

# Supplementary Materials: Diet Breadth Mediates the Prey Specificity of Venom Potency in Snakes

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**Table S1.** Models with proportion of endothermic prey items included as a fixed factor. Modes ( $\beta$ ) and 95% credibility intervals (Lower CI and Upper CI) of the posterior distributions from the three main models predicting LD<sub>50</sub> using Taxonomic richness, Phylogenetic Diversity and Species Richness as measures of diet breadth. Fixed factors include the continuous factors of mean phylogenetic distance between diet species and the LD<sub>50</sub> model (D<sub>LD50-Diet</sub>); the proportion of endothermic prey in the diet (Prey met) and Diet Breadth (DB) in models that use Phylogenetic Diversity and Species Richness. Categorical fixed factors include LD<sub>50</sub> method (subcutaneous (SC), intravenous (IV), intraperitoneal (IP) and intramuscular (IM)); the presence of eggs in the diet (Eggs in Diet; present, absent) and the Taxonomic Richness measure of Diet Breadth. For categorical factors the baseline was SC for LD<sub>50</sub> method; the absence of eggs for the Eggs in Diet and low for Taxonomic Richness. DB<sub>Low</sub>:D<sub>LD50-Diet</sub> represents the interaction term between DB and D<sub>LD50-Diet</sub>. The random terms associated with phylogenetic relatedness (Phylogeny ( $h^2$ )), intraspecific variation (Species) and residual variation (Residual) are also presented. Significant values, which are highlighted in bold, are deemed to be those with 95% of the posterior estimate above or below zero. All models have 529 LD<sub>50</sub> measures for 100 species.

	Taxonomic Richness Model			Phylogenetic Diversity Model			Species Richness Model		
	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI
<b>Fixed Terms</b>									
Intercept	0.34	−0.11	0.80	0.41	−0.01	0.88	0.41	−0.05	0.88
LD <sub>50</sub> method <sub>sc</sub>									
IV	<b>−0.52</b>	<b>−0.66</b>	<b>−0.38</b>	<b>−0.52</b>	<b>−0.66</b>	<b>0.37</b>	<b>−0.52</b>	<b>−0.67</b>	<b>−0.38</b>
IP	<b>−0.26</b>	<b>−0.41</b>	<b>−0.11</b>	<b>−0.25</b>	<b>−0.41</b>	<b>−0.10</b>	<b>−0.26</b>	<b>−0.40</b>	<b>−0.12</b>
IM	−0.12	−0.31	0.04	−0.11	−0.28	0.07	−0.11	−0.29	0.05
Eggs in Diet <sub>absent</sub>									
Present	<b>0.90</b>	<b>0.38</b>	<b>1.40</b>	<b>0.88</b>	<b>0.36</b>	<b>1.40</b>	<b>0.89</b>	<b>0.42</b>	<b>1.49</b>
D <sub>LD50-Diet</sub>	<b>0.23</b>	<b>0.13</b>	<b>0.34</b>	<b>0.12</b>	<b>0.03</b>	<b>0.21</b>	<b>0.13</b>	<b>0.04</b>	<b>0.21</b>
Diet Breadth <sub>Low</sub>				0.03	−0.06	0.12	0.02	−0.07	0.11
Intermediate				—	—	—	—	—	—
High				—	—	—	—	—	—
DB <sub>Low</sub> :D <sub>LD50-Diet</sub>				−0.06	−0.13	0.01	−0.05	−0.12	0.01
Intermediate	<b>−0.22</b>	<b>−0.38</b>	<b>−0.06</b>				—	—	—
High	<b>−0.23</b>	<b>−0.47</b>	<b>−0.01</b>				—	—	—
Prey met	0.09	−0.09	0.24	0.11	−0.04	0.27	0.12	−0.04	0.30
<b>Random Terms</b>									
Phylogeny ( $h^2$ )	0.38	0.15	0.68	0.42	0.17	0.69	0.43	0.18	0.70
Species	0.16	0.01	0.34	0.15	0.01	0.34	0.15	0.01	0.33
Residuals	0.43	0.27	0.54	0.41	0.26	0.54	0.40	0.26	0.53

