

1 **Title page**

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4 Testing the Toxicofera: comparative reptile transcriptomics casts doubt on the single, early
5 evolution of the reptile venom system

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27 **Abstract**

28

29 **Background**

30 The identification of apparently conserved gene complements in the venom and salivary
31 glands of a diverse set of reptiles led to the development of the Toxicofera hypothesis – the
32 idea that there was a single, early evolution of the venom system in reptiles. However, this
33 hypothesis is based largely on relatively small scale EST-based studies of only venom or
34 salivary glands and toxic effects have been assigned to only some of these putative
35 Toxicoferan toxins in some species. We set out to investigate the distribution of these putative
36 venom toxin transcripts in order to investigate to what extent conservation of gene
37 complements may reflect a bias in previous sampling efforts.

38 **Results**

39 We have carried out the first large-scale test of the Toxicofera hypothesis and found it
40 lacking in a number of regards. Our quantitative transcriptomic analyses of venom and
41 salivary glands and other body tissues in five species of reptile, together with the use of
42 available RNA-Seq datasets for additional species shows that the majority of genes used to
43 support the establishment and expansion of the Toxicofera are in fact expressed in multiple
44 body tissues and most likely represent general maintenance or “housekeeping” genes. The
45 apparent conservation of gene complements across the Toxicofera therefore reflects an
46 artefact of incomplete tissue sampling. In other cases, the identification of a non-toxic
47 paralog of a gene encoding a true venom toxin has led to confusion about the phylogenetic
48 distribution of that venom component.

49 **Conclusions**

50 Venom has evolved multiple times in reptiles. In addition, the misunderstanding regarding
51 what constitutes a toxic venom component, together with the misidentification of genes and
52 the classification of identical or near-identical sequences as distinct genes has led to an

53 overestimation of the complexity of reptile venoms in general, and snake venom in particular,
54 with implications for our understanding of (and development of treatments to counter) the
55 molecules responsible for the physiological consequences of snakebite.

56

57 **Keywords**

58 Snake venom, Toxicofera, Transcriptomics,

59

60 **Background**

61 Snake venom is frequently cited as being highly complex or diverse [1-3] and a large number
62 of venom toxin genes and gene families have been identified, predominantly from EST-based
63 studies of gene expression during the re-synthesis of venom in the venom glands following
64 manually-induced emptying (“milking”) [4-8] and some proteomic studies of extracted
65 venom. It has been suggested that many of these gene families have originated via the
66 duplication of a gene encoding a non-venom protein expressed elsewhere in the body
67 followed by recruitment into the venom gland where natural selection can act to increase
68 toxicity, with subsequent additional duplications leading to a diversification within gene
69 families, often in a species-specific manner [9-11]. However, since whole genome
70 duplication is a rare event in reptiles [12], the hypothesis that novelty in venom originates via
71 the duplication of a “body” gene with subsequent recruitment into the venom gland requires
72 both that gene duplication is a frequent event in the germline of venomous snakes and that the
73 promoter and enhancer sequences that regulate venom gland-specific expression are
74 relatively simple and easy to evolve. It also suggests a high incidence of neofunctionalisation
75 rather than the more common process of subfunctionalisation [13-16].
76 The apparent widespread distribution of genes known to encode venom toxins in snakes in
77 the salivary glands of a diverse set of reptiles, including both those that had previously been
78 suggested to have secondarily lost venom in favour of constriction or other predation

79 techniques and those that had previously been considered to have never been venomous led to
80 the development of the Toxicofera hypothesis – the single, early evolution of venom in
81 reptiles [17-19] (Figure 1). Analysis of a wide range of reptiles, including charismatic
82 megafauna such as the Komodo dragon, *Varanus komodoensis* [20], has shown that the basal
83 Toxicoferan venom system comprises at least 16 genes, with additional gene families
84 subsequently recruited in different lineages [18, 19, 21].

85 Although toxic effects have been putatively assigned to some Toxicoferan venom proteins in
86 some species, the problem remains that their identification as venom components is based
87 largely on their expression in the venom gland during venom synthesis and their apparent
88 relatedness to other, known toxins in phylogenetic trees. It has long been known that all
89 tissues express a basic set of “housekeeping” or maintenance genes [22] and it is therefore
90 not surprising that similar genes might be found to be expressed in similar tissues in different
91 species of reptiles and that these genes might group together in phylogenetic trees. However,
92 the identification of transcripts encoding putative venom toxins in other body tissues would
93 cast doubt on the classification of these Toxicoferan toxins as venom components, as it is
94 unlikely that the same gene could fulfil toxic and non-toxic roles without evidence for
95 alternative splicing to produce a toxic variant (as has been suggested for *acetylcholinesterase*
96 in the banded krait, *Bungarus fasciatus* [11, 23]) or increased expression levels in the venom
97 gland (where toxicity might be dosage dependent). In order to address some of these issues
98 and to test the robustness of the Toxicofera hypothesis we have carried out a comparative
99 transcriptomic survey of the venom or salivary glands, skin and cloacal scent glands of five
100 species of reptile. Unlike the pancreas and other parts of the digestive system [24, 25], these
101 latter tissues (which include a secretory glandular tissue (the scent gland) and a relatively
102 inert, non-secretory tissue (skin)) have not previously been suggested to be the source of
103 duplicated venom toxin genes and we would therefore only expect to find ubiquitous
104 maintenance or “housekeeping” genes to be commonly expressed across these tissues. Study

105 species included the venomous painted saw-scaled viper (*Echis coloratus*); the non-
106 venomous corn snake (*Pantherophis guttatus*) and rough green snake (*Ophedrys aestivus*)
107 and a member of one of the more basal extant snake lineages, the royal python (*Python*
108 *regius*). As members of the Toxicofera *sensu* Fry et al. [21] we would expect to find the basic
109 Toxicoferan venom genes expressed in the venom or salivary glands of all of these species. In
110 addition we generated corresponding data for the leopard gecko (*Eublepharis macularius*), a
111 member of one of the most basal lineages of squamate reptiles that lies outside of the
112 proposed Toxicofera clade (Figure 1). We have also taken advantage of available
113 transcriptomes or RNA-Seq data for corn snake vomeronasal organ [26] and brain [27], garter
114 snake (*Thamnophis elegans*) liver [28] and pooled tissues (brain, gonads, heart, kidney, liver,
115 spleen and blood of males and females [29]), eastern diamondback rattlesnake (*Crotalus*
116 *adamanteus*) and eastern coral snake (*Micrurus fulvius*) venom glands [7, 8, 30], king cobra
117 (*Ophiophagus hannah*) venom gland, accessory gland and pooled tissues (heart, lung, spleen,
118 brain, testes, gall bladder, pancreas, small intestine, kidney, liver, eye, tongue and stomach)
119 [31], Burmese python (*Python molurus*) pooled liver and heart [32], green anole (*Anolis*
120 *carolinensis*) pooled tissue (liver, tongue, gallbladder, spleen, heart, kidney and lung), testis
121 and ovary [33] and bearded dragon (*Pogona vitticeps*), Nile crocodile (*Crocodylus niloticus*)
122 and chicken (*Gallus gallus*) brains [27], as well as whole genome sequences for the Burmese
123 python and king cobra [31, 34].

