The evolution of island gigantism and body size variation in tortoises and turtles

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Extant cheloniens (turtles and tortoises) span almost four orders of magnitude of body size, including the startling examples of gigantism seen in the tortoises of the Galapagos and Seychelles islands. However, the evolutionary determinants of size diversity in cheloniens are poorly understood. We present a comparative analysis of body size evolution in turtles and tortoises within a phylogenetic framework. Our results reveal a pronounced relationship between habitat and optimal body size in cheloniens. We found strong evidence for separate, larger optimal body sizes for sea turtles and island tortoises, the latter showing support for the rule of island gigantism in non-mammalian amniotes. Optimal sizes for freshwater and mainland terrestrial tortoises are similar and smaller, although the range of body size variation in these forms is qualitatively greater. The greater number of potential niches in freshwater and terrestrial environments may mean that body size relationships are more complicated in these habitats.

Keywords: adaptation; body size evolution; chelonia comparative methods; island gigantism; Ornstein–Uhlenbeck; turtles

1. INTRODUCTION

The giant tortoises of the Galapagos, Seychelles and Mascarene islands represent some of the most conspicuous examples of island gigantism. These species, which fall at the upper end of the size scale for extant cheloniens (turtles and tortoises), are thought to have achieved their large size as a consequence of relaxed predation pressure, competitive release, or as an adaptation to increased environmental fluctuations on islands [1]. Remarkable as these island giants are, size diversity in the approximately 330 extant chelonia species is equally impressive. Cheloniens span almost four orders of magnitude of body mass, from tiny terrestrial species, such as the 80 g speckled padloper tortoise (Homopus signatus), to giant marine turtles, such as the 500 kg leatherback (Dermochelys coriacea) [2]. Surprisingly, the potential correlation between habitat and size in cheloniens has never, to our knowledge, been tested in a quantitative evolutionary framework. Here, we compare the fit of a series of models of body size evolution to a comparative dataset and time calibrated phylogeny of approximately 70 per cent of extant species of turtle and tortoise. Our results suggest that body size variation in cheloniens can be explained by broad habitat differences.

2. MATERIAL AND METHODS

(a) Phylogenetic reconstruction

We used BEAST v. 1.5.4 [3] to simultaneously infer phylogeny and branch lengths of cheloniens under a relaxed molecular clock. Our data comprised 1140 bp of cytochrome b for 233 species obtained from GenBank and 14 fossils, spanning a range of clades and ages from approximately 200 to 4.9 Myr ago, which represented the minimum age for the most recent common ancestor for extant crown clades. We enforced monophyly constraints on all clades represented by calibration points, and our higher level topology was consistent with previous studies of cheloniens phylogeny (e.g. [4,5]). Full details of phylogenetic analyses are provided in the electronic supplementary material.

(b) Modelling body size evolution

We collected maximum straight-line carapace length (centimetre) from the literature for 226 cheloniens species represented in our phylogenetic tree (figure 1). Each species was classified into one of four, broad habitat categories, freshwater, marine, mainland or oceanic island.

We compared the fit of a Brownian motion (BM) model of body size evolution in cheloniens with Ornstein–Uhlenbeck (OU) models that allow for different optimal body sizes according to habitat. BM has only two parameters: the evolutionary rate, $\sigma^2$, and root state of the trait, $\theta$. OU adds additional parameters, $\theta$ and $\alpha$, representing the optimal state for each of the $n$ habitat regimes modelled, as well as a parameter representing the strength of selection, $\alpha$. Also referred to as a ‘rubber-band’ parameter, larger values of $\alpha$ indicate stronger levels of selection, resulting in trait distributions that are more tightly distributed around their optima.

As $\alpha \to 0$, OU degenerates to BM. We compared the fit of models with a single optimal size for all turtles (OU1), and separate optima for each habitat type (mainland, island, freshwater and marine—OU2). If habitat influences body size, then we would expect OU2 to best fit our data. Conversely, if habitat has no influence on body size BM or OU1 should fit better.

