**Supplementary Tables**

**Table S1.** Comparative analysis of the mitogenomes of three *Laticauda*, five terrestrial elapid, and one viperid (*Gloydius*) species

|  |  |  |  |
| --- | --- | --- | --- |
|  | *Laticauda colubrina* | *Laticauda laticaudata* | *Laticauda semifasciata* |
| Gene | Startposition | Stopposition | Size(bp) | Startcodon | Stop codon | Strand | Startposition | Stopposition | Size(bp) | Startcodon | Stopcodon | Strand | Startposition | Stopposition | Size(bp) | Startcodon | Stopcodon | Strand |
| Phe | 1 | 63 | 63 |  |  | + | 1 | 62 | 62 |  |  | + | 1 | 63 | 63 |  |  | + |
| 12S rRNA | 64 | 996 | 933 |  |  | + | 63 | 995 | 933 |  |  | + | 64 | 997 | 934 |  |  | + |
| Val | 997 | 1,061 | 65 |  |  | + | 996 | 1,059 | 64 |  |  | + | 998 | 1,062 | 65 |  |  | + |
| 16S rRNA | 1,062 | 2,533 | 1,472 |  |  | + | 1,058 | 2,531 | 1,474 |  |  | + | 1,063 | 2,556 | 1,494 |  |  | + |
| *ND1* | 2,534 | 3,494 | 961 | ATT | T\_\_ | + | 2,532 | 3,492 | 961 | ATC | T\_\_ | + | 2,557 | 3,519 | 963 | ATT | TAG | + |
| Ile | 3,495 | 3,561 | 67 |  |  | + | 3,493 | 3,559 | 67 |  |  | + | 3,518 | 3,574 | 57 |  |  | + |
| CRII | 3,562 | 4,969 | 1,408 |  |  | + | 3,560 | 4,469 | 910 |  |  | + | 3,575 | 3,833 | 259 |  |  | + |
| Leu | 4,970 | 5,042 | 73 |  |  | + | 4,470 | 4,542 | 73 |  |  | + | 3,834 | 3,906 | 73 |  |  | + |
| Gln | 5,043 | 5,113 | 71 |  |  | - | 4,543 | 4,613 | 71 |  |  | - | 3,907 | 3,977 | 71 |  |  | - |
| Met | 5,114 | 5,175 | 62 |  |  | + | 4,614 | 4,675 | 62 |  |  | + | 3,978 | 4,039 | 62 |  |  | + |
| *ND2* | 5,176 | 6,207 | 1,032 | ATT | TAG | + | 4,676 | 5,707 | 1,032 | ATT | TAG | + | 4,040 | 5,071 | 1,032 | ATC | TAG | + |
| Trp | 6,206 | 6,270 | 65 |  |  | + | 5,706 | 5,770 | 65 |  |  | + | 5,070 | 5,134 | 65 |  |  | + |
| Ala | 6,273 | 6,338 | 66 |  |  | - | 5,773 | 5,838 | 66 |  |  | - | 5,137 | 5,201 | 65 |  |  | - |
| Asn | 6,339 | 6,411 | 73 |  |  | - | 5,839 | 5,910 | 72 |  |  | - | 5,202 | 5,274 | 73 |  |  | - |
| OL | 6,414 | 6,447 | 34 |  |  | + | 5,913 | 5,947 | 35 |  |  | + | 5,277 | 5,311 | 35 |  |  | + |
| Cys | 6,448 | 6,510 | 63 |  |  | - | 5,948 | 6,010 | 63 |  |  | - | 5,312 | 5,374 | 63 |  |  | - |
| Tyr | 6,511 | 6,575 | 65 |  |  | - | 6,011 | 6,073 | 63 |  |  | - | 5,375 | 5,436 | 62 |  |  | - |
| *COI* | 6,577 | 8,178 | 1,602 | GTG | AGG | + | 6,075 | 7,676 | 1,602 | GTG | AGG | + | 5,438 | 7,039 | 1,602 | GTG | AGG | + |