124 Assembled transcriptomes were searched for genes previously suggested to be venom toxins
125 in *Echis coloratus* and related species [5, 35, 36] as well as those that have been used to
126 support the Toxicofera hypothesis, namely *acetylcholinesterase*, *AVIT peptide* [9, 11, 18, 19,
127 23], *complement c3/cobra venom factor*, *epididymal secretory protein* [19, 37], *c-type lectins*
128 [38, 39], *cysteine-rich secretory protein (crisp)* [40, 41], *crotamine* [42, 43], *cystatin* [44, 45],
129 *dipeptidylpeptidase*, *lysosomal acid lipase*, *renin aspartate protease* [5, 19, 35, 46],
130 *hyaluronidase* [47, 48], *kallikrein* [49, 50], *kunitz* [51], *l-amino-acid oxidase* [52, 53], *nerve*

131 *growth factor* [54, 55], *phospholipase A₂* [15], *phospholipase b* [7, 56, 57], *ribonuclease* [58],
132 *serine protease* [59, 60], *snake venom metalloproteinase* [61, 62], *vascular endothelial*
133 *growth factor (vegf)* [9, 17, 63, 64], *veficolin* [65], *vespryn*, *waprin* [19, 66-68] and *3-finger*
134 *toxins* [69].

135 We find that many genes previously claimed to be venom toxins are in fact expressed in
136 multiple tissues (Figure 2) and that transcripts encoding these genes show no evidence of
137 consistently elevated expression level in venom or salivary glands compared to other tissues
138 (Supplemental tables S5-S9). Only two putative venom toxin genes (*l-amino acid oxidase b2*
139 and *PLA₂ IIA-c*) showed evidence of a venom gland-specific splice variant across our
140 multiple tissue data sets. We have also identified several cases of mistaken identity, where
141 non-orthologous genes have been used to claim conserved, ancestral expression and instances
142 of identical sequences being annotated as two distinct genes (see later sections). We propose
143 that the putative ancestral Toxicoferan venom toxin genes do not encode toxic venom
144 components in the majority of species and that the apparent venom gland-specificity of these
145 genes is a side-effect of incomplete tissue sampling. Our analyses show that neither increased
146 expression in the venom gland nor the production of venom-specific splice variants can be
147 used to support continued claims for the toxicity of these genes.

148

149 **Results**

150 Based on our quantitative analysis of their expression pattern across multiple species, we
151 identify the following genes as unlikely to represent toxic venom components in the
152 Toxicofera. The identification of these genes as non-venom is more parsimonious than
153 alternative explanations such as the reverse recruitment of a “venom” gene back to a “body”
154 gene [70], which requires a far greater number of steps (duplication, recruitment, selection for
155 increased toxicity, reverse recruitment) to have occurred in each species, whereas a “body”
156 protein remaining a “body” protein is a zero-step process regardless of the number of species

157 involved. The process of reverse recruitment must also be considered doubtful given the
158 rarity of gene duplication in vertebrates (estimated to be between 1 gene per 100 to 1 gene
159 per 1000 per million years [71-73]).

160 Acetylcholinesterase

161 We find identical *acetylcholinesterase* (*ache*) transcripts in the *E. coloratus* venom gland and
162 scent gland (which we call transcript 1) and an additional splice variant expressed in skin and
163 scent gland (transcript 2). Whilst the previously known splice variants in banded krait
164 (*Bungarus fasciatus*) are differentiated by the inclusion of an alternative exon, analysis of the
165 *E. coloratus ache* genomic sequence (accession number KF114031) reveals that the shorter
166 transcript 2 instead comprises only the first exon of the *ache* gene, with a TAA stop codon
167 that overlaps the 5' GT dinucleotide splice site in intron 1. *ache* transcript 1 is expressed at a
168 low level in the venom gland (6.60 FPKM) and is found in multiple tissues in all study
169 species (Figure 2), as well as corn snake vomeronasal organ and garter snake liver. The
170 shorter transcript 2 is found most often in skin and scent glands (Figure 2, Supplementary
171 figure S1). The low expression level and diverse tissue distribution of transcripts of this gene
172 suggest that *acetylcholinesterase* does not represent a Toxicoferan venom toxin. It should
173 also be noted that the most frequently cited sources for the generation of a toxic version of
174 *ache* in banded krait via alternative splicing include statements that *ache* “does not appear to
175 contribute to the toxicity of the venom” [74], is “not toxic to mice, even at very high doses”
176 [75] and is “neither toxic by itself nor acting in a synergistic manner with the toxic
177 components of venom” [76].

178 AVIT

179 We find only a single transcript encoding an AVIT peptide in our dataset, in the scent gland
180 of the rough green snake (data not shown). The absence of this gene in all of our venom and
181 salivary gland datasets, as well as the venom glands of the king cobra, eastern coral snake and
182 Eastern diamondback rattlesnake and the limited number of sequences available on Genbank

183 (one species of snake, *Dendroaspis polylepis* (accession number P25687) and two species of
184 lizard, *Varanus varius* and *Varanus komodoensis* (accession numbers AAZ75583 and
185 ABY89668 respectively)) despite extensive sampling, would suggest that it is unlikely to
186 represent a conserved Toxicoferan venom toxin.

187 Complement C3 (“cobra venom factor”)

188 We find identical transcripts encoding *complement c3* in all tissues in all species, with the
189 exception of royal python skin (Figures 2 and 3) and we find only a single *complement c3*
190 gene in the *E. coloratus* genome (data not shown). These findings, together with the
191 identification of transcripts encoding this gene in the liver, brain, vomeronasal organ and
192 tissue pools of various other reptile species (Figure 3) demonstrate that this gene does not
193 represent a Toxicoferan venom toxin. However, the grouping of additional *complement c3*
194 genes in the king cobra (*Ophiophagus hannah*) and monocled cobra (*Naja kaouthia*) in our
195 phylogenetic tree does support a duplication of this gene somewhere in the Elapid lineage.
196 One of these paralogs may therefore represent a venom toxin in at least some of these more
197 derived species and the slightly elevated expression level of this gene in the venom or
198 salivary gland of some of our study species suggests that *complement c3* has been exapted
199 [77] to become a venom toxin in the Elapids. It seems likely that the identification of the non-
200 toxic paralogue in other species (including veiled chameleon (*Chamaeleo calyptratus*), spiny-
201 tailed lizard (*Uromastyx aegyptia*) and Mitchell's water monitor (*Varanus mitchelli*) has
202 contributed to confusion about the distribution of this “Cobra venom factor” (which should
203 more rightly be called *complement c3b*), to the point where genes in alligator (*Alligator*
204 *sinensis*), turtles (*Pelodiscus sinensis*) and birds (*Columba livia*) are now being annotated as
205 venom factors (accession numbers XP 006023407-8, XP 006114685, XP 005513793, Figure
206 3).