**Table S2.** Models with presence of constriction included as a fixed factor. Modes ( $\beta$ ) and 95% credibility intervals (Lower CI and Upper CI) of the posterior distributions from the three main models predicting LD<sub>50</sub> using Taxonomic richness, Phylogenetic Diversity and Species Richness as measures of diet breadth. Fixed factors include the continuous factors of mean phylogenetic distance between diet species and the LD<sub>50</sub> model (D<sub>LD50-Diet</sub>) and Diet Breadth (DB) in the case of Phylogenetic Diversity and Species Richness. Categorical fixed factors include LD<sub>50</sub> method (subcutaneous (SC), intravenous (IV), intraperitoneal (IP) and intramuscular (IM)); the presence of eggs in the diet (Eggs in Diet; present, absent); the presence of constriction behavior (Constriction) and the Taxonomic Richness measure of Diet Breadth. For categorical factors the baseline was SC for LD<sub>50</sub> method; the absence of eggs for the Eggs in Diet; the presence of constriction behavior (Constriction) and low for Taxonomic Richness. DB<sub>Low</sub>:D<sub>LD50-Diet</sub> represents the interaction term between DB and D<sub>LD50-Diet</sub>. The random terms associated with phylogenetic

relatedness (Phylogeny ( $h^2$ )), intraspecific variation (Species) and residual variation (Residual) are also presented. Significant values, which are highlighted in bold, are deemed to be those with 95% of the posterior estimate above or below zero. All models have 529 LD<sub>50</sub> measures for 100 species.

	Taxonomic Richness Model			Phylogenetic Diversity Model			Species Richness Model		
	$\beta$	Upper CI	Upper CI	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI
<b>Fixed Terms</b>									
Intercept	0.35	−0.11	0.84	0.31	−0.21	0.79	0.31	−0.18	0.81
LD <sub>50</sub> method <sub>SC</sub>									
IV	<b>−0.53</b>	<b>−0.66</b>	<b>−0.37</b>	<b>−0.52</b>	<b>−0.67</b>	<b>−0.39</b>	<b>−0.52</b>	<b>−0.67</b>	<b>−0.39</b>
IP	<b>−0.26</b>	<b>−0.41</b>	<b>−0.11</b>	<b>−0.25</b>	<b>−0.40</b>	<b>−0.11</b>	<b>−0.25</b>	<b>−0.39</b>	<b>−0.10</b>
IM	−0.12	−0.31	0.04	−0.10	−0.27	0.07	−0.10	−0.28	0.07
Eggs in Diet <sub>absent</sub>									
Present	<b>0.90</b>	<b>0.40</b>	<b>1.43</b>	<b>0.89</b>	<b>0.33</b>	<b>1.42</b>	<b>0.91</b>	<b>0.38</b>	<b>1.45</b>
D <sub>LD50-Diet</sub>	<b>0.22</b>	<b>0.12</b>	<b>0.32</b>	<b>0.12</b>	<b>0.03</b>	<b>0.21</b>	<b>0.13</b>	<b>0.04</b>	<b>0.21</b>
Diet Breadth <sub>Low</sub>				0.04	−0.05	0.14	0.02	−0.07	0.12
Intermediate	0.08	−0.19	0.34						
High	0.13	−0.14	0.45						
DB <sub>Low</sub> :D <sub>LD50-Diet</sub>				−0.06	−0.13	0.02	−0.05	−0.12	0.02
Intermediate	<b>−0.22</b>	<b>−0.41</b>	<b>−0.06</b>						
High	<b>−0.25</b>	<b>−0.50</b>	<b>−0.02</b>						
Constriction <sub>absent</sub>									
Present	−0.14	−0.75	0.42	−0.18	−0.73	0.45	−0.17	−0.81	0.38
<b>Random Terms</b>									
Phylogeny ( $h^2$ )	0.42	0.18	0.68	0.46	0.21	0.71	0.46	0.21	0.72
Species	0.15	0.01	0.33	0.13	0.01	0.31	0.13	0.01	0.31
Residuals	0.41	0.26	0.54	0.39	0.26	0.52	0.39	0.25	0.52

