

Use of an Exemplar Versus Use of a Sample for Calculating Summary Metrics of Morphological Traits in Comparative Studies of *Anolis* Lizards

Comparative morphological analyses of large groups of species are limited by the time needed to perform multiple measurements on several individuals of each studied species. For example, taking complete external morphological data (e.g., Poe 2004) for an individual *Anolis* lizard for phylogenetic analysis takes us approximately 14 minutes. If even five individuals per species are scored for every species in the *Anolis* clade, and we estimate 400 species of *Anolis*, data collection will take over 466 hours. But is it necessary to score lots of specimens to ascertain an informative summary of the population/species? Although more data are nearly always better, researchers must optimize the time spent on data collection relative to the goals of a planned study. If measuring one specimen achieves the same results as measuring (e.g.) five specimens, then measuring one specimen is preferable.

We investigated the efficacy of a time-saving approach for performing comparative morphological analyses of lizard species. In particular, we asked whether use of a single exemplar specimen—the largest male—provides distinguishable results from using means for five conspecific male specimens in some comparative species analyses of traits commonly employed in morphological, ecological, and phylogenetic analyses. We tested for sampling effects related to the number of individuals scored for five commonly used morphological traits and three commonly employed quantitative techniques (e.g., some traits and techniques in Losos et al. 1998; Poe 2004; Latella et al. 2011) in 15 species of *Anolis* lizards.

Five morphological characters for five adult males each of 15 species of *Anolis* lizard were collected using specimens from the Poe Lab and the Museum of Southwestern Biology at the University of New Mexico. The five largest adult males available to us for each species were used without concern for geographic origin. The following characters were collected according to procedures established by Williams et al. (1995) and Poe and Yañez-Miranda (2008): body size measured as snout-vent length (SVL) from tip of snout to anterior edge of cloaca; head length (HL) measured from tip of snout to anterior edge of ear opening; femoral length (FL) measured from the midline of the body laterally to the knee; scales across snout (SNSC) counted between second canthals; and lamellae count on phalanges ii and iii of the fourth toe of the hind foot (see above cited papers for more detailed character descriptions). Measurements were taken with digital calipers to the nearest 0.1 mm.

We performed analyses of species using two sets of these data: means for each species using all measured individuals, and values for the single largest male specimen for each species. We

compared summary metrics for these two data sets for three techniques: 1) relationship of traits to body size (SVL vs. HL, FL, and lamellae; slope, R^2); 2) phylogenetic gap-coding (SNSC, SVL; Thiele 1993), a method that converts measurement data to phylogenetic codes; and 3) principal components (scores for PC I and PC II using all five variables).

Results are summarized in Table 1 and Figs. 1 and 2. We found that use of a single exemplar specimen per species produced