| Ser | 8,169 | 8,236 | 68 |  |  | - | 7,667 | 7,734 | 68 |  |  | - | 7,030 | 7,097 | 68 |  |  | - |
| Asp | 8,237 | 8,300 | 64 |  |  | + | 7,735 | 7,798 | 64 |  |  | + | 7,098 | 7,161 | 64 |  |  | + |
| *COII* | 8,302 | 8,994 | 693 | ATG | AGA | + | 7,800 | 8,492 | 693 | ATG | AGA | + | 7,163 | 7,855 | 693 | ATG | AGA | + |
| Lys | 8,987 | 9,049 | 63 |  |  | + | 8,485 | 8,546 | 62 |  |  | + | 7,848 | 7,909 | 62 |  |  | + |
| *ATP8* | 9,051 | 9,212 | 162 | ATG | TAA | + | 8,548 | 8,712 | 165 | ATG | TAA | + | 7,911 | 8,075 | 165 | ATG | TAA | + |
| *ATP6* | 9,203 | 9,883 | 681 | ATG | TAA | + | 8,703 | 9,383 | 681 | ATG | TAA | + | 8,066 | 8,746 | 681 | ATG | TAA | + |
| *COIII* | 9,883 | 10,666 | 784 | ATG | T\_\_ | + | 9,383 | 10,166 | 784 | ATG | T\_\_ | + | 8,746 | 9,529 | 784 | ATG | T\_\_ | + |
| Gly | 10,667 | 10,727 | 61 |  |  | + | 10,167 | 10,227 | 61 |  |  | + | 9,530 | 9,590 | 61 |  |  | + |
| *ND3* | 10,728 | 11,070 | 343 | ATC | T\_\_ | + | 10,228 | 10,570 | 343 | ATC | T\_\_ | + | 9,591 | 9,933 | 343 | ATT | T\_\_ | + |
| Arg | 11,071 | 11,134 | 64 |  |  | + | 10,571 | 10,635 | 65 |  |  | + | 9,934 | 9,999 | 66 |  |  | + |
| *ND4L* | 11,135 | 11,425 | 291 | ATG | TAA | + | 10,636 | 10,926 | 291 | ATG | TAA | + | 10,000 | 10,290 | 291 | ATG | TAA | + |
| *ND4* | 11,425 | 12,761 | 1,337 | ATG | TA\_ | + | 10,926 | 12,263 | 1,338 | ATG | TAG | + | 10,290 | 11,627 | 1,338 | ATG | TAG | + |
| His | 12,762 | 12,825 | 64 |  |  | + | 12,263 | 12,326 | 64 |  |  | + | 11,627 | 11,689 | 63 |  |  | + |
| Ser | 12,826 | 12,883 | 58 |  |  | + | 12,327 | 12,385 | 59 |  |  | + | 11,691 | 11,748 | 58 |  |  | + |
| Leu | 12,881 | 12,951 | 71 |  |  | + | 12,383 | 12,453 | 71 |  |  | + | 11,746 | 11,816 | 71 |  |  | + |
| *ND5* | 12,954 | 14,726 | 1,773 | ATG | TAA | + | 12,456 | 14,228 | 1,773 | ATG | TAA | + | 11,818 | 13,590 | 1,773 | ATG | TAA | + |
| *ND6* | 14,722 | 15,225 | 504 | ATG | AGA | - | 14,224 | 14,727 | 504 | ATG | AGG | - | 13,586 | 14,089 | 504 | ATG | AGG | - |
| Glu | 15,226 | 15,287 | 62 |  |  | - | 14,728 | 14,789 | 62 |  |  | - | 14,090 | 14,152 | 63 |  |  | - |
| *CYTB* | 15,288 | 16,401 | 1,114 | ATG | T\_\_ | + | 14,790 | 15,893 | 1,104 | ATG | TAA | + | 14,153 | 15,266 | 1,114 | ATG | T\_\_ | + |
| Thr | 16,402 | 16,466 | 65 |  |  | + | 15,896 | 15,962 | 67 |  |  | + | 15,267 | 15,332 | 66 |  |  | + |
| Pro | 16,467 | 16,530 | 64 |  |  | - | 15,963 | 16,024 | 62 |  |  | - | 15,333 | 15,395 | 63 |  |  | - |