**Table S3.** Models with mean prey size included as a fixed factor. Modes ( $\beta$ ) and 95% credibility intervals (Lower CI and Upper CI) of the posterior distributions from the three main models predicting LD<sub>50</sub> using Taxonomic richness, Phylogenetic Diversity and Species Richness as measures of diet breadth. Fixed factors include the continuous factors of mean phylogenetic distance between diet species and the LD<sub>50</sub> model (D<sub>LD50-Diet</sub>); mean prey size and Diet Breadth (DB) in models that use Phylogenetic Diversity and Species Richness. Categorical fixed factors include LD<sub>50</sub> method (subcutaneous (SC), intravenous (IV), intraperitoneal (IP) and intramuscular (IM)); the presence of eggs in the diet (Eggs in Diet; present, absent) and the Taxonomic Richness measure of Diet Breadth. For categorical factors the baseline was SC for LD<sub>50</sub> method; the absence of eggs for the Eggs in Diet and low for Taxonomic Richness. DB<sub>Low</sub>:D<sub>LD50-Diet</sub> represents the interaction term between DB and D<sub>LD50-Diet</sub>. The random terms associated with phylogenetic relatedness (Phylogeny ( $h^2$ )), intraspecific variation (Species) and residual variation (Residual) are also presented. Significant values, which are highlighted in bold, are deemed to be those with 95% of the posterior estimate above or below zero. All models have 396 LD<sub>50</sub> measures for 70 species.

	Taxonomic Richness Model			Phylogenetic Diversity Model			Species Richness Model		
	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI
<b>Fixed Terms</b>									
Intercept	0.33	−0.23	0.90	0.41	−0.20	0.99	0.40	−0.17	0.96
LD <sub>50</sub> method <sub>SC</sub>									
IV	<b>−0.53</b>	<b>−0.70</b>	<b>−0.36</b>	<b>−0.53</b>	<b>−0.71</b>	<b>−0.36</b>	<b>−0.54</b>	<b>−0.72</b>	<b>−0.37</b>
IP	<b>−0.32</b>	<b>−0.48</b>	<b>−0.13</b>	<b>−0.31</b>	<b>−0.46</b>	<b>−0.13</b>	<b>−0.31</b>	<b>−0.49</b>	<b>−0.14</b>
IM	−0.14	−0.35	0.06	−0.12	−0.31	0.09	−0.13	−0.33	0.09
Eggs in Diet <sub>absent</sub>									
Present	<b>0.75</b>	<b>0.18</b>	<b>1.32</b>	<b>0.71</b>	<b>0.11</b>	<b>1.26</b>	<b>0.73</b>	<b>0.14</b>	<b>1.31</b>
D <sub>LD50-Diet</sub>	<b>0.27</b>	<b>0.16</b>	<b>0.38</b>	<b>0.14</b>	<b>0.04</b>	<b>0.25</b>	<b>0.17</b>	<b>0.07</b>	<b>0.27</b>
Diet Breadth <sub>Low</sub>				0.05	−0.06	0.17	0.04	−0.07	0.15
Intermediate	0.14	−0.13	0.47						
High	0.08	−0.26	0.40						
DB <sub>Low</sub> :D <sub>LD50-Diet</sub>				−0.07	−0.17	0.02	−0.06	−0.16	0.02

<i>Intermediate</i>	<b>−0.30</b>	<b>−0.51</b>	<b>−0.09</b>						
<i>High</i>	−0.24	−0.53	0.08						
Mean prey size	0.08	−0.04	0.18	0.06	−0.07	0.18	0.07	−0.06	0.19
<b>Random Terms</b>									
Phylogeny ( $h^2$ )	0.63	0.33	0.79	0.66	0.29	0.79	0.68	0.32	0.80
Species	0.01	0.01	0.23	0.01	0.01	0.26	0.01	0.01	0.26
Residuals	0.36	0.23	0.51	0.34	0.21	0.50	0.33	0.20	0.48

