

Partitioned Bayesian Phylogenetic Analysis

We tested six different partitioning schemes based on a) known biological properties (e.g grouping 1st and 2nd codon positions); b) previously published results (Brandley *et al*, 2005) and; c) concatenating regions showing similar evolutionary properties (e.g rates and models) as shown in the table below.

Table S1.1 Partitioning strategies tested for the Bayesian analysis.

| Partitioning Scheme | N. Partitions | N. Estimated Parameters | Regions | N. Characters | % Variable | Model |
|---------------------|---------------|-------------------------|---------------------------------|---------------|------------|---------|
| a | 1 | 6 | all data combined | 3014 | 24.62% | GTR+I+G |
| | | | ND2 | 557 | 25.49% | GTR+G |
| b | 5 | 18 | ATPase 6 | 912 | 28.51% | GTR+G |
| | | | ND4 | 732 | 24.18% | GTR+G |
| | | | Cytb | 334 | 23.95% | HKY+I+G |
| | | | dLoop | 481 | 17.26% | HKY+G |
| | | | ATPase 6 1st | 222 | 15.32% | GTR+G |
| c | 9 | 27 | ND2 1st | 151 | 14.57% | HKY+G |
| | | | Cytb + ND4 1st | 326 | 7.98% | K80+I+G |
| | | | 2nd (ND2, ATPase 6, ND4, Cytb) | 699 | 1.57% | GTR+I |
| | | | ND2 + ND4 3rd | 365 | 61.64% | GTR+I+G |
| | | | ATPase 6 3rd | 222 | 72.52% | GTR+G |
| | | | Cytb 3rd | 112 | 64.29% | GTR |
| | | | Non-coding (ND2, ATPase 6, ND4) | 438 | 24.66% | GTR+G |
| | | | dloop | 481 | 17.26% | HKY+G |
| | | | ND2 1st + 2nd | 302 | 8.28% | HKY+G |
| d | 10 | 28 | ATPase 6 1st + 2nd | 444 | 8.56% | HKY+G |
| | | | ND4 1st + 2nd | 430 | 5.12% | HKY+G |
| | | | Cytb 1st + 2nd | 222 | 3.60% | GTR |
| | | | ND2 3rd | 151 | 62.91% | GTR+I |
| | | | ATPase 6 3rd | 222 | 72.52% | GTR+G |
| | | | ND4 3rd | 214 | 60.75% | GTR+I |
| | | | Cytb 3rd | 112 | 64.29% | GTR |
| | | | Non-coding (ND2, ATPase 6, ND4) | 438 | 24.66% | GTR+G |
| | | | dloop | 481 | 17.26% | HKY+G |
| e | 12 | 30 | ND2 1st + 2nd | 302 | 8.28% | HKY+G |
| | | | ATPase 6 1st + 2nd | 444 | 8.56% | HKY+G |
| | | | ND4 1st + 2nd | 430 | 5.12% | HKY+G |
| | | | Cytb 1st + 2nd | 222 | 3.60% | GTR |
| | | | ND2 3rd | 151 | 62.91% | GTR+I |
| | | | ATPase 6 3rd | 222 | 72.52% | GTR+G |
| | | | ND4 3rd | 214 | 60.75% | GTR+I |
| | | | | | | |

| | | | | | | |
|---|----|----|---------------------|-----|--------|-------|
| | | | Cytb 3rd | 112 | 64.29% | GTR |
| | | | ND2 Non-coding | 104 | 21.15% | HKY+G |
| | | | ATPase 6 Non-coding | 246 | 24.80% | HKY+G |
| | | | ND4 Non-coding | 88 | 28.41% | HKY |
| | | | dLoop | 481 | 17.26% | HKY+G |
| | | | ND2 1st | 151 | 14.57% | HKY+G |
| | | | ATPase 6 1st | 222 | 15.32% | GTR+G |
| | | | ND4 1st | 215 | 8.37% | HKY+I |
| | | | Cytb 1st | 111 | 7.21% | K80 |
| | | | ND2 2nd | 151 | 1.99% | HKY+I |
| | | | ATPase 6 2nd | 222 | 1.80% | HKY+I |
| | | | ND4 2nd | 215 | 1.86% | HKY |
| f | 16 | 36 | Cytb 2nd | 111 | 0.00% | - |
| | | | ND2 3rd | 151 | 62.91% | GTR+I |
| | | | ATPase 6 3rd | 222 | 72.52% | GTR+G |
| | | | ND4 3rd | 214 | 60.75% | GTR+I |
| | | | Cytb 3rd | 112 | 64.29% | GTR |
| | | | ND2 Non-coding | 104 | 21.15% | HKY+G |
| | | | ATPase 6 Non-coding | 246 | 24.80% | HKY+G |
| | | | ND4 Non-coding | 88 | 28.41% | HKY |
| | | | dLoop | 481 | 17.26% | HKY+G |