| CRI | 16,531 | 17,450 | 920 |  |  | + | 16,025 | 17,209 | 1,185 |  |  | + | 15,396 | 17,170 | 1,775 |  |  | + |

Table S1 continued

|  |  |  |  |
| --- | --- | --- | --- |
|  | *Naja naja* | *Naja atra* | *Ophiophagus hannah* |
| Gene | Startposition | Stopposition | Size(bp) | Startcodon | Stop codon | Strand | Startposition | Stopposition | Size(bp) | Startcodon | Stopcodon | Strand | Startposition | Stopposition | Size(bp) | Startcodon | Stopcodon | Strand |
| Phe | 1 | 63 | 63 |  |  | + | 1 | 63 | 63 |  |  | + | 1 | 62 | 62 |  |  | + |
| 12S rRNA | 64 | 995 | 932 |  |  | + | 64 | 996 | 933 |  |  | + | 63 | 996 | 934 |  |  | + |
| Val | 996 | 1,061 | 66 |  |  | + | 997 | 1,062 | 66 |  |  | + | 997 | 1,062 | 66 |  |  | + |
| 16S rRNA | 1,062 | 2,555 | 1,494 |  |  | + | 1,063 | 2,556 | 1,494 |  |  | + | 1,063 | 2,541 | 1,479 |  |  | + |
| *ND1* | 2,566 | 3,520 | 955 | ATG | T-- | + | 2,557 | 3,520 | 964 | ATT | T-- | + | 2,542 | 3,505 | 964 | ATA | T-- | + |
| Ile | 3,521 | 3,586 | 66 |  |  | + | 3,521 | 3,586 | 66 |  |  | + | 3,506 | 3,571 | 66 |  |  | + |
| CRII | 3,587 | 4,614 | 1,028 |  |  | + | 3,587 | 4,615 | 1,029 |  |  | + | 3,572 | 4,589 | 1,018 |  |  | + |
| Leu | 4,615 | 4,687 | 73 |  |  | + | 4,616 | 4,688 | 73 |  |  | + | 4,590 | 4,662 | 73 |  |  | + |
| Gln | 4,688 | 4,758 | 71 |  |  | - | 4,689 | 4,759 | 71 |  |  | - | 4,664 | 4,733 | 70 |  |  | - |
| Met | 4,759 | 4,821 | 63 |  |  | + | 4,760 | 4,822 | 63 |  |  | + | 4,735 | 4,796 | 62 |  |  | + |
| *ND2* | 4,822 | 5,851 | 1,030 | ATC | T-- | + | 4,823 | 5,852 | 1,030 | ATC | T-- | + | 4,797 | 5,826 | 1,030 | ATT | T-- | + |
| Trp | 5,852 | 5,916 | 65 |  |  | + | 5,853 | 5,917 | 65 |  |  | + | 5,827 | 5,891 | 65 |  |  | + |
| Ala | 5,919 | 5,984 | 66 |  |  | - | 5,920 | 5,985 | 66 |  |  | - | 5,894 | 5,958 | 65 |  |  | - |
| Asn | 5,986 | 6,058 | 73 |  |  | - | 5,987 | 6,059 | 73 |  |  | - | 5,959 | 6,031 | 73 |  |  | - |
| OL | 6,061 | 6,094 | 34 |  |  | + | 6,062 | 6,099 | 38 |  |  | + | 6,034 | 6,071 | 38 |  |  | + |
| Cys | 6,095 | 6,156 | 62 |  |  | - | 6,097 | 6,157 | 61 |  |  | - | 6,069 | 6,130 | 62 |  |  | - |
| Tyr | 6,157 | 6,219 | 63 |  |  | - | 6,158 | 6,220 | 63 |  |  | - | 6,131 | 6,194 | 64 |  |  | - |
| *COI* | 6,221 | 7,822 | 1,602 | GTG | AGA | + | 6,222 | 7,823 | 1,602 | GTG | AGA | + | 6,196 | 7,797 | 1,602 | GTG | AGA | + |
| Ser | 7,813 | 7,880 | 68 |  |  | - | 7,814 | 7,881 | 68 |  |  | - | 7,788 | 7,855 | 68 |  |  | - |