**Table S4.** Models with LD<sub>50</sub> duration included as a fixed factor. Modes ( $\beta$ ) and 95% credibility intervals (Lower CI and Upper CI) of the posterior distributions from the three main models predicting LD<sub>50</sub> using Taxonomic richness, Phylogenetic Diversity and Species Richness as measures of diet breadth. Fixed factors include the continuous factors of mean phylogenetic distance between diet species and the LD<sub>50</sub> model ( $D_{LD50-Diet}$ ); the duration of the LD<sub>50</sub> experiment (LD<sub>50</sub> Duration) and Diet Breadth (DB) in models that use Phylogenetic Diversity and Species Richness. Categorical fixed factors include LD<sub>50</sub> method (subcutaneous (SC), intravenous (IV), intraperitoneal (IP) and intramuscular (IM)); the presence of eggs in the diet (Eggs in Diet; present, absent) and the Taxonomic Richness measure of Diet Breadth. For categorical factors the baseline was SC for LD<sub>50</sub> method; the absence of eggs for the Eggs in Diet and low for Taxonomic Richness.  $DB_{Low:D_{LD50-Diet}}$  represents the interaction term between DB and  $D_{LD50-Diet}$ . The random terms associated with phylogenetic relatedness (Phylogeny ( $h^2$ )), intraspecific variation (Species) and residual variation (Residual) are also presented. Significant values, which are highlighted in bold, are deemed to be those with 95% of the posterior estimate above or below zero. All models have 315 LD<sub>50</sub> measures for 82 species.

	Taxonomic Richness Model			Phylogenetic Diversity Model			Species Richness Model		
	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI
<b>Fixed Terms</b>									
Intercept	0.06	−0.45	0.63	0.27	−0.21	0.82	0.24	−0.27	0.74
LD <sub>50</sub> method <sub>SC</sub>									
IV	<b>−0.54</b>	<b>−0.80</b>	<b>−0.28</b>	<b>−0.53</b>	<b>−0.80</b>	<b>−0.27</b>	<b>−0.52</b>	<b>−0.80</b>	<b>−0.27</b>
IP	−0.21	−0.46	0.05	−0.19	−0.46	0.05	−0.17	−0.42	0.12
IM	−0.05	−0.32	0.24	−0.03	−0.31	0.26	−0.01	−0.31	0.27
Eggs in Diet <sub>absent</sub>									
Present	<b>0.96</b>	<b>0.25</b>	<b>1.62</b>	<b>0.91</b>	<b>0.09</b>	<b>1.61</b>	<b>0.96</b>	<b>0.23</b>	<b>1.66</b>
$D_{LD50-Diet}$	<b>0.24</b>	<b>0.12</b>	<b>0.35</b>	<b>0.10</b>	<b>0.01</b>	<b>0.20</b>	<b>0.12</b>	<b>0.02</b>	<b>0.21</b>
Diet Breadth <sub>Low</sub>				0.05	−0.07	0.17	0.02	−0.09	0.13
Intermediate	0.27	−0.05	0.59	—	—	—	—	—	—
High	0.32	−0.07	0.69	—	—	—	—	—	—
$DB_{Low:D_{LD50-Diet}}$				−0.08	−0.17	0.02	−0.07	−0.17	0.02
Intermediate	<b>−0.28</b>	<b>−0.47</b>	<b>−0.09</b>	—	—	—	—	—	—
High	−0.26	−0.55	0.01	—	—	—	—	—	—
LD <sub>50</sub> Duration	−0.02	−0.09	0.04	−0.02	−0.08	0.04	−0.02	−0.09	0.04
<b>Random Terms</b>									
Phylogeny ( $h^2$ )	0.32	0.08	0.63	0.35	0.13	0.67	0.38	0.14	0.68
Species	0.23	0.03	0.45	0.21	0.02	0.43	0.21	0.01	0.41
Residuals	0.40	0.26	0.55	0.38	0.24	0.53	0.38	0.23	0.52

