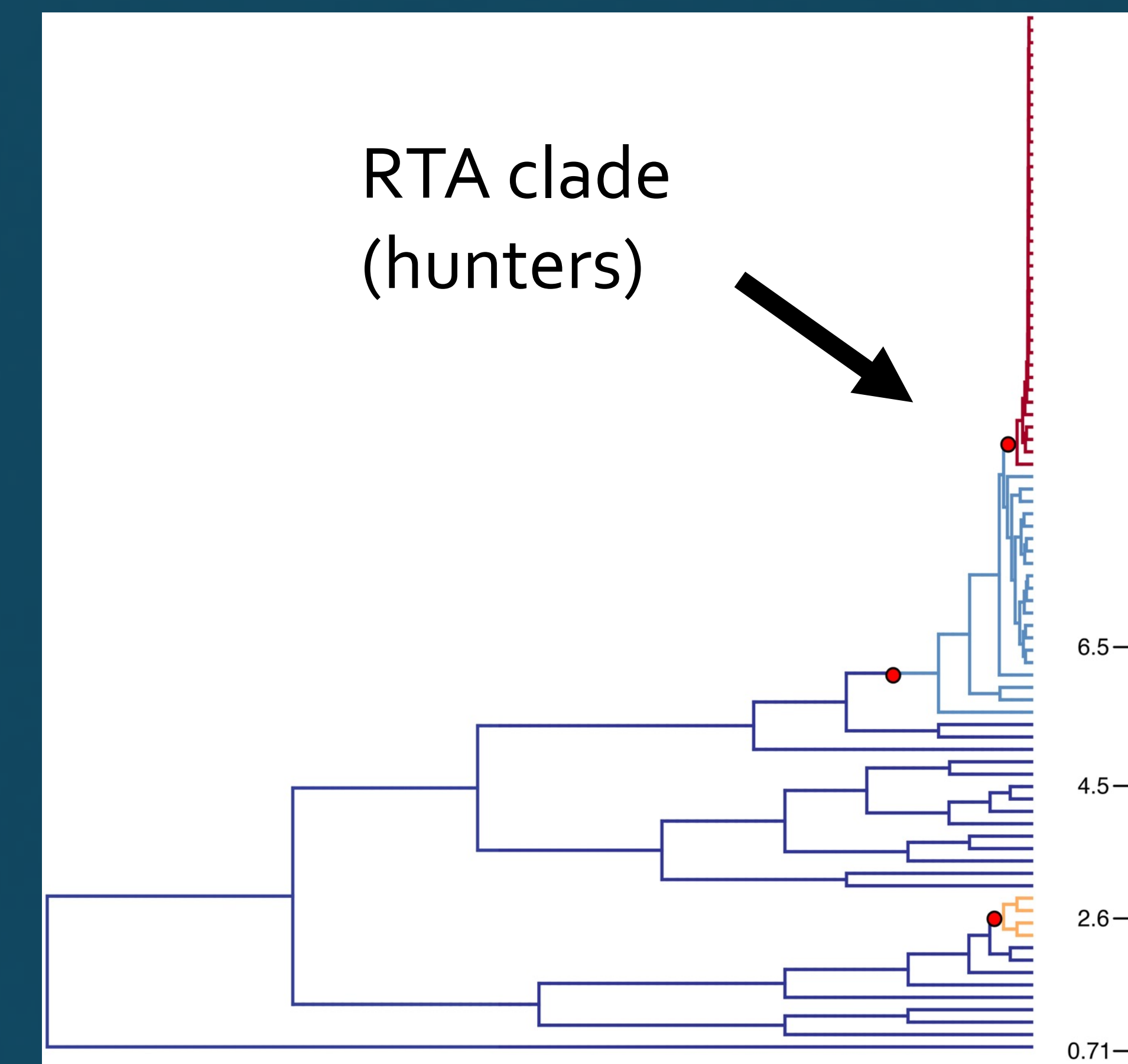


Figure 4. Ultrametric pruned phylogeny from Wheeler et al (2016), showing three shifts in rate of trait evolution (trait = PC2)

We used the recent phylogeny of Wheeler et al (2016) to understand relationships among 84 taxa that represent all major spider families and clades. Non-study taxa were pruned and the phylogeny was made ultrametric using penalized likelihood methods of Sanderson (2008). For these 84 taxa we measured seven morphological traits of the cephalothorax and one measurement of standard length per species (Figure 2). Measurements were taken, for one female per species, and all traits were natural log transformed.

The effect of size was removed by performing a phylogenetic linear regression on each measurement against the size measurement (Revell 2009).

We performed a phylogenetically corrected Principal Components Analysis and the resulting scores were extracted for each species (Revell, 2009).

To understand trait evolution we determined shifts in rate of trait evolution using the program BAMM (Rabosky 2014; Rabosky et al, 2014) for the following traits: PC1, PC2, PC3, and size (carapace width).

Discussion

The RTA clade occupies the greatest amount of morphospace (Figure 3) compared to other major spider clades. This clade (including Dionycha and the OC clade) mainly consists of hunter spiders.

Assuming that morphological adaptations reflect how species interact with their environment, morphology can determine ecological niche (Arnold 1983).

The high morphological diversity in the RTA clade suggests that this lineage occupies a diversity of niches (Figure 4).

The RTA clade shows a marked increase in the rate of cheliceral evolution for both PC1 and PC2. There is also evidence for additional rate shifts in a few other spider lineages (e.g., preceding the Entelegynae).

Conclusions

The finding of an increased rate of trait evolution in the RTA clade suggests that the evolution of a hunter lifestyle may relate to an increase in the diversification of cheliceral morphology. Although, evolution of the Entelegynae also relates to increases in trait diversification.

Future studies will include additional families and specimens, and should focus on determining the relationship between cheliceral form and function (functional morphology).

References and Acknowledgements

Special thanks to Liz Cottrell, Gene Hunt, and Virginia Power for the time and effort they put into the NHRE program. Thank you to my mentor Hannah Wood for introducing me to the world of arachnology and for making this research experience so fun and educational. This program and the resources it offers its undergraduates would not be possible without support from the Smithsonian Institution and the National Science Foundation (Grant 1560088).

- Rabosky, D.L., Grudler, M., Anderson, C., Shi, J.J., Brown, J.W., Huang, H., and Larson, J.G. (2014). BAMMtools: an R package for the analysis of evolutionary dynamics on phylogenetic trees. *Methods in Ecology and Evolution* 5, 701-707.
- Wheeler, W.C., Codrington, J.A., Crowley, L.M., Dimitrov, D., Goloboff, P.A., Griswold, C.E., Hormiga, G., Prendini, L., Ramirez, M.J., Sierwald, P., et al. (2016). The spider tree of life: phylogeny of Araneae based on target-gene analyses from an extensive taxon sampling. *Cladistics*, 1-43.
- Revell, L.J. (2009). Size-correction and principal components for interspecific comparative studies. *Evolution* 63, 3258-3268.
- Rabosky, D.L. (2014). Automatic detection of key innovations, rate shifts, and diversity-dependence on phylogenetic trees. *PLoS one* 9, e89543.
- Arnold, S.J. (1983). Morphology, performance and fitness. *American Zoologist* 23, 347-361.
- Sanderson, M.J. (2002). Estimating absolute rates of molecular evolution and divergence times: a penalized likelihood approach. *Molecular biology and evolution* 19, 101-109.