| Asp | 7,881 | 7,944 | 64 |  |  | + | 7,882 | 7,945 | 64 |  |  | + | 7,856 | 7,920 | 65 |  |  | + |
| *COII* | 7,946 | 8,630 | 685 | ATG | T-- | + | 7,947 | 8,631 | 685 | ATG | T-- | + | 7,922 | 8,606 | 685 | ATG | T-- | + |
| Lys | 8,631 | 8,694 | 64 |  |  | + | 8,632 | 8,695 | 64 |  |  | + | 8,607 | 8,670 | 64 |  |  | + |
| *ATP8* | 8,696 | 8,860 | 165 | ATG | TAA | + | 8,697 | 8,861 | 165 | ATG | TAA | + | 8,672 | 8,836 | 165 | ATG | TAA | + |
| *ATP6* | 8,851 | 9,530 | 680 | ATG | TA- | + | 8,852 | 9,532 | 681 | ATG | TAA | + | 8,827 | 9,507 | 681 | ATG | TAA | + |
| *COIII* | 9,531 | 10,314 | 784 | ATG | T-- | + | 9,532 | 10,315 | 784 | ATG | T-- | + | 9,507 | 10,290 | 784 | ATG | T-- | + |
| Gly | 10,315 | 10,375 | 61 |  |  | + | 10,316 | 10,376 | 61 |  |  | + | 10,291 | 10,351 | 61 |  |  | + |
| *ND3* | 10,376 | 10,718 | 343 | ATT | T-- | + | 10,377 | 10,719 | 343 | ATT | T-- | + | 10,352 | 10,694 | 343 | ATT | T-- | + |
| Arg | 10,719 | 10,783 | 65 |  |  | + | 10,720 | 10,784 | 65 |  |  | + | 10,695 | 10,758 | 64 |  |  | + |
| *ND4L* | 10,784 | 11,073 | 290 | ATG | TA- | + | 10,785 | 11,075 | 291 | ATG | TAA | + | 10,759 | 11,049 | 291 | ATG | TAA | + |
| *ND4* | 11,074 | 12,410 | 1,337 | ATG | TA- | + | 11,075 | 12,411 | 1,337 | ATG | TA- | + | 11,049 | 12,385 | 1,337 | ATG | TA- | + |
| His | 12,411 | 12,475 | 65 |  |  | + | 12,412 | 12,476 | 65 |  |  | + | 12,386 | 12,450 | 65 |  |  | + |
| Ser | 12,478 | 12,534 | 57 |  |  | + | 12,479 | 12,535 | 57 |  |  | + | 12,453 | 12,510 | 58 |  |  | + |
| Leu | 12,532 | 12,602 | 71 |  |  | + | 12,533 | 12,603 | 71 |  |  | + | 12,508 | 12,578 | 71 |  |  | + |
| *ND5* | 12,604 | 14,376 | 1,773 | ATG | TAA | + | 12,605 | 14,377 | 1,773 | ATG | TAA | + | 12,580 | 14,355 | 1,776 | ATG | TAA | + |
| *ND6* | 14,372 | 14,866 | 495 | ATA | AGG | - | 14,373 | 14,876 | 504 | ATG | AGG | - | 14,351 | 14,854 | 504 | ATG | AGG | - |
| Glu | 14,876 | 14,938 | 63 |  |  | - | 14,877 | 14,939 | 63 |  |  | - | 14,855 | 14,919 | 65 |  |  | - |
| *CYTB* | 14,939 | 16,055 | 1,117 | ATG | T-- | + | 14,940 | 16,056 | 1,117 | ATG | T-- | + | 14,920 | 16,036 | 1,117 | ATG | T-- | + |
| Thr | 16,056 | 16,123 | 68 |  |  | + | 16,057 | 16,124 | 68 |  |  | + | 16,037 | 16,103 | 67 |  |  | + |
| Pro | 16,124 | 16,184 | 61 |  |  | - | 16,125 | 16,185 | 61 |  |  | - | 16,104 | 16,166 | 63 |  |  | - |
| Ile | - | - | - |  |  |  | - | - | - |  |  |  | 16,194 | 16,259 | 66 |  |  | + |
