

Evolution of snake venom potency and yield is driven by trophic and macroecological factors including metabolism, prey-type and habitat

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Snake venom is best known for its ability to incapacitate and kill prey. However, venoms predatory functionality is highly variable across species, with some species possessing venoms of seemingly harmless quantities and potencies, while others, such as Russell's viper, can kill vast numbers of their prey. This suggests that venom evolution may not be predominantly influenced by drivers such as trophic ecology and macroecological factors as expected for predatory traits. In particular, venom would be predicted to be selected for prey-specific potencies while venom yield may be expected to follow macroecological patterns relating to predator-prey mass, metabolic rate and habitat dimensionality. One potential reason for the absence of these patterns is the use of non-natural prey species to measure venom potencies. Here we test a range of hypothesis relating to the drivers of venom evolution by accounting for the use of non-natural species using the evolutionary distance between model species and observed dietary species in a comparative analyses of venom potency (LD₅₀) and yield for 99 snake species. We show that snake venom evolution is driven by both trophic factors, with venom showing higher potencies when tested on species phylogenetically similar to those within their diet, and macroecological drivers, with venom yield increasing with body size as predicted by metabolic rate, and decreasing in higher dimensional habitats. These results underline the importance of trophic and macroecological forces in snake venom evolution and highlight the potential role of these factors in the evolution other venomous groups and predator traits in general.

Venom | Body size | Comparative analysis | Scaling | Macroecology

Introduction

Snake venom is perhaps best known for its ability to incapacitate biological systems, a property which has made it both a source of novel biomedical compounds (1) and also a major health concern due to the estimated millions of human envenomation cases each year (2). However, snake venom is also an ideal system of predatory trait evolution (1), particularly as its predatory functionality, the ability to subjugate prey, can be quantified by measured venom potency and the quantity a species possess. Despite significant developments in our understanding of the evolutionary origin (3-5) and the subsequent evolution of its complex compounds (1, 6), surprisingly little is known about the evolutionary pressures that drive this ability to incapacitate prey. For example, many species, such as the Gold-ringed cat snake (*Boiga dendrophila*), are incapable of subduing laboratory test model prey (7) while other species, such as Russell's viper (*Daboia russelii*), possess enough potent venom to incapacitate hundreds of thousands of potential prey items (8). This lack of a clear pattern relating to the ability to subdue prey using venom suggests drivers such as trophic factors, are thought to be less important than one might expect.

One potential explanation for this lack of a pattern is that weak selective pressures are caused by an "overkill" effect. This

is an effect were due to the capacity of many snake venoms to kill vast numbers of their prey in a single bite, as in the case of Russell's viper, it is possible that venom characteristics are not under selection with neutral process such as evolutionary drift, the main evolutionary drivers of the traits (9, 10). Such a scenario predicts that venom traits, such as potency and quantity, vary according to evolutionary drift across species. However, this then brings into question the general importance of ecological factors driving the evolution of predatory traits. Here, we use a comparative approach to test whether snake venom traits follow idiosyncratic patterns expected from neutral selection or patterns predicted from macroevolutionary and trophic theory.

As predation plays a key role in both ecosystems dynamics (11) and the evolution of the species within these ecosystems (12) much attention has been given to understanding the general patterns related to these trophic interactions and the drivers behind them. These include macroecological patterns derived from body mass and habitat complexity which predict allometric scaling relationships for traits underlining trophic interactions such as search and encounter rates (13-15); the ability to spot and track prey (16, 17); and ingestion rates (15, 18). Other general predictions for predatory traits stem from the co-evolution between both predators and their prey, were arms race dynamics may drive the co-evolution of predatory and anti-predator traits (19, 20). While these two general drivers are likely to have important influences on predator-prey co-evolution species traits are

Significance

Snake venom is best known for its ability to kill prey, a property that both makes it of biomedical interest and a public health concern. However, snake venom measured in terms of its potency and volume, also offers an opportunity to understanding a novel aspect of predator-prey co-evolution. Variation in these aspect of snake venom can be examined in relation to prey species characteristics, and snake size, metabolic rates and habitat features such as dimensionality. Here, using comparative analysis we show that trophic drivers result in venom evolving higher potency towards species closely resembling their natural diet while macroecological drivers, such as habitat dimensionality and metabolic constraints, shape the quantity of venom available.