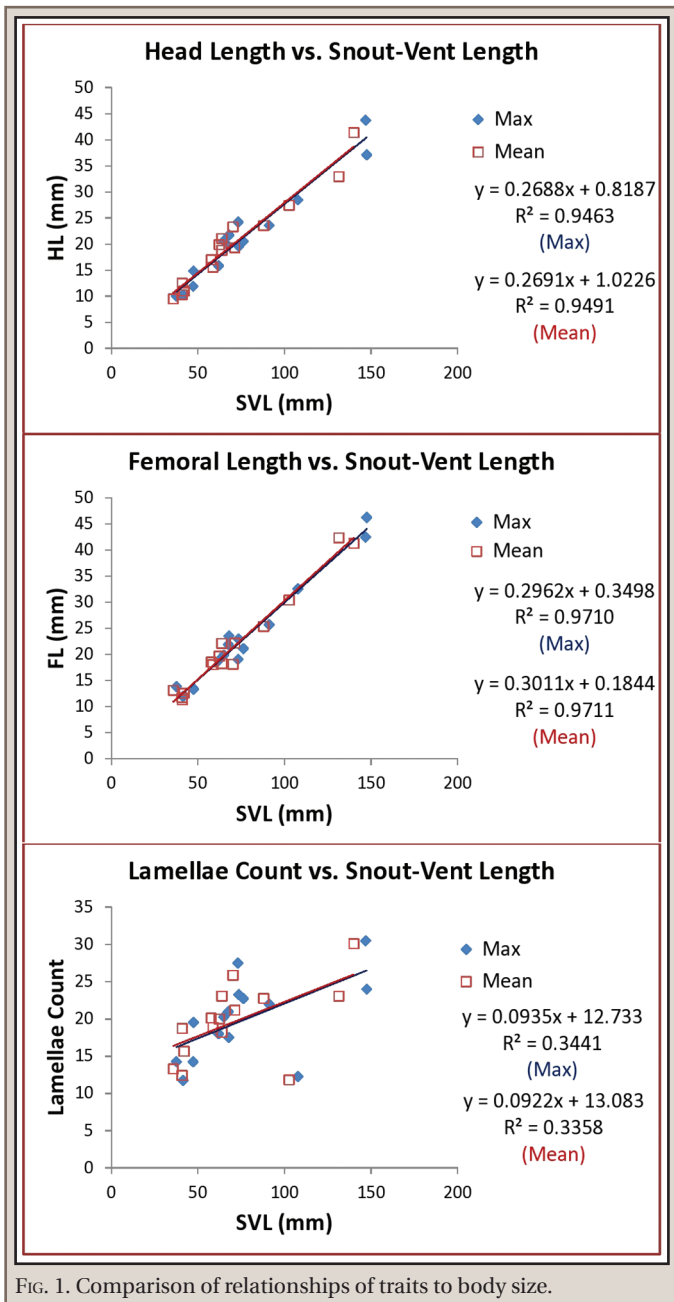


FIG. 1. Comparison of relationships of traits to body size.

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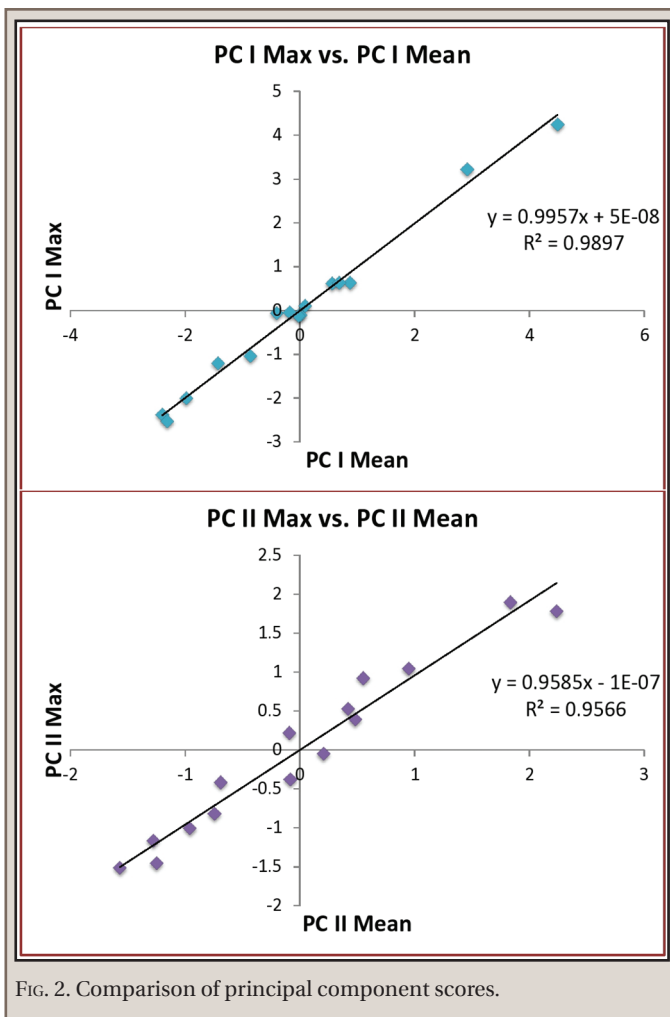


FIG. 2. Comparison of principal component scores.

nearly identical results to using summary statistics from five specimens for body size-trait relationships, phylogenetic coding, and principal component scores. Body size-trait relationships differ by less than 0.005 in slope, and by less than 0.008 in R^2 (Fig. 1). This similarity among datasets occurred both in traits expected to closely track body size (HL, FL) and in a trait known to correlate more weakly with body size (lamellae). The average difference between phylogenetic codes for each dataset was 0.4 on a scale of 0.0 to 5.0 for SVL and SNSC, and 19 of 30 codes were identical between the datasets (Table 1). Principal component scores were very strongly correlated between datasets (Fig. 2).