| CRI | 16,185 | 17,213 | 1,029 |  |  | + | 16,186 | 17,216 | 1,031 |  |  | + | 16,260 | 17,267 | 1,008 |  |  | + |

Table S1 continued

|  |  |  |  |
| --- | --- | --- | --- |
|  | *Bungarus multicinctus* | *Bungarus fasciatus* | *Gloydius brevicaudus* |
| Gene | Startposition | Stopposition | Size(bp) | Startcodon | Stop codon | Strand | Startposition | Stopposition | Size(bp) | Startcodon | Stopcodon | Strand | Startposition | Stopposition | Size(bp) | Startcodon | Stopcodon | Strand |
| Phe | 1 | 63 | 63 |  |  | + | 1 | 63 | 63 |  |  | + | 1 | 64 | 64 |  |  | + |
| 12S rRNA | 64 | 995 | 932 |  |  | + | 64 | 995 | 932 |  |  | + | 65 | 970 | 906 |  |  | + |
| Val | 996 | 1,061 | 66 |  |  | + | 996 | 1,061 | 66 |  |  | + | 971 | 1,033 | 63 |  |  | + |
| 16S rRNA | 1,062 | 2,523 | 1,462 |  |  | + | 1,062 | 2,531 | 1,470 |  |  | + | 1,034 | 2,510 | 1,477 |  |  | + |
| *ND1* | 2,524 | 3,487 | 964 | ATA | T-- | + | 2,532 | 3,495 | 964 | ATA | T-- | + | 2,511 | 3,471 | 961 | ATA | T-- | + |
| Ile | 3,488 | 3,554 | 67 |  |  | + | 3,496 | 3,562 | 67 |  |  | + | 3,472 | 3,539 | 68 |  |  | + |
| Pro | - | - | - |  |  |  | - | - | - |  |  |  | 3,540 | 3,602 | 63 |  |  | - |
| CRII | 3,555 | 4,568 | 1,014 |  |  | + | 3,563 | 4,580 | 1,018 |  |  | + | 3,603 | 4,632 | 1,030 |  |  | + |
| Leu | 4,569 | 4,641 | 73 |  |  | + | 4,581 | 4,653 | 73 |  |  | + | 4,633 | 4,705 | 73 |  |  | + |
| Gln | 4,642 | 4,712 | 71 |  |  | - | 4,654 | 4,724 | 71 |  |  | - | 4,706 | 4,774 | 69 |  |  | - |
| Met | 4,713 | 4,774 | 62 |  |  | + | 4,725 | 4,786 | 62 |  |  | + | 4,775 | 4,836 | 62 |  |  | + |
| *ND2* | 4,775 | 5,804 | 1,030 | ATC | T-- | + | 4,787 | 5,816 | 1,030 | ATT | T-- | + | 4,837 | 5,860 | 1,024 | ATG | T-- | + |
| Trp | 5,805 | 5,870 | 66 |  |  | + | 5,817 | 5,881 | 65 |  |  | + | 5,861 | 5,926 | 66 |  |  | + |
| Ala | 5,873 | 5,938 | 66 |  |  | - | 5,884 | 5,948 | 65 |  |  | - | 5,927 | 5,991 | 65 |  |  | - |
| Asn | 5,939 | 6,011 | 73 |  |  | - | 5,949 | 6,021 | 73 |  |  | - | 5,992 | 6,064 | 73 |  |  | - |
| OL | 6,014 | 6,048 | 35 |  |  | + | 6,024 | 6,061 | 38 |  |  | + | 6,067 | 6,103 | 37 |  |  | + |
| Cys | 6,046 | 6,105 | 60 |  |  | - | 6,059 | 6,119 | 61 |  |  | - | 6,101 | 6,161 | 61 |  |  | - |
| Tyr | 6,106 | 6,167 | 62 |  |  | - | 6,120 | 6,182 | 63 |  |  | - | 6,162 | 6,222 | 61 |  |  | - |
| *COI* | 6,169 | 7,776 | 1,608 | GTG | AGG | + | 6,184 | 7,785 | 1,602 | GTG | AGA | + | 6,224 | 7,825 | 1,602 | GTG | AGA | + |