Each partitioning strategy was analyzed in MrBayes using the following MCMC parameters: 10^6 generations using four runs and with sampling every 100^{th} generation. 25% of the samples were discarded as burnin and the remaining log file of each run was combined.

Comparison between the different partitioning schemes was performed by comparing Bayes Factors (BF) calculated using Tracer v1.4.1. We followed previous suggestions of interpretation of BF's (Brandley *et al*, 2005) but also took into account the total number of parameters estimated, since overpartitioning can lead to sampling error (Li *et al*, 2008). Therefore, if two partitioning schemes could not be distinguished based on lnBF, the simplest one (with least estimated parameters) was chosen. The results of this selection are shown below.

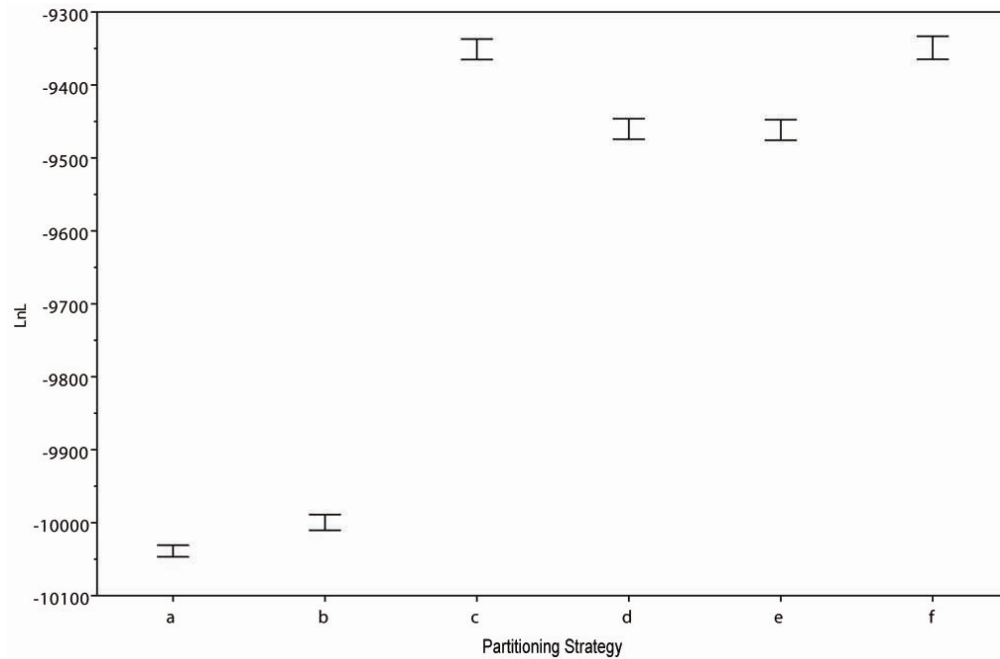


Figure S1.1 Distribution of the ln likelihoods of the trees obtained using the six partitioning strategies, labeled in order of complexity (i.e number of estimated parameters) from a-f (see Table S1.1). Bars represent 95% confidence intervals of the estimates.

Estimation of divergence times

The dataset containing coding regions from three mitochondrial genes from two *Eigenmannia* species pairs and 9 teleosts (described in the Materials and Methods section) was tested for two different partitioning schemes.

Partitioning strategies were compared using Bayes Factors and are described in the table below.