207 Cystatin

208 We find two transcripts encoding cystatins expressed in the venom gland of *E. coloratus*
209 corresponding to *cystatin-e/m* and *f* (Supplementary figures S2 and S3). *cystatin-e/m* was
210 found to be expressed in all tissues from all species used in this study (Figure 2), as well as
211 corn snake vomeronasal organ and brain and garter snake liver and pooled tissues. The
212 transcript encoding *cystatin-f* (which has not previously been reported to be expressed in a
213 snake venom gland) is also expressed in the scent gland of *E. coloratus* and in the majority of
214 other tissues of our study species. We find no evidence for a monophyletic clade of
215 Toxicoferan cystatin-derived venom toxins and would agree with Richards et al. [45] that low
216 expression level and absence of *in vitro* toxicity represents a “strong case for snake venom
217 cystatins as essential housekeeping or regulatory proteins, rather than specific prey-targeted
218 toxins...” Indeed, it is unclear why cystatins should be considered to be conserved venom
219 toxins, since even from its earliest discovery in the venom of the puff adder (*Bitis arietans*)
220 there has been “...no evidence that it is connected to the toxicity of the venom” [44].

221 Dipeptidyl peptidases

222 We find identical transcripts encoding *dipeptidyl peptidase 3* and *4* in all tissues in all species
223 except the leopard gecko (Figures 2, 4a and 4b), and both of these have a low transcript
224 abundance in the venom gland of *E. coloratus*. *dpp4* is expressed in garter snake liver and
225 Anole testis and ovary and *dpp3* is also expressed in garter snake liver, king cobra pooled
226 tissues and Bearded dragon brain (Figures 4a and b). It is therefore unlikely the either *dpp3* or
227 *dpp4* represent venom toxins.

228 Epididymal secretory protein

229 We find one transcript encoding epididymal secretory protein (ESP) expressed in the venom
230 gland of *Echis coloratus* corresponding to type E1. This transcript is also found to be
231 expressed at similar levels in the scent gland and skin of this species and orthologous
232 transcripts are expressed in all three tissues of all other species used in this study (Figure 2
233 and Supplementary figure S4a), suggesting that this is a ubiquitously expressed gene and not

234 a venom component. Previously described epididymal secretory protein sequences from
235 varanids [78] and the colubrid *Cylindrophis ruffus* [21] do not represent *esp-e1* and their true
236 orthology is currently unclear. However, our analysis of these and related sequences suggests
237 that they are likely part of a reptile-specific expansion of esp-like genes and that the *Varanus*
238 and *Cylindrophis* sequences do not encode the same gene (Supplementary figure S4b).
239 Therefore there is not, nor was there ever, any evidence that epididymal secretory protein
240 sequences represent venom components in the Toxicofera.

241 Ficolin (“veficolin”)

242 We find one transcript encoding *ficolin* in the *E. coloratus* venom gland and identical
243 transcripts in both scent gland and skin (Figure 2, Supplementary figure S5) and orthologous
244 transcripts in all corn snake and leopard gecko tissues, as well as rough green snake salivary
245 and scent glands and royal python salivary gland. Paralogous genes expressed in multiple
246 tissues were also found in corn snake and rough green snake (Supplementary figure S5).
247 These findings, together with additional data from available transcriptomes of pooled garter
248 snake body tissues and bearded dragon and chicken brains show that *Ficolin* does not
249 represent a Toxicoferan venom component.

250 Hyaluronidase

251 Hyaluronidase has been suggested to be a “venom spreading factor” to aid the dispersion of
252 venom toxins throughout the body of envenomed prey, and as such it does not represent a
253 venom toxin itself [79]. We do however find two hyaluronidase genes expressed in the
254 venom gland of *E. coloratus*. The first appears to be venom gland specific (based on
255 available data) and has two splice variants including a truncated variant similar to sequences
256 previously characterised from *Echis carinatus sochureki* (accession number DQ840262) and
257 *Echis pyramidum leakeyi* (accession number DQ840255) venom glands [48]. Although we
258 cannot rule out hyaluronidase in playing an active (but non-toxic) role in *Echis* venom, it is
259 worth commenting that hyaluronan has been suggested to have a role in wound healing and

260 the protection of the oral mucosa in human saliva [80]. The expression of hyaluronidases
261 involved in hyaluronan metabolism in venom and/or salivary glands is therefore perhaps
262 unsurprising.

263 Kallikrein

264 We find two Kallikrein-like sequences in *E. coloratus*, one of which is expressed in all three
265 tissues in this species (at a low level in the venom gland) and a variety of other tissues in the
266 other study species, and one of which is found only in scent gland and skin (Figure 2,
267 Supplementary figure S6). These genes do not represent venom toxins in *E. coloratus* and
268 appear to be most closely-related to a group of mammalian Kallikrein (KLK) genes
269 containing *KLK1*, *11*, *14* and *15* and probably represent the outgroup to a mammalian-
270 specific expansion of this gene family. The orthology of previously published Toxicoferan
271 Kallikrein genes is currently unclear and the majority of these sequences can be found in our
272 serine protease tree (see later section and Supplementary figure S19).

273 Kunitz

274 We find a number of transcripts encoding Kunitz-type protease inhibitors in our tissue data,
275 with the majority of these encoding *kunitz1* and *kunitz2* genes (Figure 2 and Supplementary
276 figure S7). The tissue distribution of these transcripts, together with the phylogenetic position
277 of lizard and venomous snake sequences does not support a monophyletic clade of venom
278 gland-specific Kunitz-type genes in the Toxicofera. The presence of protease inhibitors in
279 reptile venom and salivary glands should perhaps not be too surprising and it again seems
280 likely that the involvement of Kunitz-type inhibitors in venom toxicity in some advanced
281 snake lineages (in this case mamba (*Dendroaspis sp.*) dendrotoxins and krait (*Bungarus*
282 *multicinctus*) bungarotoxins [81, 82]) has led to confusion when non-toxic orthologs have
283 been identified in other species.