| Ser | 7,767 | 7,836 | 70 |  |  | - | 7,776 | 7,846 | 71 |  |  | - | 7,816 | 7,883 | 68 |  |  | - |
| Asp | 7,837 | 7,900 | 64 |  |  | + | 7,847 | 7,910 | 64 |  |  | + | 7,884 | 7,946 | 63 |  |  | + |
| *COII* | 7,902 | 8,586 | 685 | ATG | T-- | + | 7,912 | 8,596 | 685 | ATG | T-- | + | 7,947 | 8,631 | 685 | ATG | T-- | + |
| Lys | 8,587 | 8,649 | 63 |  |  | + | 8,597 | 8,658 | 62 |  |  | + | 8,632 | 8,694 | 63 |  |  | + |
| *ATP8* | 8,650 | 8,808 | 159 | ATG | TAA | + | 8,660 | 8,824 | 165 | ATG | TAA | + | 8,695 | 8,859 | 165 | ATG | TAA | + |
| *ATP6* | 8,799 | 9,478 | 680 | ATG | TA- | + | 8,815 | 9,484 | 680 | ATG | TA- | + | 8,850 | 9,530 | 681 | ATG | TAA | + |
| *COIII* | 9,479 | 10,262 | 784 | ATG | T-- | + | 9,495 | 10,278 | 784 | ATG | T-- | + | 9,530 | 10,313 | 784 | ATG | T-- | + |
| Gly | 10,263 | 10,323 | 61 |  |  | + | 10,279 | 10,339 | 61 |  |  | + | 10,314 | 10,374 | 61 |  |  | + |
| *ND3* | 10,324 | 10,666 | 343 | ATC | T-- | + | 10,340 | 10,682 | 343 | ATT | T-- | + | 10,375 | 10,717 | 343 | ATC | T-- | + |
| Arg | 10,667 | 10,730 | 64 |  |  | + | 10,683 | 10,748 | 66 |  |  | + | 10,718 | 10,781 | 64 |  |  | + |
| *ND4L* | 10,731 | 11,020 | 290 | ATG | TA- | + | 10,749 | 11,038 | 290 | ATG | TA- | + | 10,782 | 11,072 | 291 | ATG | TAA | + |
| *ND4* | 11,021 | 12,357 | 1,337 | ATG | TA- | + | 11,039 | 12,375 | 1,337 | ATA | TA- | + | 11,072 | 12,409 | 1,338 | ATG | AGA | + |
| His | 12,358 | 12,420 | 63 |  |  | + | 12,376 | 12,440 | 65 |  |  | + | 12,411 | 12,472 | 62 |  |  | + |
| Ser | 12,422 | 12,479 | 58 |  |  | + | 12,444 | 12,500 | 57 |  |  | + | 12,473 | 12,527 | 55 |  |  | + |
| Leu | 12,477 | 12,547 | 71 |  |  | + | 12,498 | 12,568 | 71 |  |  | + | 12,529 | 12,599 | 71 |  |  | + |
| *ND5* | 12,549 | 14,309 | 1,761 | ATG | TAA | + | 12,570 | 14,336 | 1,767 | ATG | TAA | + | 12,601 | 14,388 | 1,788 | ATG | TAA | + |
| *ND6* | 14,305 | 14,799 | 495 | ATG | AGA | - | 14,332 | 14,826 | 495 | ATA | AGA | - | 14,384 | 14,896 | 513 | ATG | AGG | - |
| Glu | 14,806 | 14,868 | 63 |  |  | - | 14,836 | 14,898 | 63 |  |  | - | 14,897 | 14,959 | 63 |  |  | - |
| *CYTB* | 14,869 | 15,979 | 1,111 | ATG | T-- | + | 14,899 | 16,009 | 1,111 | ATG | T-- | + | 14,960 | 16,073 | 1,114 | ATG | T-- | + |
| Thr | 15,980 | 16,042 | 63 |  |  | + | 16,010 | 16,075 | 66 |  |  | + | 16,074 | 16,137 | 64 |  |  | + |
| Pro | 16,043 | 16,103 | 61 |  |  | - | 16,076 | 16,137 | 62 |  |  | - | - | - | - |  |  |  |