Table S1.2 Partitioning strategies tested for the estimation of divergence times.

| Partitioning Scheme | Mean Likelihood | ln P(model data) | S.E | ln BF | Partitions | Model |
|---------------------|-----------------|--------------------|--------------|---------|--------------|---------|
| By Gene | -11154.9847 | -11163.93 | +/- 0.108 | -345.08 | ND2 | HKY+G |
| | | | | | ATPase 6 | HKY+I+G |
| | | | | | Cytb | GTR+I+G |
| By Codon | -10805.2921 | -10818.851 | +/- 0.132 | 345.079 | ND2 1st | GTR+G |
| | | | | | ND2 2nd | GTR+I |
| | | | | | ND2 3rd | HKY+I+G |
| | | | | | ATPase 6 1st | SYM+G |
| | | | | | ATPase 6 2nd | GTR+G |
| | | | | | ATPase 6 3rd | HKY+I+G |
| | | | | | Cytb 1st | HKY+I |
| | | | | | Cytb 2nd | GTR+I+G |
| | | | | | Cytb 3rd | SYM+G |

The tree obtained using the abovementioned data set and is shown below (Figure S1.2). The analysis parameters are given in the Materials and Methods section.

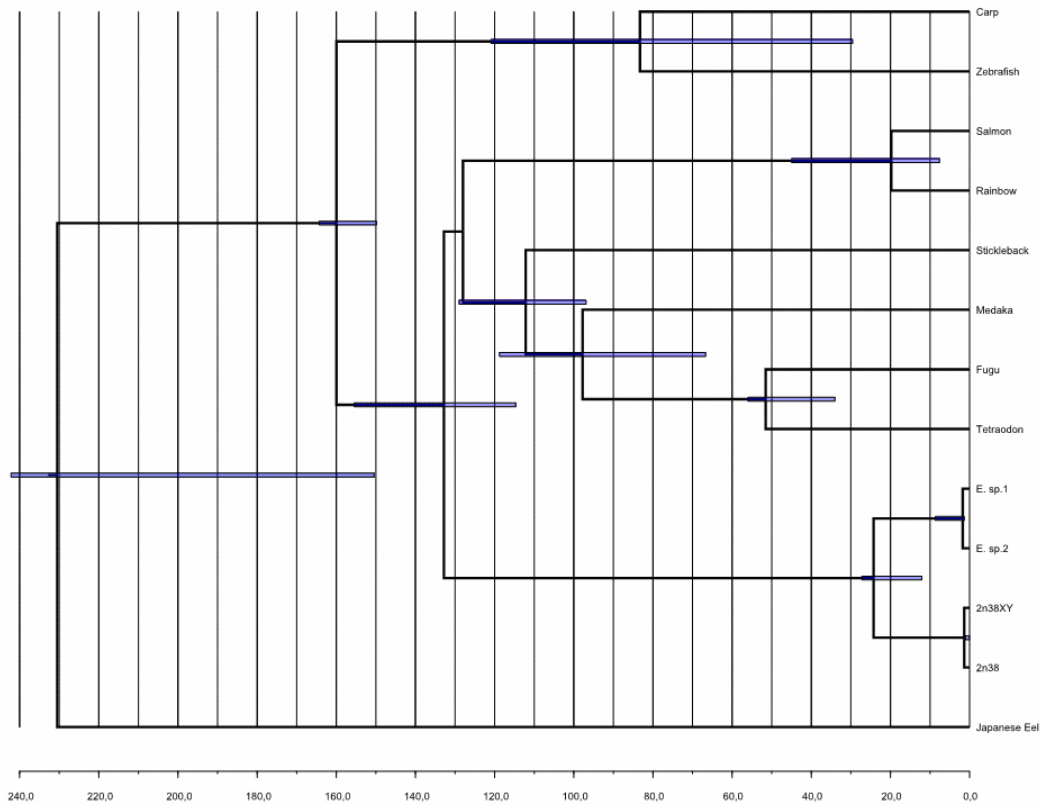


Figure S1.2 Estimation of divergence times of the *Eigenmannia* sister-species. Times from present are given in million years and bars represent the estimated dates and confidence intervals.

Cited References

Brandley MC. Schmitz A. Reeder TW (2005). Partitioned Bayesian analyses. partition choice. and the phylogenetic relationships of scincid lizards. *Syst Biol* **54**(3): 373-390.

Li CH. Lu GQ. Orti G (2008). Optimal data partitioning and a test case for ray-finned fishes (Actinopterygii) based on ten nuclear loci. *Syst Biol* **57**(4): 519-539.