Reserved for Publication Footnotes

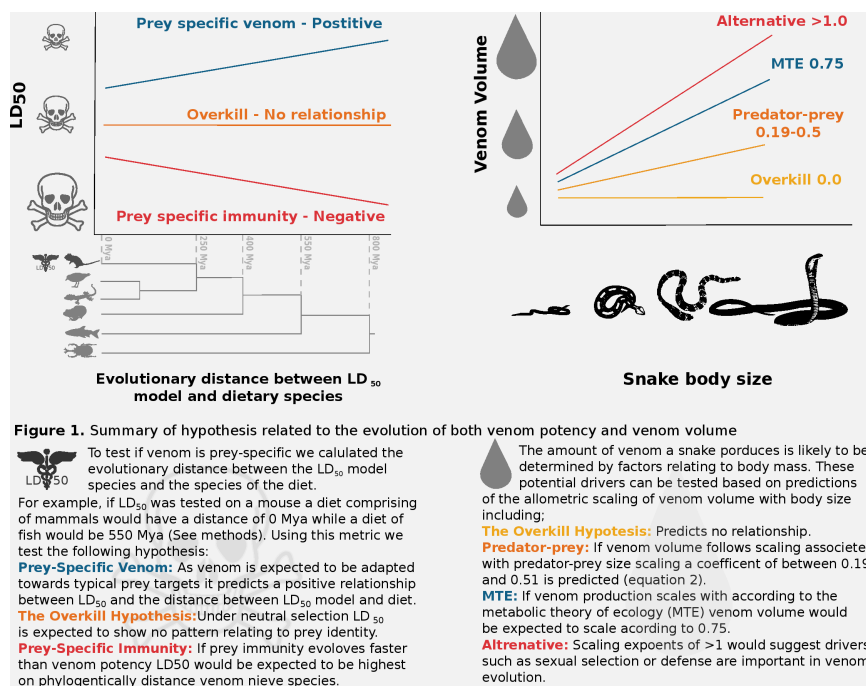


Fig. 1.

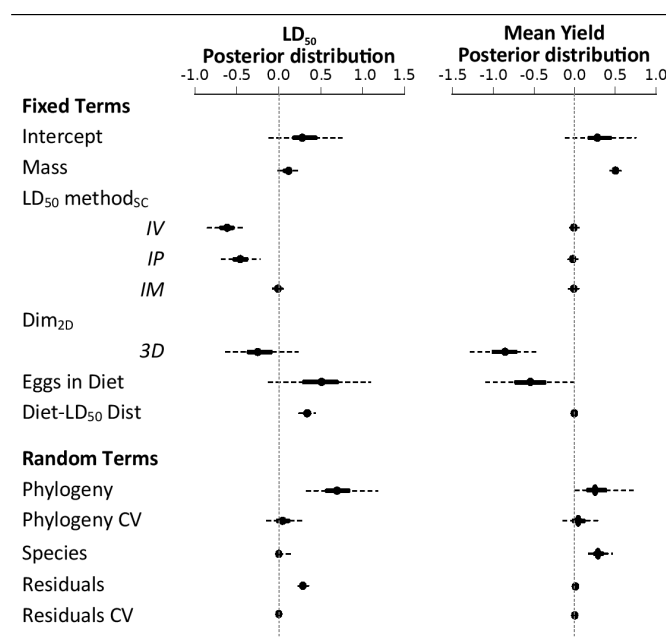


Fig. 2. Posterior distributions of LD₅₀ and mean venom volume estimates (represented by dots) and higher and lower 95% credibility intervals (represented by dotted horizontal bar). Fixed factors include mass; LD₅₀ method (subcutaneous (SC), intravenous (IV), intrapulmonary (IP) and intramuscular (IM)); habitat dimensionality (Dim- 2D and 3D); Presence of eggs in diet (Eggs in Diet) and the mean phylogenetic distance between diet species and the LD₅₀ model (Diet-LD₅₀ Dist). The random terms and the co-variance (CV) between LD₅₀ and yield are also presented. Significance is determined when 95% of the data is above or below zero. The model was run with 12,000,000 iterations with a 2,000,000 burn-in and a thinning of 5000.

of diverse species allowing us to evaluate whether environmental and physiological factors influence its evolution.