| CRI | 16,104 | 17,144 | 1,041 |  |  | + | 16,138 | 17,234 | 1,097 |  |  | + | 16,138 | 17,227 | 1,090 |  |  | + |

**Table S2.** Nucleotide composition of three *Laticauda*, five terrestrial elapid, and one viperid (*Gloydius*) species.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Size (bp) | Nucleotide composition (%) | AT skew | GC skew |
| A | T | G | C  | A+T |
| *Laticauda**colubrina* | PCG | 11,277 | 33.9  | 28.2  | 11.4  | 26.4  | 62.1  | 0.092  | -0.397  |
| tRNA | 1,437 | 33.4  | 25.3  | 17.0  | 24.2  | 58.7  | 0.138  | -0.175  |
| rRNA | 2,405 | 37.5  | 22.2  | 16.9  | 23.4  | 59.7  | 0.256  | -0.161  |
| OL | 34 | 38.2  | 29.4  | 20.6  | 11.8  | 67.6  | 0.130  | 0.272  |
| CR | 2,328 | 27.1  | 35.7  | 11.1  | 26.1  | 62.8  | -0.137  | -0.403  |
| Total | 17,450 | 33.4 | 28.2 | 12.6 | 25.8 | 61.6 | 0.084 | -0.344 |
| *Laticauda**laticaudata* | PCG | 11,271 | 33.4  | 26.8  | 11.9  | 27.9  | 60.2  | 0.110  | -0.402  |
| tRNA | 1,433 | 33.4  | 24.3  | 16.7  | 25.6  | 57.6  | 0.158  | -0.210  |
| rRNA | 2,407 | 37.6  | 21.8  | 16.9  | 23.8  | 59.4  | 0.266  | -0.170  |
| OL | 35 | 28.6  | 34.3  | 25.7  | 11.4  | 62.9  | -0.091  | 0.385  |
| CR | 2,095 | 27.9  | 34.5  | 13.5  | 24.2  | 62.4  | -0.106  | -0.284  |
| Total | 17,209 | 33.2  | 26.9  | 13.2  | 26.7  | 60.1 | 0.105 | -0.338 |
| *Laticauda**semifasciata* | PCG | 11,283 | 33.2  | 26.0  | 12.2  | 28.6  | 59.2  | 0.122  | -0.402  |
| tRNA | 1,424 | 32.4  | 25.4  | 18.0  | 24.3  | 57.7  | 0.121  | -0.149  |
| rRNA | 2,428 | 37.2  | 21.2  | 16.8  | 24.7  | 58.4  | 0.274  | -0.190  |
| OL | 35 | 40.0  | 31.4  | 17.1  | 11.4  | 71.4  | 0.120  | 0.200  |
| CR | 2,034 | 30.4  | 33.2  | 10.5  | 25.9  | 63.6  | -0.044  | -0.423  |
| Total | 17,170 | 33.4  | 26.1  | 13.1  | 27.3  | 59.5  | 0.123  | -0.351  |
| *Naja naja* | PCG | 11,256 | 33.4 | 25.0 | 12.2 | 29.5 | 58.3 | 0.144 | -0.415 |
| tRNA | 1,438 | 32.1 | 24.4 | 17.7 | 25.8 | 56.5 | 0.136 | -0.186 |
| rRNA | 2,426 | 37.2 | 20.4 | 17.1 | 25.4 | 57.6 | 0.292 | -0.195 |
| OL | 34 | 35.3 | 29.4 | 20.6 | 14.7 | 64.7 | 0.091 | 0.167 |
| CR | 2,057 | 26.8 | 33.3 | 11.8 | 28.0 | 60.2 | -0.108 | -0.407 |
| Total | 17,213 | 33.0 | 25.3 | 13.3 | 28.4 | 58.3 | 0.132 | -0.362 |
| *Naja atra* | PCG | 11,276 | 33.5 | 25.0 | 12.1 | 29.4 | 58.5 | 0.145 | -0.417 |
| tRNA | 1,437 | 31.9 | 24.5 | 17.8 | 25.7 | 56.4 | 0.131 | -0.182 |
