(A) Species-set A - the Western Palearctic Colubrinae clade

| **Analysis** | **Dataset**  | **Partition** | **Length** | **Model** | **Clock model (unlinked)** | **Rate** | **Tree model (linked)** | **Other Priors/Parameters** | **Runs** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phylogenetic trees**Maximum****Likelihood** | mtDNA+nDNA(N=82)**Dataset 1** | *12S* | 581 | GTR+G |  | Replicates x100 Bootstrap x1000 |  |
| *16S* | 505 |
| *cytb* codons 1+2 | 664 |
| *cytb* codon 3 | 332 |
| c-*mos* codon 1+2 | 272 |
| c-*mos* codon 3 | 136 |
| Phylogenetic trees**Bayesian** **Inference** | *12S* | 581 | GTR+I+G | Relaxed Uncorrelated Lognormal | Rate fixed to 1 | YuleRandom starting tree | Alpha Uniform (0, 10); Base substitution Uniform (0, 100)  | 3 runs; 108 generations; 104 sampling frequency; 10% burn-in |
| *16S* | 505 | GTR+I+G | Relaxed Uncorrelated Lognormal |
| *cytb* codons 1+2 | 664 | GTR+I+G | Relaxed Uncorrelated Lognormal |
| *cytb* codon 3 | 332 | GTR+G | Relaxed Uncorrelated Lognormal |
| c-*mos* codons 1+2 | 272 | TrN+I+G | Strict clock |
| c-*mos* codon 3 | 136 | TrN+G | Strict clock |
| Estimation of divergence times **Bayesian** **Inference** | mtDNA+nDNA(N=48)**Dataset 2**Including one representative of each mPTP entity for *Rhynchocalamus* only | *12S* | 583 | GTR+I+G | Relaxed Uncorrelated Lognormal | 0.0001 (0-1) | YuleRandom starting tree | Alpha Uniform (0, 10); Base substitution Uniform (0, 100) | 3 runs; 3x108 generations; 3x104 sampling frequency; 10% burn-in |
| *16S* | 507 | GTR+I+G | Relaxed Uncorrelated Lognormal |
| *cytb* codons 1+2 | 664 | GTR+I+G | Relaxed Uncorrelated Lognormal |
| *cytb* codon 3 | 332 | GTR+G | Relaxed Uncorrelated Lognormal |
| c-*mos* codons 1+2 | 272 | TrN+I | Strict clock |
| c-*mos* codon 3 | 136 | GTR+G | Strict clock |

(B) Species-set B - *Rhynchocalamus* and *Lytorhynchus*

| **Analysis** | **Dataset** | **Partition** | **Length** | **Model** | **Clock model (unlinked)** | **Rate** | **Tree model (linked)** | **Other Priors/Parameters** | **Runs** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phylogenetic trees**Maximum****Likelihood** | mtDNA+nDNA(N=36)**Dataset 3** | *12S* | 618 |  | Replicates x100 Bootstrap x1000 |
| *16S* | 510 |
| *cytb* codons 1+2 | 728 |
| *cytb* codon 3 | 364 |
| c-*mos* codon 1+2 | 272 |
| c-*mos* codon 3 | 136 |
| Phylogenetictrees**Bayesian** **Inference** | *12S* | 618 | GTR+G | Relaxed Uncorrelated Lognormal | Rate fixed to 1 | YuleRandom starting tree | Alpha Uniform (0, 10); Base substitution Uniform (0, 100)  | 3 runs; 8x107 generations; 8x103 sampling frequency; 10% burn-in |
| *16S* | 510 | GTR+I+G | Relaxed Uncorrelated Lognormal |
| *cytb* codons 1+2 | 728 | HKY+I | Relaxed Uncorrelated Lognormal |
| *cytb* codon 3 | 364 | GTR+G | Relaxed Uncorrelated Lognormal |
| c-*mos* codons 1+2 | 272 | HKY | Strict clock |
| c-*mos* codon 3 | 136 | HKY | Strict clock |

(C) Species-set C - *Rhynchocalamus* only

| **Analysis** | **Dataset** | **Partition** | **Length** | **Model** | **Other Priors/Parameters** |
| --- | --- | --- | --- | --- | --- |
| Phylogenetic trees**Maximum****Likelihood** | mtDNAHaplotypes (N=28)**Dataset 4** | *12S* | 618 |  |  |
| *16S* | 510 | GTR+G | Replicates x100 Bootstrap x1000 |
| *cytb* codons 1+2 | 728 |
| *cytb* codon 3 | 364 |  |  |