Predatory foraging traits are expected to be adapted towards their main target prey species. For example, jaw morphology in cichlid fish is strongly selected by factors such as prey type (21). Similar selection pressures driven by prey type also appears to influence snake venom traits such as its quantity. For example, a switch in diet from fish to eggs has resulted in the almost complete atrophy of the venom apparatus in the egg eating marble sea snake *Aipysurus eydouxii* (22), demonstrating the importance of predation in venom evolution. Further such trophic selection is also seen in cases of prey-specific venoms where potency is higher when tested on species commonly found within the snakes diet, such as observed in Malayan pitvipers (23), coral snakes (24), the viper genus *Echis* (25), saw-scaled vipers (26) and insect eating *Pelias* vipers (27). However, such co-evolution is not apparent in all snake species, such as in tiger snakes where variation in venom across populations is independent of dietary differences (28). Furthermore, prey species can also respond in such co-evolutionary arms races through the development of immunity. Evidence for this is seen in venoms that show weaker potencies in potential prey items such as in the cases of Opossums and Neotropical pitvipers (29); eels and *Laticauda colubrine* (30); and between ground squirrels and rattlesnakes (31, 32). This idiosyncratic pattern of some species displaying prey-specific venom while others do not may mirror a pattern predicted from the Overkill hypotheses where neutral processes are the main driver of venom potency (10). However, many measures of venom potency are not typically tested on natural prey species leading to the question of whether these examples represent an idiosyncratic pattern expected under weak or neutral selection or whether a general pattern might emerge if analyses controlled for the relatedness of the model species to its normal prey. While measures of potency using natural prey species are becoming more common, these are taxonomically restricted making large comparative analysis difficult (24, 25). Here we utilize these measures of venom potency on non-natural species by testing if potency is higher when measured on test species phylogenetically closer to natural dietary species. Through accounting for the model species used for measuring po-

