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Short Title: XXX

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Conflicts of Interests: The authors declare no conflicts of interest.

Data Archiving: Data are available on DRYAD (doi:10.5061/dryad.xwdbrv1f6 (Tejero-Cicuéndez et al. 2021b)). R-scripts are found in the Supplemental Information.

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³¹ **Abstract**

³² asdf

Introduction

some general paragraph on the evolution of phenotypic diversity

when organisms colonize new and unique habitats, they are subjected to novel ecological selection pressures in those habitats. Often these selective pressures elicit changes in body form, as organisms adapt to their new habitats (examples: some comment on ecomorphs, etc.). . . . leads to so-called ecomorphs, with such well known examples in Anolis lizards, cichlid fishes, etc. It follows that . . . Some comment on the fact that clades living in diverse ecological conditions often display greater diversity in form and function (REFS).

However, while the above patterns have been well documented in a variety of vertebrate taxa, what remains less known is how allometry plays a role in this phenotypic diversification. We know that XYZPDQ (about allometry). Then links to diversity..

The Afro-Arabian geckos in the genus *Pristurus* afford the opportunity to elucidate the interdigitating effects of allometry and habitat specialization on clade-level patterns of phenotypic diversity. Prior work on this system (Tejero-Cicuéndez et al. 2021a) has revealed that . . . (sentence or 2 about your prior study, getting to diversity and . . . Importantly, . . . something about habitat. . . . What remains unexamined however, is XYZPDQ. . .

In this study, we . . .

Materials and Methods

Data

For this study, we combined phenotypic, phylogenetic, and ecological data to evaluate macroevolutionary trends in allometry, and to discern the extent to which those patterns differed across species occupying distinct ecological habitats. The data were obtained from our prior work on this system (Tejero-Cicuéndez et al. 2021a, 2022), and are briefly described here. First we used a time-dated, molecular phylogeny that included all members of the genus *Pristurus*, including several currently undescribed taxa. The tree was estimated in a Bayesian framework, using five mitochondrial markers, six nuclear markers, and 21 calibration points (for details see Tejero-Cicuéndez et al. 2022). Next we categorized each species as belonging to one of three ecological groups (ground, rock, or tree), based on descriptions in the literature (see Tejero-Cicuéndez et al. 2021a). Finally, we obtained a phenotypic data set containing body size (snout-vent length: SVL) and eight linear measurements that describe overall body proportions: trunk length (TrL), head length (HL),

head width (HW), head height (HH), humerus length (Lhu), ulna length (Lun), femur length (Lfe), and tibia length (Ltb) (Tejero-Cicuéndez et al. 2021a). From the original dataset we restricted our study to those species represented by five or more individuals; resulting in a dataset of 687 individuals from 25 species ($\mu_N = 27$; min = 9, max = 56). These species were then matched to the phylogeny, which was subsequently pruned to arrive at our final dataset. All measurements were log-transformed prior to statistical analyses. Additional details regarding data collection and formal descriptions of each linear measurement may be found in the original sources (see Tejero-Cicuéndez et al. 2021a, 2022). The data are found on DRYAD: <https://doi.org/10.5061/dryad.xwdbrv1f6> (Tejero-Cicuéndez et al. 2021b).

Statistical Analyses

To test the hypothesis...

- Mancova body \sim SVL*hab.gp
 - PW of slopes, and inspected reg. coefficients to identify biological trends
 - Visualized multivariate regressions via regression scores (sensu Drake and Klingenberg 2008) and predicted lines (sensu Adams and Nistri 2010)
- Examine allometry phylogenetically.
 - PLS of head vs. SVL and limb vs SVL. Obtained scores on 1st axis for each.
 - within-species regressions of Head.sc \sim SVL & limb.sc \sim SVL; obtained regression coefficients (slopes)
 - mapped slopes on phylogeny under BM and generated traitgrams to identify changes in allometric relationships across the phylogeny
- Finally, to link allometric patterns with trends in phenotypic diversification we obtained size-standardized species means, following procedures in H TC paper (residuals from phylo-regressions of traits on SVL, residuals). We then performed an ordination to obtain a phylomorphospace, where habitat types and species could be observed.

Results

Discussion

References

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Figures

Figure 1. Linear Measurements used in this study. SVL = snout-vent length, TL = trunk length, HL = head length, HW = head width, HH = head height, Lhu = humerus length, Lun = ulna length, Lfe = femur length, Ltb = tibia length (for details see Tejero-Cicuéndez et al. 2021a).