| rRNA | 2,427 | 37.2 | 20.2 | 16.9 | 25.6 | 57.5 | 0.296 | -0.205 |
| OL | 38 | 39.5 | 26.3 | 21.1 | 13.2 | 65.8 | 0.201 | 0.230 |
| CR | 2,060 | 26.7 | 33.6 | 11.7 | 27.9 | 60.3 | -0.114 | -0.409 |
| Total | 17,216 | 33.0 | 25.4 | 13.2 | 28.4 | 58.4 | 0.130 | -0.365 |
| *Ophiophagus hannah* | PCG | 11,279 | 34.2 | 24.7 | 11.0 | 30.1 | 58.9 | 0.161 | -0.465 |
| tRNA | 1,505 | 32.0 | 23.9 | 16.9 | 27.2 | 55.9 | 0.145 | -0.234 |
| rRNA | 2,413 | 37.0 | 19.8 | 17.0 | 26.2 | 56.8 | 0.303 | -0.213 |
| OL | 38 | 39.5 | 26.3 | 21.1 | 13.2 | 65.8 | 0.201 | 0.230 |
| CR | 2,026 | 27.5 | 33.1 | 12.4 | 26.9 | 60.6 | -0.092 | -0.369 |
| Total | 17,267 | 33.6 | 24.9 | 12.5 | 29.0 | 58.5 | 0.149 | -0.398 |

Table S2. Continued

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | Size (bp) | Nucleotide composition (%) | AT skew | GC skew |
| A | T | G | C  | A+T |
| *Bungarus multicinctus* | PCG | 11,247 | 33.4 | 28.7 | 11.2 | 26.6 | 62.2 | 0.076 | -0.407 |
| tRNA | 1,430 | 32.6 | 26.9 | 17.2 | 23.4 | 59.4 | 0.096 | -0.153 |
| rRNA | 2,394 | 36.7 | 22.1 | 16.8 | 24.4 | 58.9 | 0.248 | -0.184 |
| OL | 35 | 31.4 | 25.7 | 31.4 | 11.4 | 57.1 | 0.100 | 0.467 |
| CR | 2,055 | 26.2 | 35.7 | 10.2 | 27.9 | 61.9 | -0.153 | -0.465 |
| Total | 17,144 | 32.9 | 28.5 | 12.4 | 26.2 | 61.4 | 0.072 | -0.358 |
| *Bungarus fasciatus* | PCG | 11,253 | 34.8 | 30.0 | 10.4 | 24.8 | 64.8 | 0.074 | -0.409 |
| tRNA | 1,437 | 33.6 | 26.8 | 15.9 | 23.7 | 60.4 | 0.113 | -0.197 |
| rRNA | 2,402 | 38.1 | 22.8 | 16.2 | 22.9 | 60.9 | 0.251 | -0.171 |
| OL | 38 | 47.4 | 26.3 | 15.8 | 10.5 | 73.7 | 0.286 | 0.202 |
| CR | 2,115 | 27.4 | 34.8 | 11.1 | 26.7 | 62.2 | -0.119 | -0.413 |
| Total | 17.234 | 34.3 | 29.3 | 11.7 | 24.7 | 63.6 | 0.079 | -0.357 |
| *Gloydius brevicaudus* | PCG | 11,289 | 31.2 | 26.1 | 12.3 | 30.4 | 57.3 | 0.089 | -0.424 |
| tRNA | 1,422 | 33.6 | 25.6 | 17.1 | 23.7 | 59.2 | 0.135 | -0.162 |
| rRNA | 2,383 | 37.3 | 22.5 | 16.7 | 23.5 | 59.8 | 0.247 | -0.169 |
| OL | 37 | 32.4 | 21.6 | 32.4 | 13.5 | 54.1 | 0.200 | 0.412 |
| CR | 2,120 | 28.3 | 32.2 | 12.4 | 27.2 | 60.5 | -0.064 | -0.374 |
| Total | 17.227 | 31.8 | 26.3 | 13.4 | 28.5 | 58.2 | 0.095 | -0.360 |

**Supplementary Figure 1**

**Figure S1.** Bayesian inference phylogenetic tree reconstructed with 13 mitochondrial genes (ATP synthase 6 and 8, cytochrome oxidase (CO) I to III, cytochrome b (Cyt*b*) and NADH dehydrogenase (ND) 1 to 6) for eight representative elapid species and one viperid species.