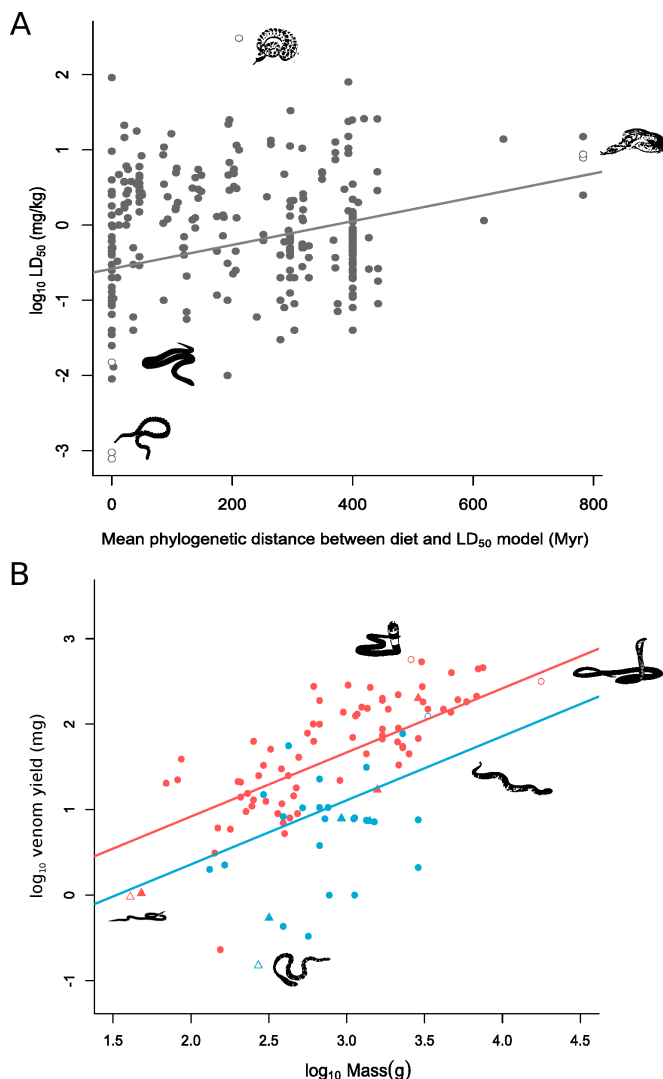


Fig. 3. (A) Mean phylogenetic distance between diet species and LD50 model (Myr) against log₁₀ LD₅₀ (intercept = -0.58, slope = 0.002). Hollow points represent silhouette species which are from left to right; *Bungarus multicinctus*; *Oxyuranus microlepidotus*; *Echis carinatus*; *Causus rhombeatus*. (B) Relationship between log₁₀ mass (g) against log₁₀ venom yield (mg). Red points and fitted line (intercept = -0.58, slope = 0.75) represent species in 2D habitats and the blue points and fitted line (intercept = -1.14, slope = 0.75) represent species in 3D habitats. Hollow points represent silhouette species which are from left to right *Atractaspis bibronii*; *Emydocephalus annulatus*; *Naja melanoleuca*; *Agkistrodon piscivorus*; *Ophiophagus hannah*. All intercepts and slopes are back transformed from the values in Figure 1 and Table A1.

tency the importance of other potentially important evolutionary drivers of venom, such as Macroecological factors, can be tested on other venom traits such as volume available.

Similar to venom potency we also predict that venom yield is under positive selection from potential trophic and macroecological factors. As venom production incurs a metabolic cost (33) (although the level of this cost is debated (34)) and requires storage, the volume of venom a snake species can produce is likely to be heavily linked to one of the strongest determinants of trophic ecology; body size. In general, larger predators eat larger prey (18). If venom is under selection for its ability to kill prey it would be expected that larger snake species would need to produce larger quantities of venom to keep pace with the subsequent increased in prey size. The metering of venom in response to prey size seen in several species (35, 36) represents

an example of this. However, while bigger snakes are known to have larger amounts of venom in general (37) it is not known whether venom yield scales interspecifically according to any general pattern. One prediction is that venom yield increases with snake body size with an exponent relating to their predator-prey body size scaling as described by (equation 1);

$$M_{prey} \propto M_{predator}^a$$

Were for snakes the scaling exponent a is approximately 0.88 (18). However, venom yield would not be expected to scale according to this exponent as the effects of toxicological agents also follows an allometric relationship (38) were the amount of venom required (V) to induce the same incapacitating effect on a prey of mass (M_{prey}) would be expected to follow (equation 2);

$$V \propto M_{prey}^b$$

were b is the scaling coefficient, commonly estimated as 0.75, of venoms toxicological effects (38). Hence to calculate the expected allometry of venom yield with snake body mass in a case were yield increases at a rate to match predator-prey size scaling after accounting for scaling of toxicological effects we substitute $M_{predator}^a$ from equation 1 for M_{prey} to get (equation 3);

$$V \propto M_{predator}^{ab}$$

If we take the commonly used value of 0.75 for the interspecific scaling of drug dosages (38) for b and the value of 0.68 for a from the scaling predator-prey mass relationship for snakes (18) we would expect a scaling exponent of approximately 0.51 between snake venom yield and snake mass. Other predictions include the overkill hypothesis which predicts no relationship between venom yield and prey size, or alternatively venom yield may scale according to constraints such as metabolic costs, were a scaling of 0.75 would be expected (39). At the other extreme superlinear allometries would suggests patterns associated with drivers such as sexual selection, such as proposed by the weapons hypothesis (40), or defenses requiring increased effectiveness with size, such as seen in the allometry of horn growth in horned lizards (41) (Figure 1).