284 Lysosomal acid lipase

285 We find two transcripts encoding Lysosomal acid lipase genes in the *E. coloratus* venom
286 gland transcriptome, one of which (*lipa-a*) is also expressed in skin and scent gland in this
287 species and all three tissues in our other study species. *lipa-a*, despite not being venom gland
288 specific, is more highly expressed in the venom gland (3,337.33 FPKM) than in the scent
289 gland (484.49 FPKM) and skin (22.79 FPKM) of *E. coloratus*, although there is no evidence
290 of elevated expression in the salivary glands of our other study species. As this protein is
291 involved in lysosomal lipid hydrolysis [83] and the venom gland is a highly active tissue, we
292 suggest that this elevated expression is likely related to high cell turnover. Transcripts of *lipa-*
293 *b* are found at a low level in the venom and scent glands of *E. coloratus* and the scent gland
294 of royal python (Figure 2, Supplementary figure S8). Neither *lipa-a* or *lipa-b* therefore
295 encode venom toxins.

296 Natriuretic peptide

297 We find only a single natriuretic peptide-like sequence in our dataset, in the skin of the royal
298 python. The absence of this gene from the rest of our study species suggests that it is not a
299 highly conserved Toxicoferan toxin.

300 Nerve growth factor

301 We find identical transcripts encoding *nerve growth factor (ngf)* in all three *E. coloratus*
302 tissues. Transcripts encoding the orthologous gene are also found in the corn snake salivary
303 gland and scent gland; rough green snake scent gland and skin; royal python skin and leopard
304 gecko salivary gland, scent gland and skin (Figure 2 and Supplementary figure S9). *ngf* is
305 expressed at a higher level in the venom gland (525.82 FPKM) than in the scent gland (0.18
306 FPKM) and skin (0.58 FPKM) of *E. coloratus*, but not at an elevated level in the salivary
307 gland of other species, again hinting at the potential for exaptation of this gene. Based on
308 these findings, together with the expression of this gene in garter snake pooled tissues, we
309 suggest that *ngf* does not encode a Toxicoferan toxin. However, we do find evidence for the
310 duplication of *ngf* in cobras (Supplementary figure S9) suggesting that it may represent a

311 venom toxin in at least some advanced snakes [84]. As with *complement c3*, it seems likely
312 that the identification of non-toxic orthologs in distantly-related species has led to the
313 conclusion that *ngf* is a widely-distributed venom toxin and confused its true evolutionary
314 history.

315 Phospholipase A₂ (PLA₂ Group IIE)

316 We find transcripts encoding Group IIE PLA₂ genes in the venom gland of *E. coloratus* and
317 the salivary glands of all other species (Figure 2, Supplementary figure S10). Although this
318 gene appears to be venom and salivary-gland-specific (based on available data), its presence
319 in all species (including the non-Toxicoferan leopard gecko) suggests that it does not
320 represent a toxic venom component.

321 Phospholipase B

322 We find a single transcript encoding *phospholipase b* expressed in all three *E. coloratus*
323 tissues (Figures 2 and 5) and transcripts encoding the orthologous gene are found in all other
324 tissues from all study species with the exception of rough green snake salivary gland. We also
325 find *plb* transcripts in corn snake vomeronasal organ, garter snake liver, Burmese python
326 pooled tissues (liver and heart) and bearded dragon brain (Figure 5). The two transcripts in
327 each of rough green snake and corn snake are likely alleles or the result of individual
328 variation, and actually represent a single *phospholipase b* gene from each of these species.
329 Transcript abundance analysis shows this gene to be expressed at a low level in all tissues
330 from all study species. Based on the phylogenetic and tissue distribution of this gene it is
331 unlikely to represent a Toxicoferan venom toxin.

332 Renin (“renin aspartate protease”)

333 We find a number of transcripts encoding renin-like genes in the *E. coloratus* venom gland
334 (Figures 2 and 6), one of which (encoding the canonical *renin*) is also expressed in the scent
335 gland and is orthologous to a previously described sequence from the venom gland of the
336 ocellated carpet viper (*Echis ocellatus*, accession number CAJ55260). We also find that the

337 recently-published *Boa constrictor renin aspartate protease (rap)* gene (accession number
338 JX467165 [21]) is in fact a *cathepsin d* gene, transcripts of which are found in all three
339 tissues in all five of our study species. We suggest that this misidentification may be due to a
340 reliance on BLAST-based classification, most likely using a database restricted to squamate
341 or serpent sequences. It is highly unlikely that either *renin* or *cathepsin d* (or indeed any
342 renin-like aspartate proteases) constitute venom toxins in *E. coloratus* or *E. ocellatus*, nor do
343 they represent basal Toxicoferan toxins.

344 Ribonuclease

345 Ribonucleases have been suggested to have a role in the generation of free purines in snake
346 venoms [58] and the presence of these genes in the salivary glands of two species of lizard
347 (*Gerrhonotus infernalis* and *Celestus warreni*) and two colubrid snakes (*Liophis peocilogyrus*
348 and *Psammophis mossambicus*) has been used to support the Toxicofera [78, 85]. We did not
349 identify orthologous ribonuclease genes in any of our salivary or venom gland data, nor do
350 we find them in venom gland transcriptomes from the Eastern diamondback rattlesnake, king
351 cobra and eastern coral snake (although we have identified a wide variety of other
352 ribonuclease genes). The absence of these genes in seven Toxicoferans, coupled with the fact
353 that they were initially described from only 2 out of 11 species of snake [85] and 3 out of 18
354 species of lizard [78] would cast doubt on their status as conserved Toxicoferan toxins.

355 Three finger toxins (3ftx)

356 We find 2 transcripts encoding three finger toxin (3ftx)-like genes expressed in the *E.*
357 *coloratus* venom gland, one of which is expressed in all 3 tissues (*3ftx-a*) whilst the other is
358 expressed in the venom and scent glands (*3ftx-b*). Orthologous transcripts of *3ftx-a* are found
359 to be expressed in all three tissues of corn snake, rough green snake salivary gland and skin,
360 and royal python salivary gland. An ortholog of *3ftx-b* is expressed in rough green snake
361 scent gland. We also find a number of different putative *3ftx* genes in our other study species,
362 often expressed in multiple tissues (Figure 2, Supplementary figure S11). Based on the

363 phylogenetic and tissue distribution of both of these genes we suggest that they do not
364 represent venom toxins in *E. coloratus*. As with other proposed Toxicoferan genes such as
365 *complement c3* and *nerve growth factor*, it seems likely that *3ftx* genes are indeed venom
366 components in some species, especially cobras and other elapids [31, 69], and that the
367 identification of their non-venom orthologs in other species has led to much confusion
368 regarding the phylogenetic distribution of these toxic variants.

369 Vespryn

370 We do not find *vespryn* transcripts in any *E. coloratus* tissues, although this gene is present in
371 the genome of this species (accession number KF114032). We do however find transcripts
372 encoding this gene in the salivary and scent glands of the corn snake, and skin and scent
373 glands of the rough green snake, royal python and leopard gecko (Figure 2, Supplementary
374 figure S12). We suggest that the tissue distribution of this gene in these species casts doubt
375 on its role as a venom component in the Toxicofera.