We subsequently compared the fit of three additional models that account for more generalized evolutionary hypotheses. OU3 condensed mainland and freshwater cheloniens into one category, accounting for the possibility that only oceanic islands and marine adaptation required different optimal sizes. OU4 condensed mainland and oceanic island cheloniens into one terrestrial category, accounting for the possibility that there is only one optimal size for terrestrial taxa. OU5 condensed all species to one of two categories, marine or terrestrial. We fit all models using OUCH 2.6-1 [6] in R v. 2.11.1 [7].

An advantage of model-fitting approaches over phylogenetically informed analogues of conventional statistics (e.g. phylogenetic ANOVA [8]) is that uncertainty and error in phylogenetic reconstruction and branch length estimation easily be incorporated by averaging model fits over a sample of trees. We fitted each model of body size evolution to 500 trees drawn at random from the post burn-in sample retained in our BEAST analysis. For each tree, we assigned habitat states to internal branches using maximum-likelihood estimates of ancestral states computed using functions in the APE package [9] for R. The state with the highest marginal likelihood was assigned in each case (e.g. figure 2). Where two or more states had equal marginal likelihoods, we selected a state at random. We averaged parameter estimates over the 500 models and assessed model fit using average Akaike's Information Criterion scores with small sample correction (AICc).

3. RESULTS

The model allowing each habitat to take a separate optimal body size (OU2) was best supported (table 1). Taking $\Delta$AICc > 4 as indicating strong support for the best model over other candidate models [10], all other models performed poorly with respect to this model.
This result supports our hypothesis that habitat differences can explain body size diversity in chelonians. Average parameter estimates for the strength of selection and Brownian rate parameters proved sensitive to a few outlying values. We therefore present median rather than mean values for those parameters here. Selection and Brownian rate parameters were greatest for OU2, the best-fitting model (table 2).

Focusing on the best model, OU2, we found evidence for large optimal sizes in oceanic island and marine chelonians (island optimum = 82.6 cm, marine optimum = 132.6 cm). Optimal size in freshwater and mainland chelonians were smaller and more similar to one another (freshwater optimum = 33.7 cm, mainland optimum = 24.18 cm).

4. DISCUSSION

We found strong support for different optimal sizes in turtles and tortoises that occupy different habitats. Notably, we recovered similar, large optimal body sizes for both oceanic island tortoises and sea turtles. Despite these similarities, the reasons why these lineages evolved large body size are probably quite different.

Although several studies have examined the relationship between body size and island endemism, particularly in birds and mammals (e.g. [11] and references therein), ours is the first that we are aware of to demonstrate strong evolutionary signal for gigantism as an optimal condition in oceanic island tortoises. It has been suggested that large optimal size was a preadaptation for increased dispersal abilities that allowed the ancestors of these populations to initially colonize islands [1]. However, the retention of large size, combined with convergent loss of anti-predator behavioural and morphological characteristics [12,13], suggests that this condition was at least selectively maintained in the descendants of these initial immigrants. Oceanic Islands are susceptible to unpredictable periods of adverse conditions, while larger size is associated with increased
fastering ability. Gigantism may have been selectively maintained to allow island tortoises to survive prolonged periods of reduced resource availability and drought, or to facilitate long distance travelling between watering holes and feeding sites [1,11,12,14].

Sea turtles exhibited the largest optimal size in our analysis. As has been suggested for ancestors of island tortoise lineages, large size in sea turtles may reflect adaptation for increased dispersal abilities as many sea tortoise lineages, large size in sea turtles may reflect adaptation for increased dispersal abilities as many sea turtles seasonally migrate vast distances. For example, green turtles (Chelonia mydas) have been recorded to trek 2300 km on their journey from the remote Atlantic Ascension Island to the Brazilian coast [15]. Some species such as green (C. mydas) and loggerhead (Caretta caretta) turtles range from equatorial regions to colder areas of the northern or southern oceans [16], and larger body size also becomes advantageous in cold waters because lower surface area to volume ratios reduce heat lost to the environment. Arguing against large size purely as a thermoregulatory adaptation is the observation that the leatherback turtle can use changes in blood flow to maintain body temperatures above ambient in colder waters [16,17]. Furthermore, the largest turtles to have ever lived, such as the 4.6 m Archelon ischyros [18], inhabited Mesozoic seas that would have been much warmer than today’s oceans [19–21].