Figure 2. Plot of regression scores and predicted lines representing the relationship between linear body measurements and size (SVL). Individuals are colored by habitat use: rock (beige), ground (dark purple), and tree (magenta).

Figure 3. Traitgrams showing the evolution of body size (SVL) through time based on the phylogenetic tree of *Pristurus*. Colors represent an evolutionary mapping of regression slopes describing the relationship of (A) head morphology versus body size, and (B) limb proportions versus body size (see text for descriptions). Species names are colored by habitat use: rock (beige), ground (dark purple), and tree (magenta).

Figure 4. Phylomorphospace of *Pristurus*, based on residuals from a phylogenetic regression of body measurements on size (SVL). Species means are colored by habitat use: rock (beige), ground (dark purple), and tree (magenta). Large and small rock-dwelling and ground-dwelling are highlighted with darker colors to highlight their differentiation and relative positions in morphospace.

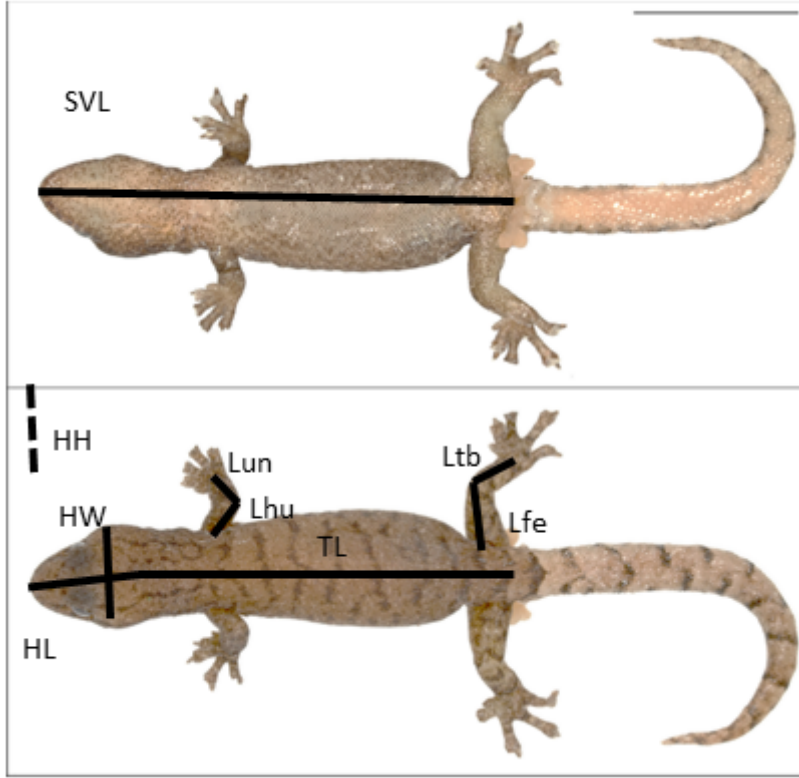


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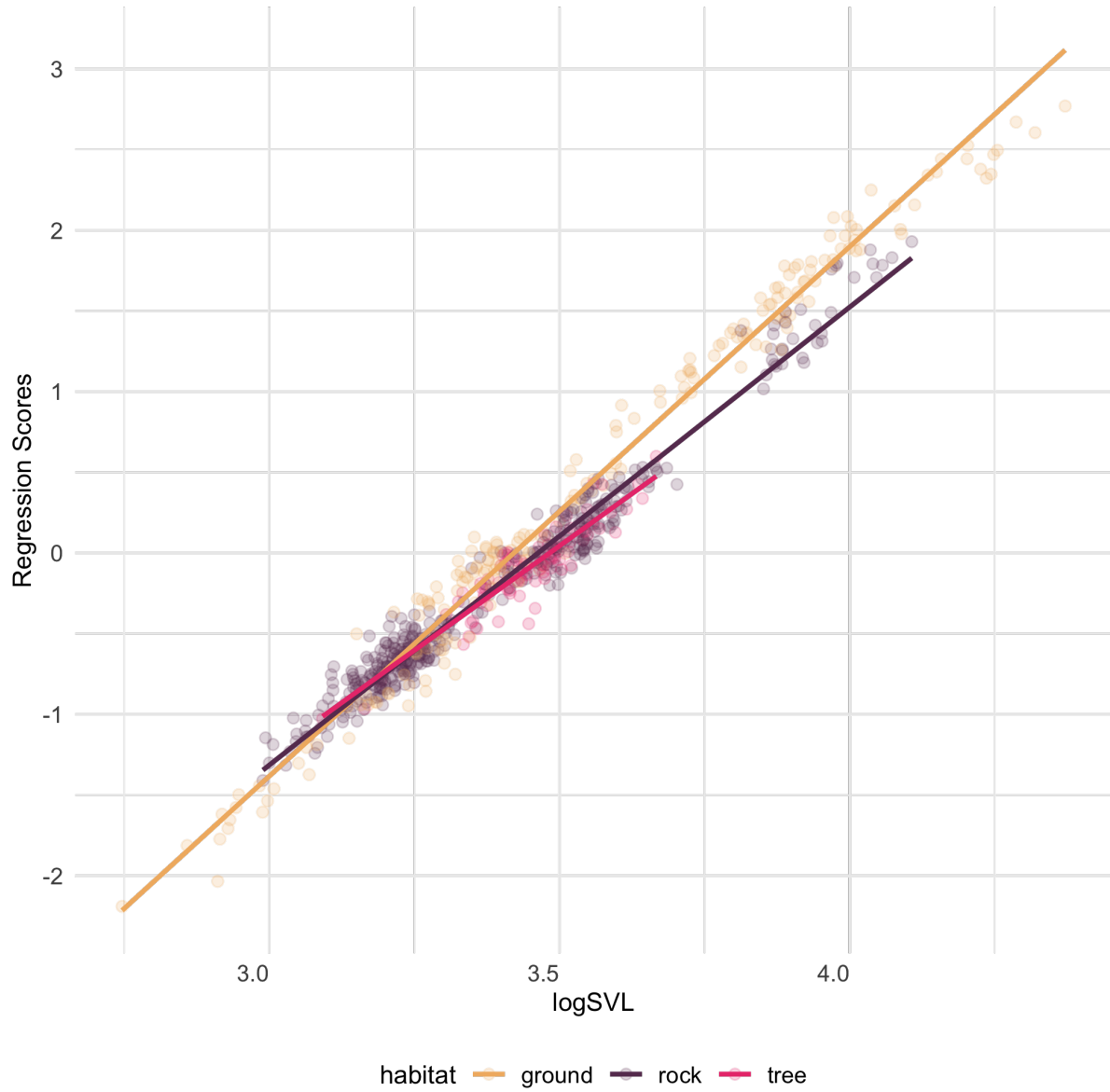


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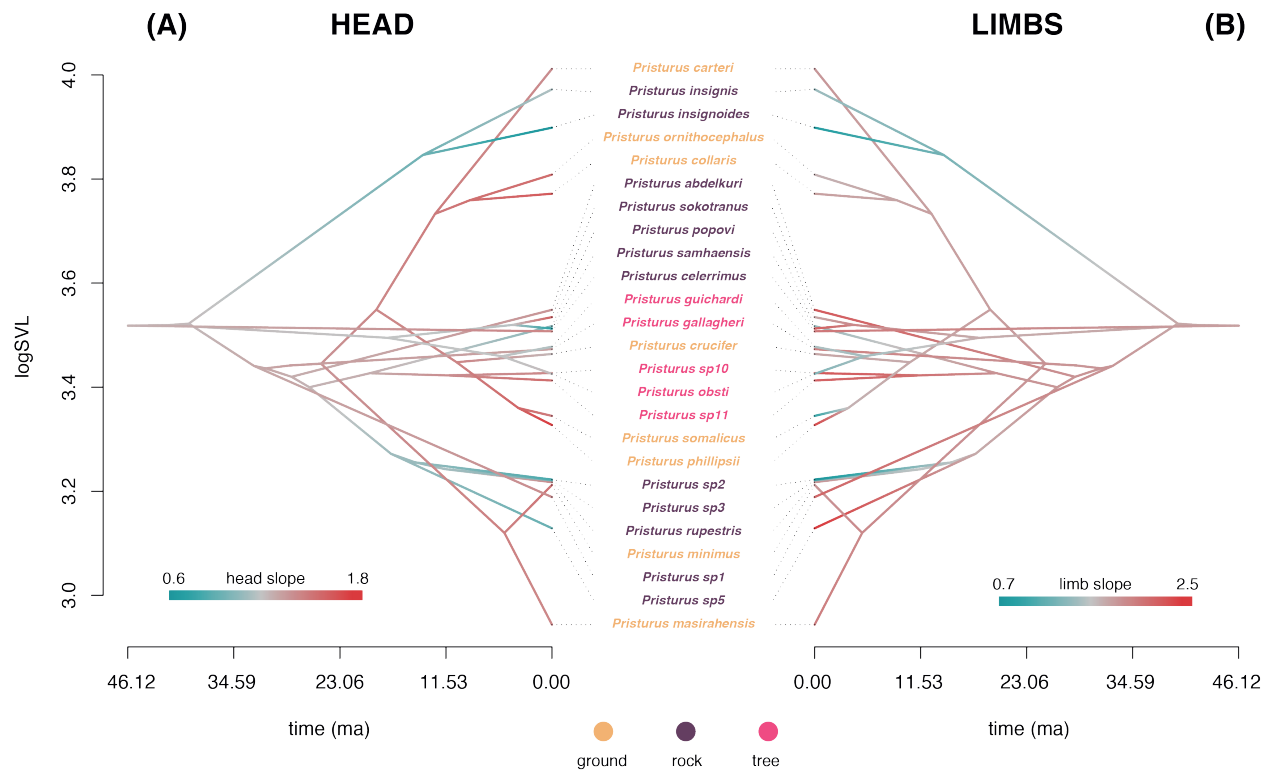