376 Waprin

377 We find a number of “waprin”-like genes in our dataset, expressed in a diverse array of body
378 tissues. Our phylogenetic analyses (Supplementary figure S13) show that previously
379 characterised “waprin” genes [8, 66, 68, 86, 87] most likely represent *WAP four-disulfide*
380 *core domain 2 (wfdc2)* genes which have undergone a squamate-specific expansion and that
381 there is no evidence for a venom gland-specific paralog. It is unlikely therefore that these
382 genes represent a Toxicoferan venom toxin. Indeed, the inland taipan (*Oxyuranus*
383 *microlepidotus*) “Omwaprin” has been shown to be “...non-toxic to Swiss albino mice at
384 doses of up to 10 mg/kg when administered intraperitoneally” [68] and is more likely to have
385 an antimicrobial function in the venom or salivary gland.

386 Implications for venom composition and complexity in *Echis coloratus*

387 The following genes show either a venom gland-specific expression or an elevated expression
388 level in this tissue, but not both and as such we suggest that whilst they *may* represent venom
389 toxins in *E. coloratus*, further analysis is needed in order to confirm this.

390 Vascular endothelial growth factor

391 We find four transcripts encoding vascular endothelial growth factor (VEGF) expressed in
392 the venom gland of *E. coloratus*. These correspond to *vegf-a*, *vegf-b*, *vegf-c* and *vegf-f* and of
393 these *vegf-a*, *b* and *c* are also expressed in the skin and scent gland of this species (Figure 2).
394 Transcripts encoding orthologs of these genes are expressed in all three tissues of all other
395 species used in this study (with the exception of the absence of *vegf-a* in corn snake skin). In
396 accordance with previous studies [7] we find evidence of alternative splicing of *vegf-a*
397 transcripts in all species although no variant appears to be tissue-specific. It is likely that a
398 failure to properly recognise and classify alternatively spliced *vegf-a* transcripts (Aird et al.
399 2013) may have contributed to an overestimation of snake venom complexity. *vegf-d* was
400 only found to be expressed in royal python salivary gland and scent gland and all three tissues
401 from leopard gecko (Figure 2, Supplementary figure S14). The transcript encoding VEGF-F
402 is found only in the venom gland of *E. coloratus* and, given the absence of any Elapid *vegf-f*
403 sequences in public databases as well as absence of this transcript in the two species of
404 colubrid in our study, we suggest that *vegf-f* is specific to vipers. Whilst *vegf-f* has a higher
405 transcript abundance in *E. coloratus* venom gland (186.73 FPKM) than *vegf-a* (3.24 FPKM),
406 *vegf-b* (1.28 FPKM) and *vegf-c* (1.54 FPKM), compared to other venom genes in this species
407 (see next section) it has a considerably lower transcript abundance suggesting it represents at
408 most a minor venom component in *E. coloratus*.

409 L-amino acid oxidase

410 We find transcripts encoding two *l-amino acid oxidase (laao)* genes in *E. coloratus*, one of
411 which (*laao-b*) has two splice variants (Figure 2, Supplementary figure S15). *laao-a*
412 transcripts are found in all three *E. coloratus* and leopard gecko tissues. *laao-b* is venom

413 gland-specific in *E. coloratus* (based on the available data) and transcripts of the orthologous
414 gene are found in the scent glands of corn snake, rough green snake and royal python. The
415 splice variant *laao-b2* may represent a venom toxin in *E. coloratus* based on its specific
416 expression in the venom gland of this species and elevated expression level (628.84 FPKM).

417 Crotamine

418 We find a single *crotamine*-like transcript in *E. coloratus*, in the venom gland (Figure 2).
419 Related genes are found in a variety of tissues in other study species (including the scent
420 gland of the rough green snake, the salivary gland and skin of the leopard gecko, and in all
421 three corn snake tissues), although the short length of these sequences precludes a definitive
422 statement of orthology. This gene may represent a toxic venom component in *E. coloratus*
423 based on its tissue distribution, but due to its low transcript abundance (10.95 FPKM) it is
424 likely to play a minor role, if any.

425

426 The following genes are found only in the venom gland of *E. coloratus* and clearly show an
427 elevated expression level (Figure 7). Whilst we classify these genes as encoding venom
428 toxins in this species (Table 1) it should be noted that none of these genes support the
429 monophyly of Toxicoferan venom toxins.

430 Cysteine-rich secretory proteins (CRISPs)

431 We find transcripts encoding two distinct CRISPs expressed in the *E. coloratus* venom gland,
432 one of which is also found in skin and scent gland (Figure 2). Phylogenetic analysis of these
433 genes (which we call *crisp-a* and *crisp-b*) reveals that they appear to have been created as a
434 result of a gene duplication event earlier in the evolution of advanced snakes (Supplementary
435 Figure S16). *crisp-a* transcripts are also found in all three corn snake tissues, as well as rough
436 green snake skin and scent gland and royal python scent gland. *crisp-b* is also found in corn
437 snake salivary gland (Figure 2 and Supplementary figure S16) and the phylogenetic and
438 tissue distribution of this gene suggest that it does indeed represent a venom toxin, produced

439 via duplication of an ancestral *crisp* gene that was expressed in multiple tissues, including the
440 salivary gland. The elevated transcript abundance of *crisp-b* (3,520.07 FPKM) in the venom
441 gland of *E. coloratus* further supports its role as a venom toxin in this species (Figure 7). The
442 phylogenetic and tissue distribution and low transcript abundance of *crisp-a* (0.61 FPKM in
443 *E. coloratus* venom gland) shows that it is unlikely to be a venom toxin. We also find no
444 evidence of a monophyletic clade of reptile venom toxins and therefore suggest that, contrary
445 to earlier reports [20, 78], the CRISP genes of varanid and helodermatid lizards do not
446 represent shared Toxicoferan venom toxins and, if they are indeed toxic venom components,
447 have been recruited independently from those of the advanced snakes. Regardless of their
448 status as venom toxins, it appears likely that the diversity of CRISP genes in varanid lizards
449 in particular [17] has been overestimated as a result of the use of negligible levels of
450 sequence variation to classify transcripts as representing distinct gene products
451 (Supplementary figures S23 and S24).

