

SUPPLEMENTARY MATERIALS FOR THE ARTICLE

**A New Species of the Genus *Crenubiotus* (Tardigrada: Eutardigrada: Adorybiotidae) from Salt Spring Island, Strait of Georgia, British Columbia (Canada)**

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**SM.02.** Model selection results on the concatenated alignment.

Settings used

alignment : .\Crenubiotus\_salishani.phy

branchlengths : linked

models : JC, K80, SYM, F81, HKY, GTR, JC+G, K80+G, SYM+G, F81+G, HKY+G, GTR+G, JC+I, K80+I, SYM+I, F81+I, HKY+I, GTR+I, JC+I+G, K80+I+G, SYM+I+G, F81+I+G, HKY+I+G, GTR+I+G

model\_selection : aicc

search : all

Best partitioning scheme

Scheme Name : 203

Scheme lnL : -12009.5803223

Scheme AICc : 24221.6459386

Number of params : 98

Number of sites : 3091

Number of subsets : 6

Subset	Best Model	# sites	subset id	Partition names
1	GTR+I	1101	9dc69645fa3dc40f05f867b267cafea	18S
2	GTR+G	793	ee310033ababd0520c1c785c019a81bd	28S
3	HKY+G	220	520e13da01e3d3430350526210abcc69	COI1
4	SYM+G	219	9ce930a8c88635b671f2f178fe6a4b19	COI2
5	GTR+I+G	219	29c209c648216a0b54bd1460f20b6f19	COI3
6	GTR+G	539	f346d0bb07e4b592b3693711292de489	ITS2

## Scheme Description in PartitionFinder format

Scheme\_203 = (18S) (28S) (COI1) (COI2) (COI3) (ITS2);

## Nexus formatted character sets

begin sets;

charset Subset1 = 1-1101;

charset Subset2 = 1102-1894;

charset Subset3 = 1895-2552\3;

charset Subset4 = 1896-2552\3;

charset Subset5 = 1897-2552\3;

charset Subset6 = 2553-3091;

charpartition PartitionFinder = Group1:Subset1, Group2:Subset2, Group3:Subset3,  
Group4:Subset4, Group5:Subset5, Group6:Subset6;

end;

## Nexus formatted character sets for IQtree

Warning: the models written in the charpartition are just the best model found in this analysis. Not all models are available in IQtree, so you may need to set up specific model lists for your analysis

#nexus

begin sets;

charset Subset1 = 1-1101;

charset Subset2 = 1102-1894;

charset Subset3 = 1895-2552\3;

charset Subset4 = 1896-2552\3;

charset Subset5 = 1897-2552\3;

charset Subset6 = 2553-3091;

charpartition PartitionFinder = GTR+I:Subset1, GTR+G:Subset2, HKY+G:Subset3,  
SYM+G:Subset4, GTR+I+G:Subset5, GTR+G:Subset6;

end;

## RaxML-style partition definitions

Warning: RAxML allows for only a single model of rate heterogeneity in partitioned analyses. I.e. all partitions must be assigned one of three types of model: No heterogeneity (e.g. GTR); +G (e.g. GTR+G); or +I+G (e.g. GTR+I+G). If the best models for your dataset contain different types of model for different subsets you will need to decide on the best rate heterogeneity model before you run RAxML. If you prefer to do things more rigorously, you can run separate PartitionFinder analyses for each type of rate heterogeneity. Then choose the scheme with the lowest AIC/AICc/BIC score. Note that these re-runs will be quick!

DNA, Subset1 = 1-1101

DNA, Subset2 = 1102-1894

DNA, Subset3 = 1895-2552\3

DNA, Subset4 = 1896-2552\3

DNA, Subset5 = 1897-2552\3

DNA, Subset6 = 2553-3091

## MrBayes block for partition definitions

Warning: MrBayes only allows a relatively small collection of models. If any model in your analysis is not one that is included in MrBayes (e.g. by setting nst = 1, 2, or 6 for DNA sequences; or is not in the available list of protein models for MrBayes) then this MrBayes block will just set that model to nst = 6 for DNA, or 'wag' for Protein. Similarly, the only additional parameters that this MrBayes block will include are +I and +G. Other parameters, such as +F and +X, are ignored. If you want to use this MrBayes block for your analysis, please make sure to check it carefully before you use it we've done our best to make it accurate, but there may be errors that remain!

```
begin mrbayes;
```

```
charset Subset1 = 1-1101;
```

```
charset Subset2 = 1102-1894;
```

```
charset Subset3 = 1895-2552\3;
```

```
charset Subset4 = 1896-2552\3;
```

```
charset Subset5 = 1897-2552\3;
```

```
charset Subset6 = 2553-3091;
```

```
partition PartitionFinder = 6:Subset1, Subset2, Subset3, Subset4, Subset5, Subset6;
set partition=PartitionFinder;

lset applyto=(1) nst=6 rates=propinv;
lset applyto=(2) nst=6 rates=gamma;
lset applyto=(3) nst=2 rates=gamma;
lset applyto=(4) nst=6 rates=gamma;
prset applyto=(4) statefreqpr=fixed(equal);

lset applyto=(5) nst=6 rates=invgamma;
lset applyto=(6) nst=6 rates=gamma;

prset applyto=(all) ratepr=variable;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all) tratio=(all);

end;
```

\*Citations for this analysis\*

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If you use this analysis in your published work, please cite the following papers on which your analysis relied.

For the version of PartitionFinder you used, please cite:

Lanfear, R., Frandsen, P. B., Wright, A. M., Senfeld, T., Calcott, B. (2016) PartitionFinder 2: new methods for selecting partitioned models of evolution formolecular and morphological phylogenetic analyses. *Molecular biology and evolution*. DOI: [dx.doi.org/10.1093/molbev/msw260](https://doi.org/10.1093/molbev/msw260)

For the all algorithm you used, please cite:

Your analysis also used PhyML, so please cite:

Guindon, S., Dufayard, J. F., Lefort, V., Anisimova, M., Hordijk, W., & Gascuel, O. (2010). New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Systematic biology*, 59(3), 307-321.