Finally, an overlooked feature that may also drive the evolution of both venom quantity and toxicity is habitat structure (42). The structural complexity of a habitat, such as whether it's a 2-dimensional terrestrial surface or a complex 3-dimensional forest canopy, can influence both encounter rates (14, 18) and the escape rates of prey, with higher dimensional spaces increasing both (43, 44). Hence predators in high dimensional habitats with associated increased escape rates may compensate through larger yields of more potent venom in order to increase capture rates. For example, strike and release behaviors may be less successful in either 3-dimensional arboreal or aquatic environments requiring higher toxicities to incapacitate prey quickly. Conversely there may be less of a requirement for high potencies and large reservoirs of venom due to increases in encounter rates, and hence feeding opportunities, in high dimensional habitats which may compensate for possible increases in escape rates.

Here we test the importance of these multiple potential drivers of both venom quantity and potency, as measured using median lethal dose (LD₅₀), in a phylogenetically corrected comparative analysis of ninety-nine species of venomous snakes. Using the phylogenetic distance between species used to measure LD₅₀ and dietary species, we test;

(1) the overkill hypothesis: that there is no relationship between venom potency and the species on which it was measured or between venom yield and prey size.

(2) the importance of trophic drivers on venom evolution including: that venom potency is higher (lower LD₅₀) when tested on model species phylogenetically closer to species found in the diet; and that snake species which include eggs in their diets have lower venom potencies (higher LD₅₀) or yields.

(3) the importance of macroecological drivers on venom evolution with scaling of venom yield with snake body mass predicted from predator-prey size scaling to be approximately 0.51; from metabolic constraints to be 0.75; and from other potential drivers such as sexual selection and the weapons hypothesis to be superlinear.

(4) the importance of habitat dimensionality on venom evolution, in particular that; species in high dimensional habitats show either higher or lower potencies.

We show that both trophic and macroecological factors are important in driving venom evolution with patterns supporting prey-specific venom in general and venom quantity both scaling as predicted by metabolic cost constraints and lower in higher dimensional habitats.

Results

Our final compiled dataset of venom traits and corresponding trophic and macroecological data consisted of 275 observations over 99 species which corresponds to the data used in the main analysis. We also conducted supplementary analysis where we included whether species to are known to using constricting behaviours; the inclusion of habitat type and finally an analysis including prey body size which was conducted using a reduced dataset of 177 observations across 68 species. We report the results across all models relating to the importance of each driving factor in order below.

Predator-prey coevolution

Despite the presence of only eight egg eating species in our dataset LD₅₀ was found to be significantly higher in species with eggs in their diet in both the main and constriction models, while venom yield had a negative, but non-significant, association with ovivorous behavior in all models (Table 2; Tables A2-4).

Of the species included within the analysis only 14 species had a diet completely matching that of the LD₅₀ model their venom was tested on, i.e. the LD₅₀ of a species with a diet including 100% mammals tested using a mouse model. Most species in the dataset had a diet with a least some component not matching the LD₅₀ model as reflected by a median evolutionary distance of 211.3 million years between the common ancestors of the dietary taxa and the LD₅₀ species. In all models species LD₅₀ increased with mean phylogenetic distance between the diet and the LD₅₀ model with snake species with diets phylogenetically close to the LD₅₀ model species hence having higher potencies (table 2; tableA2-3; Figure 1B). From the main model, after back transforming the mean centered log₁₀ value, LD₅₀ was found to increase by 1.44 for every 100 million years between the species in the diet and that of the LD₅₀ model. This was after correcting for LD₅₀ injection route were intravenous and Intraperitoneal routes were found to have lower LD₅₀ values in comparison to a subcutaneous route (table 2; tableA2-3).

Macroecological drivers; body size and habitat dimensionality

The mean yield of venom, as measured using dried weight, ranged from 0.15 mg in the egg-eating sea snake (*Emydocephalus annulatus*) to 571 mg in the forest cobra (*Naja melanoleuca*). Body size, prey size and habitat dimensionality all correlated with yield. The main correlate with average yield was snake body size with a log-log scaling of between 0.74 and 0.76 across all models, after back transforming (Figure 2, Tables A2-4; Figure 1), an exponent far higher than the predicted scaling of 0.51 for predator-prey body size scaling. Venom yield also showed a positive increase with prey body mass, with a log₁₀-log₁₀ increase of 0.139, however

only 90% of the posterior samples are above the zero threshold (Table A2). Snake body size was also found to have a significantly positively correlation with LD₅₀, meaning larger snakes showed decreased potency (Figure 3. However, this relationship was only significant in the main analysis (Table A2-3).