**Table S5.** Models with the wild/captive status of the LD<sub>50</sub> model included as a fixed factor. Modes ( $\beta$ ) and 95% credibility intervals (Lower CI and Upper CI) of the posterior distributions from the three main models predicting LD<sub>50</sub> using Taxonomic richness, Phylogenetic Diversity and Species Richness as measures of diet breadth. Fixed factors include the continuous factors of mean phylogenetic distance between diet species and the LD<sub>50</sub> model ( $D_{LD50-Diet}$ ) and Diet Breadth (DB) in models that use Phylogenetic Diversity and Species Richness. Categorical fixed factors include LD<sub>50</sub> method (subcutaneous (SC), intravenous (IV), intraperitoneal (IP) and intramuscular (IM)); the presence of eggs in the diet (Eggs in Diet; present, absent); the wild/captive origin of the LD<sub>50</sub> model (LD<sub>50</sub> captive, wild captive) and the Taxonomic Richness measure of Diet Breadth. For categorical factors the baseline was SC for LD<sub>50</sub> method; the absence of eggs for the Eggs in Diet; Captive for LD<sub>50</sub> captive and low for Taxonomic Richness.  $DB_{Low:D_{LD50-Diet}}$  represents the interaction term between DB and  $D_{LD50-Diet}$ . The random terms associated

with phylogenetic relatedness (Phylogeny ( $h^2$ )), intraspecific variation (Species) and residual variation (Residual) are also presented. Significant values, which are highlighted in bold, are deemed to be those with 95% of the posterior estimate above or below zero. All models have 492 LD<sub>50</sub> measures for 100 species.

Taxonomic Richness Model				Phylogenetic Diversity Model			Species Richness Model		
	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI
<b>Fixed Terms</b>									
Intercept	0.33	−0.14	0.77	0.38	−0.07	0.87	0.37	−0.12	0.83
LD <sub>50</sub> method <sub>SC</sub>									
IV	<b>−0.43</b>	<b>−0.56</b>	<b>−0.30</b>	<b>−0.43</b>	<b>−0.56</b>	<b>−0.30</b>	<b>−0.43</b>	<b>−0.56</b>	<b>−0.30</b>
IP	<b>−0.30</b>	<b>−0.43</b>	<b>−0.18</b>	<b>−0.30</b>	<b>−0.43</b>	<b>−0.17</b>	<b>−0.30</b>	<b>−0.44</b>	<b>−0.17</b>
IM	−0.13	−0.29	0.02	−0.14	−0.29	0.04	−0.14	−0.30	0.04
Eggs in Diet <sub>absent</sub>									
Present	<b>0.87</b>	<b>0.40</b>	<b>1.34</b>	<b>0.86</b>	<b>0.37</b>	<b>1.35</b>	<b>0.89</b>	<b>0.43</b>	<b>1.43</b>
D <sub>LD50-Diet</sub>	<b>0.27</b>	<b>0.17</b>	<b>0.36</b>	<b>0.17</b>	<b>0.10</b>	<b>0.26</b>	<b>0.19</b>	<b>0.11</b>	<b>0.27</b>
Diet Breadth <sub>Low</sub>				0.01	−0.07	0.10	0.01	−0.07	0.10
Intermediate	0.05	−0.21	0.29	—	—	—	—	—	—
High	0.11	−0.18	0.40	—	—	—	—	—	—
DB <sub>Low</sub> :D <sub>LD50-Diet</sub>				−0.04	−0.10	0.03	−0.02	−0.09	0.05
Intermediate	−0.13	−0.30	0.02	—	—	—	—	—	—
High	<b>−0.38</b>	<b>−0.61</b>	<b>−0.14</b>	—	—	—	—	—	—
LD <sub>50</sub> captive									
Wild	<b>0.25</b>	<b>0.07</b>	<b>0.41</b>	<b>0.25</b>	<b>0.09</b>	<b>0.43</b>	<b>0.27</b>	<b>0.09</b>	<b>0.44</b>
<b>Random Terms</b>									
Phylogeny ( $h^2$ )	0.48	0.24	0.73	0.53	0.28	0.77	0.56	0.28	0.78
Species	0.16	0.01	0.34	0.14	0.01	0.30	0.11	0.01	0.30
Residuals	0.35	0.22	0.47	0.33	0.21	0.46	0.31	0.21	0.45