Predation risk presents an additional explanation for large optimal sizes in sea turtles. The largest sea turtle species evolved during the Late Mesozoic, and co-occurred with massive reptilian predators, such as mosasaurs and pliosaurs [19,20]. During the Cenozoic, smaller sharks and toothed whales have become the dominant predators of marine turtles [22], relaxing selection for extreme body size in more recent species. However, extant marine predators remain larger than most of their terrestrial counterparts, and this may be sufficient to maintain an optimal size difference between marine turtles and terrestrial or freshwater species.

Despite our striking results for oceanic island and marine chelonians, optimal size estimates for freshwater and mainland terrestrial chelonians were similar. Based on our raw data, members of these two groups also span qualitatively similar large body size ranges (figure 1b). A more complicated set of ecological factors may be responsible for determining body size in these species. Terrestrial and freshwater chelonians occur in diverse environments, from arid deserts to temperate forests, and often coexist with several other turtle species. Body size also appears to be correlated with diet in chelonians, possibly owing to size-related increases in bite force [23,24]. Given that many freshwater and terrestrial chelonian clades exhibit considerable ecologically diversity (e.g. [25]), their similar, broad distributions of body size variation are perhaps to be expected.

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Table 1. Mean scores for body size models fit to 500 trees randomly sampled from the post-burn in output of BEAST. (Refer to text for model descriptions.)

<table>
<thead>
<tr>
<th>model</th>
<th>AICc</th>
<th>ΔAICc</th>
<th>weights</th>
</tr>
</thead>
<tbody>
<tr>
<td>OU2</td>
<td>297.34</td>
<td>—</td>
<td>0.89</td>
</tr>
<tr>
<td>OU3</td>
<td>301.65</td>
<td>4.30</td>
<td>0.10</td>
</tr>
<tr>
<td>OU4</td>
<td>310.91</td>
<td>13.57</td>
<td>1 × 10⁻³</td>
</tr>
<tr>
<td>OU5</td>
<td>328.97</td>
<td>31.62</td>
<td>1 × 10⁻⁷</td>
</tr>
<tr>
<td>OU1</td>
<td>330.42</td>
<td>33.08</td>
<td>5.88 × 10⁻⁸</td>
</tr>
<tr>
<td>BM</td>
<td>426.74</td>
<td>129.39</td>
<td>7.15 × 10⁻²⁹</td>
</tr>
</tbody>
</table>

Table 2. Summary parameter values for models of body evolution for turtles. (Models were fit to 500 random phylogenies from the post burn-in posterior sample. θ values are ln-transformed and averaged over the 500 model fits while σ² and α values are medians. Refer to text for model descriptions.)

<table>
<thead>
<tr>
<th>BM</th>
<th>OU1</th>
<th>OU2</th>
<th>OU3</th>
<th>OU4</th>
<th>OU5</th>
</tr>
</thead>
<tbody>
<tr>
<td>σ²</td>
<td>4.28</td>
<td>6.82</td>
<td>7.91</td>
<td>7.42</td>
<td>7.52</td>
</tr>
<tr>
<td>α</td>
<td>7.34</td>
<td>11.63</td>
<td>10.16</td>
<td>10.11</td>
<td>7.95</td>
</tr>
<tr>
<td>γ₀</td>
<td>3.59</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>γ₁water</td>
<td>—</td>
<td>3.52</td>
<td>—</td>
<td>3.54</td>
<td>—</td>
</tr>
<tr>
<td>γ₁marine</td>
<td>—</td>
<td>4.89</td>
<td>4.91</td>
<td>4.91</td>
<td>—</td>
</tr>
<tr>
<td>γ₁mainland</td>
<td>—</td>
<td>3.19</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>γ₁water/</td>
<td>—</td>
<td>4.41</td>
<td>4.52</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>γ₁terrestrial</td>
<td>—</td>
<td>—</td>
<td>3.45</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>γ₁aquatic</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>3.31</td>
<td>3.31</td>
</tr>
</tbody>
</table>

*aBest-fitting model.*


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