The next most significant driver of venom yield was the dimensionality of the habitat with the 27 species in high dimensional environments (arboreal = 9, aquatic = 18) showing lower venom yields in comparison to species in lower dimensional habitats (Table 2). A sensitivity analysis where habitat was included as terrestrial, arboreal and aquatic also showed similar significant reductions in both arboreal and aquatic habitats (Table A4).

Phylogeny, constriction behaviour and covariance between venom yield and LD₅₀

In all models there is was an intermediate to high phylogenetic signal for both LD₅₀ and venom yield with h² values of 0.69 for LD₅₀ and 0.49 for venom yield (Table 2, A2-4). with LD₅₀ showing a higher phylogenetic signal in all models (Table 2, A2-4). The presence of constricting behaviour was found to have no effect on either yield or LD₅₀ (Table A3). Finally, there is no significant covariance between either the residuals of phylogenetic terms of both yield and LD₅₀ across all models (Table 2, A2-4).

Discussion

Predator traits are thought to be heavily shaped by both predator-prey evolutionary dynamics and macroecological forces such as imposed by the limitations of body size and habitat structure. Here we show that traits associated with snake venom follow patterns predicted from a scenario where these factors are important evolutionary drivers of predator trait. This includes that venom potency is prey specific, with higher potencies found when venom is tested on species more phylogenetically similar to a snakes natural diet, and that venom yield scales with snake body size according to an allometry expected if energetic costs of venom production are the main driver. We also find that snake venom is influenced, as expected by the presence of ovivorous feeding behaviours and, in a less expected direction, by the dimensionality of the environment. Hence, our results show that while aspects of neutral selection, such as genetic drift, play an important role in generated the observed variance in predator traits, positive selection forces associated with trophic and macroevolutionary drivers play a key role in shaping the evolution of these traits.

Trophic factors have been known to play an important role in the maintenance of venom. This is supported by cases of its evolutionary loss with dietary changes that no longer require venom (22), the absence of an increased lifespan associated with venomous as generally seen in species with toxic defence systems (45), and also by our findings here that ovivorous feeding is associated with lower potencies and venom yield. However, the role of trophic drivers in shaping the subsequent evolution of venom has been much more hotly debated, in particularly relating to the generality of prey-specific venoms (1, 9, 10). By flipping the inconvenience usually associated with the use of non-natural test models for venom potency (24) we show that venom is generally prey-specific with higher potencies associated with species that more closely resemble a species diet. The prey-specific effect demonstrated in our analysis is also likely to underestimate the prey specific nature of venom in general due to our use of LD₅₀. While LD₅₀ measures the lethality of a venom, it is likely that venom is selected to simply subdue prey, as opposed to cause mortality, in order to reduce the chances of prey escaping or retaliating (25). Even though prey mortality achieves this, other measures of venoms ability to subdue prey, such as the speed at which a venom affects prey or a measure of its sub-lethal incapacitating effects, may give clearer reflection of venoms prey-specificity (25). However, despite such limitations, we find a clear pattern of prey-specificity suggesting that cases of non-prey

specific venom (28-32) are more likely to be the exception to the general rule.