**Table S6.** Sensitivity analysis of Taxonomic Richness Models. Modes ( $\beta$ ) and 95% credibility intervals (Lower CI and Upper CI) of the posterior distributions from the sensitivity analysis models predicting LD<sub>50</sub> using Taxonomic richness with differing category definitions. Fixed factors include the continuous factors mean phylogenetic distance between diet species and the LD<sub>50</sub> model (D<sub>LD50-Diet</sub>). Categorical fixed factors include LD<sub>50</sub> method (subcutaneous (SC), intravenous (IV), intraperitoneal (IP) and intramuscular (IM)); the presence of eggs in the diet (Eggs in Diet; present, absent) and Taxonomic richness (Diet Breadth, Low, Intermediate and high). The baseline was SC for LD<sub>50</sub> method, the absence of eggs for the Eggs in Diet and Low for Diet Breadth. For the sensitivity analysis 1 taxonomic richness was split as low (1 taxonomic group present in the diet), intermediate (2–3 taxonomic groups) and high (more than 3 taxonomic groups) and for sensitivity analysis 2 taxonomic richness was split as low (1 taxonomic group), intermediate (2–4 taxonomic groups) and high (more than 4 taxonomic groups). DB<sub>Low</sub>:D<sub>LD50-Diet</sub> represents the interaction term between DB and D<sub>LD50-Diet</sub>. The random terms associated with phylogenetic relatedness (Phylogeny ( $h^2$ )), intraspecific variation (Species) and residual variation (Residual) are also presented. Significant values, which are highlighted in bold, are deemed to be those with 95% of the posterior estimate above or below zero. All models have 529 LD<sub>50</sub> measures for 100 species.

	Sensitivity Analysis 1			Sensitivity analysis 2		
	$\beta$	Lower CI	Upper CI	$\beta$	Lower CI	Upper CI
<b>Fixed Terms</b>						
Intercept	0.33	−0.11	0.85	0.34	−0.14	0.83
LD <sub>50</sub> method <sub>SC</sub>						
IV	<b>−0.53</b>	<b>−0.65</b>	<b>−0.37</b>	<b>−0.53</b>	<b>−0.68</b>	<b>−0.40</b>
IP	<b>−0.27</b>	<b>−0.41</b>	<b>−0.13</b>	<b>−0.26</b>	<b>−0.41</b>	<b>−0.12</b>
IM	−0.12	−0.28	0.07	−0.12	−0.29	0.05
Eggs in Diet <sub>absent</sub>						
Present	<b>0.89</b>	<b>0.36</b>	<b>1.38</b>	<b>0.89</b>	<b>0.38</b>	<b>1.39</b>
D <sub>LD50-Diet</sub>	<b>0.22</b>	<b>0.12</b>	<b>0.32</b>	<b>0.22</b>	<b>0.11</b>	<b>0.33</b>
Diet Breadth <sub>Low</sub>						

<i>Intermediate</i>	0.07	−0.20	0.30	0.07	−0.17	0.31
<i>High</i>	0.17	−0.29	0.59	0.16	−0.25	0.64
DB <sub>Low</sub> :D <sub>LD50-Diet</sub>						
<i>Intermediate</i>	<b>−0.22</b>	<b>−0.37</b>	<b>−0.06</b>	<b>−0.22</b>	<b>−0.39</b>	<b>−0.06</b>
<i>High</i>	<b>−0.26</b>	<b>−0.50</b>	<b>−0.01</b>	−0.25	−0.50	0.01
<b>Random Terms</b>						
Phylogeny (h <sup>2</sup> )	0.44	0.20	0.68	0.44	0.20	0.68
Species	0.15	0.01	0.32	0.15	0.01	0.31
Residuals	0.40	0.26	0.54	0.39	0.27	0.53