452 C-type lectins

453 We find transcripts encoding 11 distinct C-type lectin genes in the *E. coloratus* venom gland,
454 one of which (*ctl-a*) is also expressed in the scent gland of this species. The remaining 10
455 genes (*ctl-b* to *k*) are found only in the venom gland and form a clade with other viper C-type
456 lectin genes (Figure 2, Supplementary figure S17). Of these, 6 are highly expressed in the
457 venom gland (*ctl-b* to *d*, *ctl-f* to *g* and *ctl-j*) with a transcript abundance range of 3,706.21-
458 24,122.41 FPKM (Figure 7). The remainder of these genes (*ctl-e*, *ctl-h* to *i* and *ctl-k*) show
459 lower transcript abundance (0.80-1,475.88 FPKM), with two (*ctl-i* and *k*) being more lowly
460 expressed than *ctl-a* (230.06 FPKM). A number of different C-type lectin genes are found in
461 our other study species, often expressed in multiple tissues (Supplementary figure S17). We
462 suggest therefore that the 6 venom-gland specific C-type lectin genes which are highly
463 expressed are indeed venom toxins in *E. coloratus* and that these genes diversified via the
464 duplication of an ancestral gene with a wide expression pattern, including in salivary/venom

465 glands. Based on their selective expression in the venom gland (from available data) the
466 remaining four C-type lectin genes cannot be ruled out as putative toxins, although their
467 lower transcript abundance suggests that they are likely to be minor components in *E.*
468 *coloratus* venom. It should also be noted that a recent analysis of king cobra (*Ophiophagus*
469 *hannah*) venom gland transcriptome and proteome suggested that “...lectins do not contribute
470 to king cobra envenoming” [31].

471 Phospholipase A₂ (PLA₂ Group IIA)

472 We find five transcripts encoding Group IIA PLA₂ genes in *E. coloratus*, three of which are
473 found only in the venom gland and two of which are found only in the scent gland (these
474 latter two likely represent intra-individual variation in the same transcript) (Figure 2,
475 Supplementary figure S18). The venom gland-specific transcript *PLA₂ IIA-c* is highly
476 expressed (22,520.41 FPKM) and likely represents a venom toxin, and may also be a putative
477 splice variant although further analysis is needed to confirm this. *PLA₂ IIA-d* and *IIA-e* show
478 an elevated, but lower, expression level (1,677.15 FPKM and 434.67 FPKM respectively,
479 Figure 7). Based on tissue and phylogenetic distribution we would propose that these three
480 genes may represent putative venom toxins (Table 1).

481 Serine proteases

482 We find 6 transcripts encoding Serine proteases in *E. coloratus* (Figure 2, Supplementary
483 figure S19) which (based on available data) are all venom gland specific. Four of these
484 transcripts are highly expressed in the venom gland (*serine proteases a-c* and *e*; 3,076.01-
485 7,687.03 FPKM) whilst two are expressed at a lower level (*serine proteases d* and *f*; 1,098.45
486 FPKM and 102.34 FPKM respectively, Figure 7). Based on these results we suggest *serine*
487 *proteases a, b, c* and *e* represent venom toxins whilst *serine proteases d* and *f* may represent
488 putative venom toxins (Table 1).

489 Snake venom metalloproteinases

490 We find 21 transcripts encoding snake venom metalloproteinases in *E. coloratus* and of these
491 14 are venom gland-specific, whilst another (*svmp-n*) is expressed in the venom gland and
492 scent gland. Five remaining genes are expressed in the scent gland only whilst another is
493 expressed in the skin (Figure 2, Supplementary figure S20). Of the 14 venom gland-specific
494 SVMPs we find 4 to be highly expressed (5,552.84-15,118.41 FPKM, Figure 7). In the
495 absence of additional data, we classify the 13 venom gland-specific *svmp* genes as venom
496 toxins in this species (Table 1).

497

498 **Discussion**

499 Our transcriptomic analyses have revealed that all 16 of the basal venom toxin genes used to
500 support the hypothesis of a single, early evolution of venom in reptiles (the Toxicofera
501 hypothesis [17-21, 78]), as well as a number of other genes that have been proposed to
502 encode venom toxins in multiple species are in fact expressed in multiple tissues, with no
503 evidence for consistently higher expression in venom or salivary glands. Additionally, only
504 two genes in our entire dataset of 74 genes in five species were found to encode possible
505 venom gland-specific splice variants (*l-amino acid oxidase b2* and *PLA₂ IIA-c*). We therefore
506 suggest that many of the proposed basal Toxicoferan genes most likely represent
507 housekeeping or maintenance genes and that the identification of these genes as conserved
508 venom toxins is a side-effect of incomplete tissue sampling. This lack of support for the
509 Toxicofera hypothesis therefore prompts a return to the previously held view [88] that venom
510 in different lineages of reptiles has evolved independently, once at the base of the advanced
511 snakes, once in the helodermatid (gila monster and beaded lizard) lineage and, possibly, one
512 other time in monitor lizards, although evidence for a venom system in this latter group [20,
513 78, 89] may need to be reinvestigated in light of our findings. The process of reverse
514 recruitment [70], where a venom gene undergoes additional gene duplication events and is
515 subsequently recruited from the venom gland back into a body tissue (which was proposed on

516 the basis of the placement of garter snake and Burmese python “physiological” genes within
517 clades of “venom” genes) must also be re-evaluated in light of our findings.

518 Bites by venomous snakes are thought to be responsible for as many as 1,841,000
519 envenomings and 94,000 deaths annually, predominantly in the developing world [90, 91]
520 and medical treatment of snakebite is reliant on the production of antivenoms containing
521 antibodies, typically from sheep or horses, that will bind and neutralise toxic venom proteins
522 [92]. Since these antivenoms are derived from the injection of crude venom into the host
523 animal they are not targeted to the most pathogenic venom components and therefore also
524 include antibodies to weakly- or non-pathogenic proteins, requiring the administration of
525 large or multiple doses [11], increasing the risks of adverse reactions. A comprehensive
526 understanding of snake venom composition is therefore vital for the development of the next
527 generation of antivenoms [2, 11, 93] as it is important that research effort is not spread too
528 thinly through the inclusion of non-toxic venom gland transcripts. Our results suggest that
529 erroneous assumptions about the single origination and functional conservation of venom
530 toxins across the Toxicofera has led to the complexity of snake venom being overestimated
531 by previous authors, with the venom of the painted saw-scaled viper, *Echis coloratus* likely
532 consisting of just 34 genes in 8 gene families (Table 1, based on venom gland-specific
533 expression and a ‘high’ expression, as defined by presence in the top 25% of transcripts [94]
534 in at least two of four venom gland samples), fewer than has been suggested for this and
535 related species in previous EST or transcriptomic studies [5, 35]. However, it is noteworthy
536 that the results of our analyses accord well with proteomic analyses of venom composition in
537 snakes, which range from an almost identical complement of 35 toxins in 8 gene families for
538 the related ocellated carpet viper, *Echis ocellatus* [36] to between 24-61 toxins in 6-14
539 families in a range of other species (Table 2). Far from being a “complex cocktail” [10, 11,
540 95, 96], snake venom may in fact represent a relatively simple mixture of toxic proteins

541 honed by natural selection for rapid prey immobilisation, with limited lineage-specific
542 expansion in one or a few particular gene families.
543 In order to avoid continued overestimation of venom complexity, we propose that future
544 transcriptome-based analyses of venom composition must include quantitative comparisons
545 of multiple body tissues from multiple individuals and robust phylogenetic analysis that
546 includes known paralogous members of gene families. We would also encourage the use of
547 clearly explained, justifiable criteria for classifying highly similar sequences as new paralogs
548 rather than alleles or the result of PCR or sequencing errors, as it seems likely that some
549 available sequences from previous studies have been presented as distinct genes on the basis
550 of extremely minor (or even non-existent) sequence variation (see Supplementary figures
551 S21-S24 for examples of identical or nearly identical ribonuclease and CRISP sequences and
552 Supplementary figures S25 and S26 for examples of the same sequence being annotated as
553 two different genes). As a result, the diversity of “venom” composition in these species may
554 have been inadvertently inflated.