In terms of macroecological patterns, we unsurprisingly we found that larger snakes had larger quantities of venom. More surprisingly these increases did not follow the expected scaling allometry of 0.51 from a predator-prey scaling perspective (18) with venom yield increasing faster with snake body size than expected. Even when considering potential variation in the allometric scaling of toxicological effects (equation 3) (38), a value far in excess of 1 is required for b , the scaling of toxicological effects, in order for the observed scaling of 0.75 between venom volume and snake mass to agree with this prediction. Furthermore, our analysis found that the predatory-prey body mass scaling of venomous snakes, (a in equation 3) is much lower in comparison to snakes as a whole (18), with larger venomous snakes feeding on much smaller prey items than expected. This lower scaling of prey size may explain the reduced venom potency with snake size seen in our main analysis. A more likely explanation for our results regarding venom yield scaling is that it relates to limitations relating to metabolic rate (46), which also has a similar scaling coefficient of 0.75 with respect to body mass (39, 46). In particular, it might be expected that the production of a potentially metabolically costly material such as venom (33), would follow such a metabolic scaling, particularly if the costs of venom were maintained at a constant proportion of overall energy budgets across snake species. While we focus on the average yield a snake can produce the amount of venom administered in a single bite does seem to show stronger associations with trophic factors (36). Interestingly, such a decoupling of trophic and metabolic determinants between the amount of venom in a single bite and the total reservoir may have strong implications on the predation strategies available with body size. As yield scales with body size according to a higher exponent in comparison to any trophic factor, such as prey size, larger species would be expected to have the capacity for more envenomation's before depleting their reservoir. These larger reservoirs may hence allow for strategies such as the use of multiple envenomation's on a single prey item or strike and release strategies which may require "back-up" venom for cases where prey items are not recovered.

Another potential macroecological factor we found shaping the available volume of venom to a species is habitat dimensionality. While we expected that species in high dimensional habitats may have higher venom yields to compensate for higher escape rates of prey (42) we found that, counter to our expectation, these species had lower yields in comparison species in low dimensional habitats (terrestrial and fossorial). This may be associated with differences in prey capturing behaviour as it might be expected that high dimensional environments require more holding behaviours during attacks in order to prevent the loss of prey, hence allowing a more accurate delivery of venom. However, the presence of constriction in venomous snakes (47), the most extreme form of prey holding behaviours, is present in both arboreal and terrestrial species and was found to have no effect when included within the analysis. Furthermore bite and release behaviours are known in arboreal species such as the black mamba (*Dendroaspis polylepis*) suggesting this behaviour is not fully restricted to low dimensional environments (48). Another potential explanation is that higher encounter rates in high dimensional environments (14) may reduce the missed opportunity of feeding cost associated with replenishing venom. Rates of replenishing venom can be substantial with estimates of replenishment rate ranging from 3-7 days (49) to 30-50 days (36, 50-52). These long periods of replenishment may hence select for larger reserves in species where encounter rates with prey are lower in order to minimise potential missed opportunity costs. While further research on the role of habitat dimensionality will allow more detailed understanding of the mechanisms driving this trend our results highlight that

venom may also be selected according to factors relate to prey encounter rates.

Our analysis shows that both predator-prey dynamics and macroecological factors shape the evolution of venom in snakes. While other mechanisms, such as gene duplication events (53), are important in driving the evolution of these traits positive selection pressures are important in shaping the pattern seen in the variation of traits relating to venom. This is also expected to be the case in other venomous groups, where patterns relating to prey specificity and energetic constraints are also likely to play key roles in their evolution (1). Examples of prey-specific venom is seen in cone snails and spiders (1), while the energetic costs of producing venom is also suggested by venom metering in taxa such as scorpions (54). The generality of prey-specific and macroecological constraints is also likely to extent across non-venomous predatory traits, such as related to tooth morphology and gap limitation scaling, or other traits such as predator pursuit speed. By using snake venom as a system of predator trait evolution we show the importance of multiple evolutionary drivers allowing not only a window into the evolution of venomous systems, but of predatory traits and trophic ecology as a whole.

Methods

Data

We collected data on venom yield and toxicity from the literature, along with our predicted drivers. We used mean dry weight (mg) extracted as a measure of venom yield as it represents the amount of active ingredients available and is the most available reported measure. As a measure of venom lethality we used median lethal dose (LD_{50}) due to its wide availability. We only included intravenous (IV), subcutaneous (SC), intraperitoneal (IP) or intramuscular routes (IM) of injecting the venom as other routes were too uncommon to include within the analysis. We include LD_{50} values measured on all animal models as we were interested in including variation relating to the potential prey specific nature of venom.