These results suggest that little would be gained by measuring five specimens rather than one specimen for these analyses (body size-trait relationships; phylogenetic coding; PC scores) for these traits in these *Anolis* species. A five-fold decrease in data collection time is not trivial in comparative studies of large clades. In the case of *Anolis*, the time saved by measuring one specimen rather than five would be on the scale of months, rather than hours. We conclude that some comparative interspecific morphological studies of lizards such as *Anolis* may proceed more efficiently by measurement of a single exemplar per species rather than multiple individuals.

Although results are conclusive for the traits, methods, species, and scale studied here, we do not recommend general extrapolation to other studies. There certainly are studies of morphology—perhaps most studies—wherein measurement of several or even hundreds of individuals per species or population

TABLE 1. Comparison of phylogenetic codes for snout-vent length (SVL) and scales across snout (SNSC).

Species (<i>Anolis</i>)	SVL (Max)	SVL (Mean)	SNSC (Max)	SNSC (Mean)
<i>baleatus</i>	5	5	1	0
<i>biporcatus</i>	2	3	2	3
<i>concolor</i>	1	2	2	3
<i>crisatellus</i>	1	1	1	1
<i>cybotes</i>	1	1	0	0
<i>frenatus</i>	5	5	5	5
<i>fuscoauratus</i>	0	0	4	5
<i>gingivinus</i>	1	1	0	0
<i>grahami</i>	2	1	4	4
<i>kunayalae</i>	3	3	4	5
<i>limifrons</i>	0	0	5	5
<i>porcatus</i>	1	1	1	0
<i>pulchellus</i>	0	0	1	0
new species	0	0	5	4
<i>townsendi</i>	1	1	4	4

is warranted. Studies of intraspecific variation, of growth within species, and of traits with high variance are obvious examples where many individuals must be measured in order to gain biologically meaningful results. Other cases similar to our study (e.g., interspecific principal component analyses) may produce similar results—i.e., adequacy of use of a single exemplar for some quantitative summary metrics. But these inferences are best made on a case-by-case basis. We believe that the null expectation for a study with unknown variance properties should be that measurement of more than one individual per species/population is warranted. A conservative implication of our results is simply that large sample sizes should not be assumed to be necessary for all studies.

LITERATURE CITED

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APPENDIX

Specimens Examined

- Anolis baleatus*: POE 0373–0375, 0395, 0485.
Anolis biporcatus: POE 1520, 2151, 2155, 2170–2171.
Anolis concolor: UNM 46696, 46703, 46721, 46724, 46746.

Anolis cristatellus: POE 0137–0138, 0155, 0157, 0164.

Anolis cybotes: POE 0453, 0480–0481, 0603, 0610.

Anolis frenatus: EWS 0103, POE 1435, 1639, 1880, 1907.

Anolis fuscoauratus: POE 2715, 2720, 2730, 2775–2776.

Anolis gingivinus: UNM 44410, 44413, 44420–44421, 44425.

Anolis grahami: POE 1314, 1332, 1343, 1349, 1357.

Anolis kunayalae: EWS 0102, POE 1623, 1969–1970, 2100.

Anolis limifrons: EWS 0014, 0091, 0093, 0099, 0104.

Anolis porcatus: POE 0706–0707, 0724–0725, 1117.

Anolis pulchellus: POE 0151–0152, 0238–0239, 3689.

Anolis new species: POE 1426, 1436, 1558, 1580, 1963.

Anolis townsendi: UNM 58081, 58093, 58095, 58097, 58101.