555 Additionally, we would encourage the adoption of a standard nomenclature for reptile genes,
556 as the overly-complicated and confusing nomenclature used currently (Table 3) may also
557 contribute to the perceived complexity of snake venom. We propose that such a nomenclature
558 system should be based on the comprehensive standards developed for Anole lizards [97], for
559 example:

- 560 • “Gene symbols for all...species should be written in lower case only and in italics,
561 e.g., *gene2*.”
- 562 • “Whenever criteria for orthology have been met... the gene symbol should be
563 comparable to the human gene symbol, e.g., if the human gene symbol is *GENE2*,
564 then the gene symbol would be *gene2*.”

- 565 • “Duplication of the ortholog of a mammalian gene will be indicated by an “a” or “b”
566 suffix, e.g., *gene2a* and *gene2b*. If the mammalian gene symbol already contains a
567 suffix letter, then there would be a second letter added, e.g., *gene4aa* and *gene4ab*.”

568 It seems likely that the application of our approach to other species (together with proteomic
569 studies of extracted venom) will lead to a commensurate reduction in claimed venom
570 diversity, with clear implications for the development of next generation antivenoms: since
571 most true venom genes are members of a relatively small number of gene families, it is likely
572 that a similarly small number of antibodies may be able to bind to and neutralise the toxic
573 venom components, especially with the application of “string of beads” techniques [98]
574 utilising fusions of short oligopeptide epitopes designed to maximise the cross-reactivity of
575 the resulting antibodies [2].

576

577 **Conclusions**

578 We suggest that identification of the apparently conserved Toxicofera venom toxins in
579 previous studies is most likely a side effect of incomplete tissue sampling, compounded by
580 incorrect interpretation of phylogenetic trees and the use of BLAST-based gene identification
581 methods. It should perhaps not be too surprising that homologous tissues in related species
582 would show similar gene complements and the restriction of most previous studies to only the
583 “venom” glands means that monophyletic clades of reptile sequences in phylogenetic trees
584 have been taken to represent monophyletic clades of venom toxin genes. Whilst it is true that
585 some of these genes do encode toxic proteins in some species (indeed, this was often the
586 basis for their initial discovery) the discovery of orthologous genes in other species does not
587 necessarily demonstrate shared toxicity. In short, toxicity in one does not equal toxicity in all.

588

589 **Methods**

590 Experimental methods involving animals followed institutional and national guidelines and
591 were approved by the Bangor University Ethical Review Committee.

592 *RNA-Seq*

593 Total RNA was extracted from four venom glands taken from four individual specimens of
594 adult Saw-scaled vipers (*Echis coloratus*) at different time points following venom extraction
595 in order to capture the full diversity of venom genes (16, 24 and 48 hours post-milking).

596 Additionally, total RNA from two scent glands and two skin samples of this species and the
597 salivary, scent glands and skin of two adult corn snakes (*Pantherophis guttatus*), rough green
598 snakes (*Opheodrys aestivus*), royal pythons (*Python regius*) and leopard geckos (*Eublepharis*
599 *macularius*) was also extracted using the RNeasy mini kit (Qiagen) with on-column DNase
600 digestion. Only a single corn snake skin sample provided RNA of high enough quality for
601 sequencing. mRNA was prepared for sequencing using the TruSeq RNA sample preparation
602 kit (Illumina) with a selected fragment size of 200-500bp and sequenced using 100bp paired-
603 end reads on the Illumina HiSeq2000 or HiSeq2500 platform.

604 *Quality control, assembly and analysis*

605 The quality of all raw sequence data was assessed using FastQC [99] and reads for each
606 tissue and species were pooled and assembled using Trinity [100] (sequence and assembly
607 metrics are provided in Supplemental tables S1-S3). Putative venom toxin amino acid
608 sequences were aligned using ClustalW [101] and maximum likelihood trees constructed
609 using the Jones-Taylor-Thornton (JTT) model with 500 Bootstrap replicates. Transcript
610 abundance estimation was carried out using RSEM [102] as a downstream analysis of Trinity
611 (version trinityrnaseq_r2012-04-27). Sets of reads were mapped to species-specific reference
612 transcriptome assemblies (Supplementary table S4) to allow comparison between tissues on a
613 per-species basis and all results values shown are in FPKM (Fragments Per Kilobase of exon
614 per Million fragments mapped). Individual and mean FPKM values for each gene per tissue
615 per species are given in Supplementary tables S5-S9. All transcript abundance values given

616 within the text are based on the average transcript abundance per tissue per species to account
617 for variation between individual samples.

618 Transcriptome reads were deposited in the European Nucleotide Archive (ENA) database
619 under accession #ERP001222 and GenBank under accession numbers XXX and XXX and
620 genes used to reconstruct phylogenies are deposited in GenBank under accession numbers
621 XXXX-XXXX

622

623 **Competing interests**

624 The authors declare that they have no competing interests

625

626 **Authors' contributions**

627 JFM, ADH and DWL designed the experiments and all authors carried out them out. JFM
628 and ADH prepared the manuscript and this was seen, modified and approved by all authors.

629

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639

640

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1077 **Tables**

1078

1079 **Table 1.** Predicted venom composition of the painted saw-scaled viper, *Echis coloratus*

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Gene family		Number of genes
SVMP		13
C-type lectin		8
Serine protease		6
PLA2		3
CRISP		1
L-amino acid oxidase		1
VEGF		1
Crotamine		1
Total	8	34

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1098 **Table 2.** Predicted numbers of venom toxins and venom toxin families from proteomic
1099 studies of snake venom accord well with our transcriptome results.
1100

Species	Number of toxins	Number of toxin families
<i>Bitis caudalis</i> [103]	30	8
<i>Bitis gabonica gabonica</i> [104]	35	12
<i>Bitis gabonica rhinoceros</i> [103]	33	11
<i>Bitis nasicornis</i> [103]	28	9
<i>Bothriechis schlegelii</i> [105]	?	7
<i>Cerastes cerastes</i> [106]	25-30	6
<i>Crotalus atrox</i> [107]	~24	~9
<i>Echis ocellatus</i> [36]	35	8
<i>Lachesis muta</i> [108]	24-26	8
<i>Naja kaouthia</i> [109]	61	12
<i>Ophiophagus hannah</i> [31]	?	14
<i>Vipera ammodytes</i> [110]	38	9

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1118 **Table 3.** Venom gene nomenclature. Lack of a formal set of nomenclatural rules for venom
 1119 toxins has led to an explosion of different gene names and may have contributed to the
 1120 overestimation of reptile venom diversity.