To test whether venom is prey specific we calculated the phylogenetic distance between the model animal species used to measure LD_{50} for each snake species and the species naturally present in its diet. We calculated this as the sum of the phylogenetic distance, using mean estimates from TimeTree (55), between each prey taxa and the LD_{50} model multiplied by the proportion of each prey group reported in each snake species diet. For example, a species with a diet comprising of 20% mammals, 50% fish and 30% reptiles with a LD_{50} measured using mice would have a diet with an average phylogenetic distance of $0.2(0) + 0.5(400.1) + 0.3(296) = 288.85$ million years from the common ancestor of the LD_{50} model. Diet data was collated from the literature using studies with quantitative estimates of prey proportions, mainly from studies of stomach contents. As prey items were rarely identified to lower taxonomic levels diet was categorized into six prey categories; invertebrates, fish, amphibians, lizards, birds and mammals.

Species habitat was categorized as either terrestrial, fossorial, aquatic or arboreal based on accounts in the literature. In order to directly test the expected effect of the dimensionality of habitat environment each environment was scored, as in Pawar et al (14), with terrestrial and fossorial environments scored as two-dimensional and arboreal and aquatic scored as three-dimensional. As some venomous species also engage in constriction behavior we collected data on any observation of constriction behavior in capturing prey from the literature (47).

For snake body size we used total length values from the literature and field guides as these were the most common measures available (See Appendix A). All lengths were then converted to mass using family-level allometric scaling (56). Prey size data was included from dietary studies when available. When prey size was not reported in the dietary studies and were prey species were identified to the species level, we used mean prey species body mass from available databases (56-58). In cases where only body lengths were available for prey species allometric scaling were used to convert to mass (57, 59). For species that were only identified to the genus level the genus mean body mass was used if possible. The estimate mean prey size for each snake species was then calculated using a weighted mean based on the proportion each prey species/genus or group within the diet.

Snake mass, prey mass, LD_{50} , venom yield and phylogenetic distance between diet and model were all \log_{10} transformed, mean centered and expressed in units of standard deviation prior to analysis. Significance was determined for the fixed effects when 95% of the data is greater or less than 0. The phylogeny from Pyron RA & Burbrink (60) was included in all analyses to account for non-independence in traits due to common descent.

Analysis

To test our hypotheses we fit Bayesian multivariate phylogenetic mixed models using the MCMCglmm package (61) in R v 3.2.4 (62). As venom yield and LD_{50} are likely to have co-evolved, both were included as response variables in a series of multivariate analysis. Phylogeny was controlled by

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including it using the animal term in the MCMCglmm model while variation due to multiple measures on individual species was included using a separate random term. For the main model snake body mass; LD₅₀ inoculation method (SC, IM, IV, IP); habitat dimensionality (2D, 3D); the presence of eggs in the diet (absent, present); and the phylogenetic distance of diet species to LD₅₀ model were included as explanatory variables to give the analysis;

(1) Yield + LD₅₀ = $f(\text{Snake mass} + \text{LD}_{50} \text{ method} + \text{Presence of eggs in diet} + \text{Phylogenetic distance between diet and model species} + \text{Habitat dimensionality})$ (275 observations over 99 species).

A similar model was also fit including prey size as an explanatory model which resulted in a smaller dataset of 177 observations across 68 species. To estimate the direct scaling exponents relating to prey mass, venom yield and predator mass as referred to in equations (1 and 3) we also ran the following model;

(2) Yield = $f(\text{Prey mass})$

(3) Prey mass = $f(\text{Predator mass})$

Finally, we also fitted a final set of sensitivity analysis including the main model with constriction behavior included as a categorical factor

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(absent, present) and a model with habitat type included instead of habitat dimension with the levels of terrestrial; aquatic and arboreal.

All models were fitted with parameter expanded priors (Hedfield 2010) with standard non-informative priors also tested separately to ensure that choice of prior had no effect on model results. A burn-in, thinning and number of iterations was determined for each model separately to ensure effective sample sizes exceeded 1000 for all parameter estimates. We tested for convergence using the Gelman-Rubin statistic over three separate chains (63).

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