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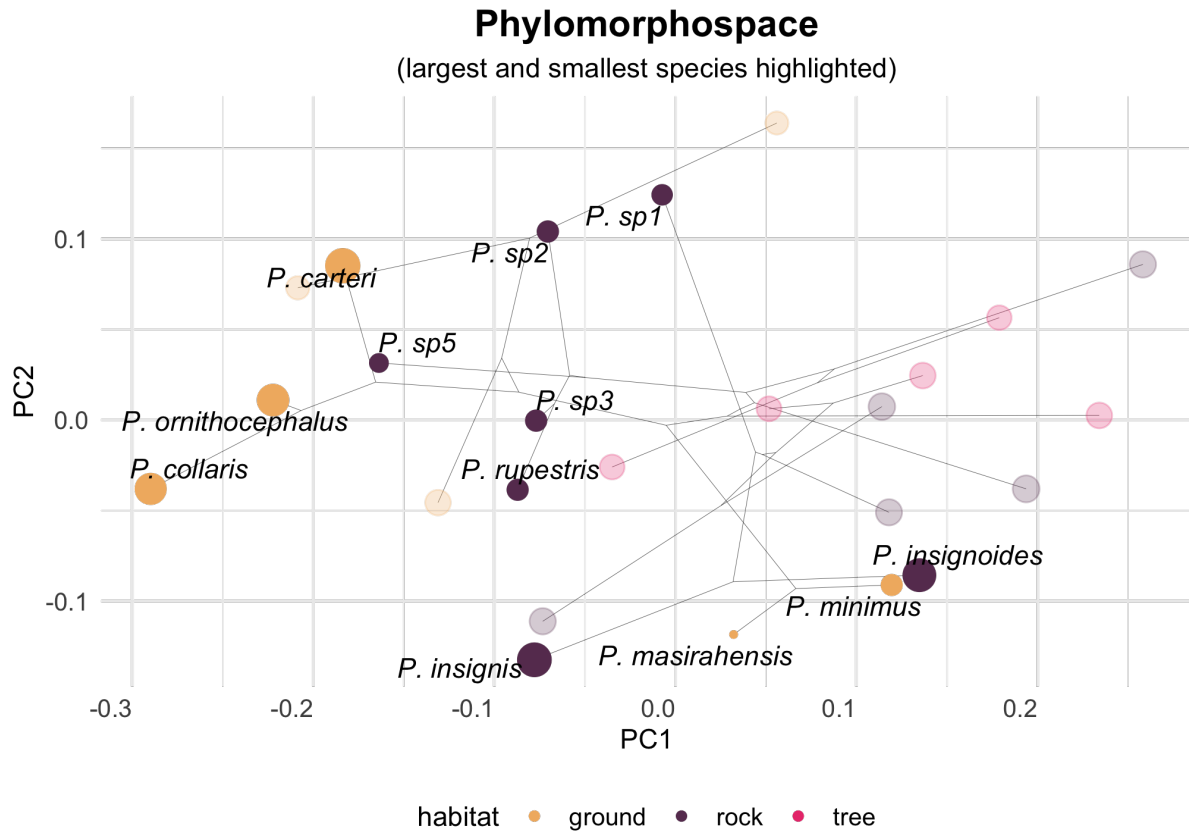


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