Gene/gene family	Alternative name and accession number
3 Finger toxin (3Ftx)	Denmotoxin [Q06ZW0] Candoxin [AY142323]
CRISP	Piscivorin [AAO62994] Catrin [AAO62995] Ablomin [AAM45664] Tigrin [Q8JGT9] Kaouthin [ACH73167, ACH73168] NatrIn-1 [Q7T1K6] CRVP [Q8UW25, Q8UW11] Pseudechetoxin [Q8AVA4] Pseudechin [Q8AVA3] Serotriflin [POCB15] Latisemin [Q8JI38] Ophanin [AAO62996] Opharin [ACN93671] Bc-CRP [ACE73577, ACE73578]
Ficolin	Veficolin [ADK46899] Ryncolin [D8VNS7-9, D8VNT0]
Serine proteases	Acubin [CAB46431] Gyroxin [B0FXM3] Ussurase [AAL48222] Serpentokallikrein [AAG27254] Salmobin [AAC61838] Batroxobin [AAA48553] Nikobin [CBW30778] Gloshedobin [POC5B4] Gussurobin [Q8UVX1] Pallabin [CAA04612] Pallase [AAC34898]
Snake venom metalloproteinase (SVMP)	Stejnihagin-B [ABA40759] Bothropasin [AAC61986] Atrase B [ADG02948] Mocarhagin 1 [AAM51550] Scutatease-1 [ABQ01138] Austrelease-1 [ABQ01134]
Vascular endothelial growth factor (VEGF)	Barietin [ACN22038] Cratrin [ACN22040] Apiscin [ACN22039] Vammin [ACN22045]
Vespryn	Ohanin [AAR07992] Thaicobrin [P82885]
Waprin	Nawaprin [P60589] Porwaprin [B5L5N2] Stewaprin [B5G6H3] Veswaprin [B5L5P5] Notewaprin [B5G6H5] Carwaprin [B5L5P0]

1121 **Figure legends**

1122

1123 **Figure 1. Relationships of key vertebrate lineages and the placement of species**

1124 **discussed in this paper.** A monophyletic clade of reptiles (which includes birds) is

1125 shaded green and the Toxicofera [21] are shaded red. Modified taxon names

1126 have been used for simplicity.

1127

1128 **Figure 2. Tissue distribution of proposed venom toxin transcripts.** The majority of

1129 transcripts proposed to encode Toxicoferan venom proteins are expressed in multiple body

1130 tissues. Transcripts found in the assembled transcriptomes but which are assigned transcript

1131 abundance of <1 FPKM are shaded orange. Eco, painted saw-scaled viper (*Echis coloratus*);

1132 Pgu, corn snake (*Pantherophis guttatus*); Oae, rough green snake (*Opheodrys aestivus*); Pre,

1133 royal python (*Python regius*); Ema, leopard gecko (*Eublepharis macularius*). VG, venom

1134 gland; SAL, salivary gland; SCG, scent gland; SK, skin.

1135

1136 **Figure 3. Maximum likelihood tree of *complement c3* (“cobra venom factor”) sequences.**

1137 Whilst most sequences likely represent housekeeping or maintenance genes, a gene

1138 duplication event in the elapid lineage (marked with *) may have produced a venom-specific

1139 paralog. An additional duplication (marked with +) may have taken place in *Austrelaps*

1140 *superbus*, although both paralogs appear to be expressed in both liver and venom gland.

1141 Geographic separation in king cobras (*Ophiophagus hannah*) from Indonesia and China is

1142 reflected in observed sequence variation. Numbers above branches are Bootstrap values for

1143 500 replicates. Tissue distribution of transcripts is indicated using the following

1144 abbreviations: VG, venom gland; SK, skin; SCG, scent gland, AG, accessory gland; VMNO,

1145 vomeronasal organ and those genes found to be expressed in one or more body tissues are

1146 shaded blue.

1147

1148 **Figure 4. Maximum likelihood tree of dipeptidylpeptidase 3 (*dpp3*) and**

1149 ***dipeptidylpeptidase 4 (*dpp4*) sequences.*** Transcripts encoding *dpp3* and *dpp4* are found in a

1150 wide variety of body tissues, and likely represent housekeeping genes. Numbers above

1151 branches are Bootstrap values for 500 replicates. Tissue distribution of transcripts is indicated

1152 using the following abbreviations: VG, venom gland; SK, skin; SCG, scent gland, AG,

1153 accessory gland; VMNO, vomeronasal organ and those genes found to be expressed in one or

1154 more body tissues are shaded blue.

1155

1156 **Figure 5. Maximum likelihood tree of phospholipase b (*plb*) sequences.** Transcripts

1157 encoding *plb* are found in a wide variety of body tissues, and likely represent housekeeping

1158 genes. Numbers above branches are Bootstrap values for 500 replicates. Tissue distribution of

1159 transcripts is indicated using the following abbreviations: VG, venom gland; SK, skin; SCG,

1160 scent gland, AG, accessory gland; VMNO, vomeronasal organ and those genes found to be

1161 expressed in one or more body tissues are shaded blue.

1162

1163 **Figure 6. Maximum likelihood tree of renin-like sequences.** Renin-like genes are

1164 expressed in a diversity of body tissues. The recently published *Boa constrictor* “RAP-Boa-

1165 1” sequence is clearly a *cathepsin d* gene and is therefore not orthologous to the *Echis*

1166 *ocellatus* renin sequence as has been claimed [21]. Numbers above branches are Bootstrap

1167 values for 500 replicates. Tissue distribution of transcripts is indicated using the following

1168 abbreviations: VG, venom gland; SK, skin; SCG, scent gland and those genes found to be

1169 expressed in one or more body tissues are shaded blue.

1170

1171 **Figure 7. Graph of transcript abundance values of proposed venom transcripts in the**

1172 ***Echis coloratus* venom gland.** The majority of Toxicoferan transcripts are expressed at

1173 extremely low level, with the most highly expressed genes falling into only four gene
1174 families (C-type lectins, Group IIA phospholipase A₂, serine proteases and snake venom
1175 metalloproteinases). FPKM = Fragments Per Kilobase of exon per Million fragments
1176 mapped.