

Supplementary material 3

PAUP output

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Data type: pdf

Explanation notes: Output of the PAUP analysis, including the majority consensus and bootstrap consensus trees.

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P A U P *

Version 4.0a (build 169) for 32-bit Microsoft Windows (built on Feb 10 2021 at 22:12:44)

Tue Feb 28 18:23:09 2023

-----NOTICE-----

This is a test version that is still changing rapidly.

Please report bugs to dave@phylosolutions.com

Running on Intel(R) Core(TM) i7-2600 CPU @ 3.40GHz

Current processor contains 4 CPU cores on 1 socket (hyperthreaded to 8 logical cores)

Executable built for IA-32 architecture (64-bit word length)

SSE vectorization enabled

SSSE3 instructions supported

Multithreading enabled using Pthreads

paup> set errorStop=no;

Processing of file "F:\Table_S1.nex" begins...

Data matrix has 24 taxa, 110 characters

Valid character-state symbols: 01234

Missing data identified by '?'

Gaps identified by '-'

Case significant for alphabetic character-state symbols

Processing of input file "Table_S1.nex" completed.

```
paup> outgroup 21;
```

Outgroup status changed:

1 taxon transferred to outgroup

Total number of taxa now in outgroup = 1

Number of ingroup taxa = 23

```
paup> set maxtrees=40000 increase=no;
```

Maxtrees reset to 40000

```
paup> hsearch;
```

Heuristic search settings:

Optimality criterion = parsimony

Character-status summary:

Of 110 total characters:

All characters are of type 'unord'

All characters have equal weight

20 characters are constant (proportion = 0.181818)

34 variable characters are parsimony-uninformative

Number of parsimony-informative characters = 56

Gaps are treated as "missing"

Starting tree(s) obtained via stepwise addition

Addition sequence: simple (reference taxon = Elseya (Pelocomastes) albagula)

Number of trees held at each step = 1

Branch-swapping algorithm: tree-bisection-reconnection (TBR) with reconnection limit = 8

Steepest descent option not in effect

'Maxtrees' setting = 40000 (will not be increased)

Branches collapsed (creating polytomies) if maximum branch length is zero

'MulTrees' option in effect

No topological constraints in effect

Trees are unrooted

Heuristic search completed

Total number of rearrangements tried = 40157333

Score of best tree(s) found = 153

Number of trees retained = 10236

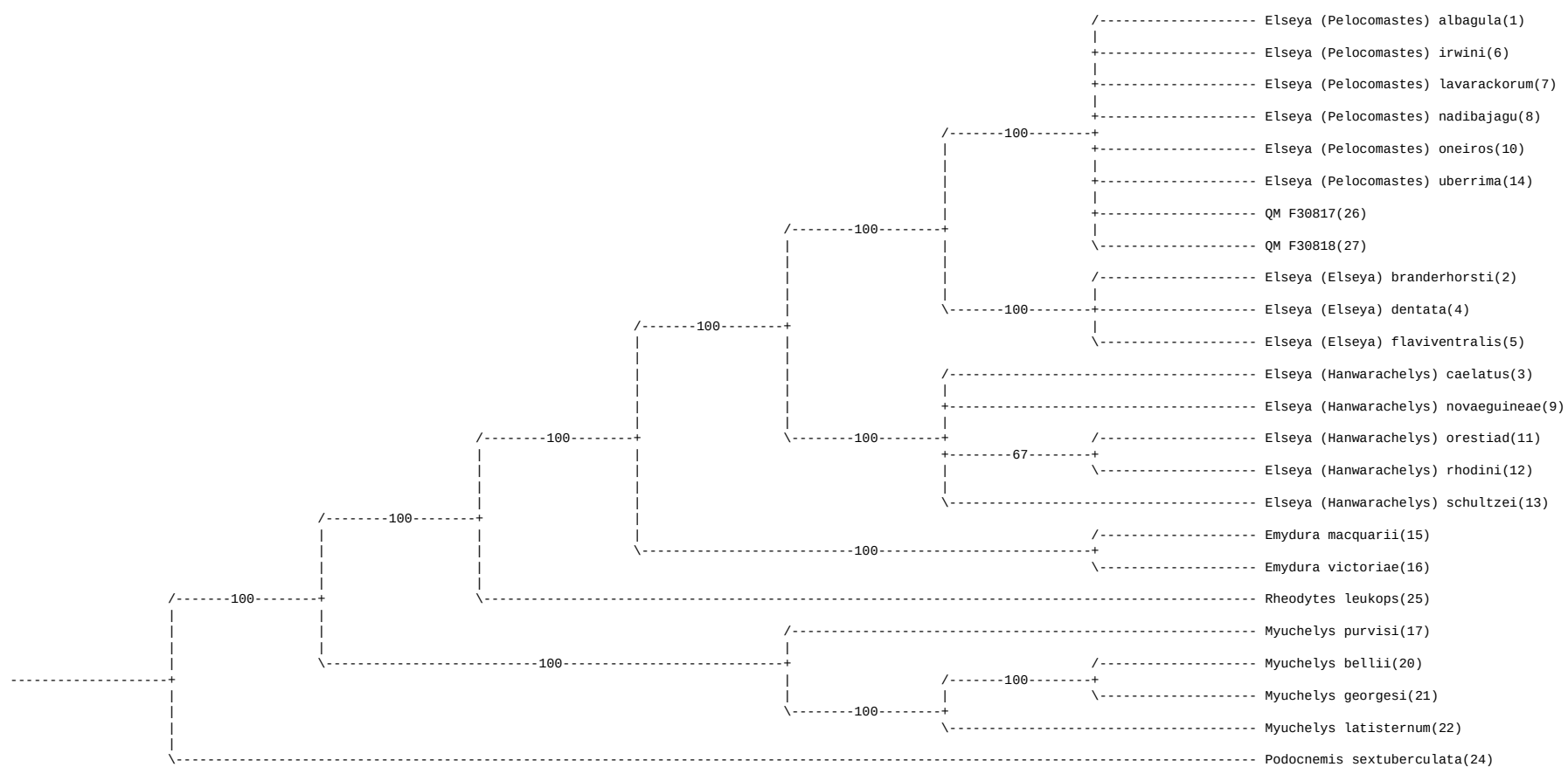
Time used = 15.11 sec (CPU time = 15.11 sec)

```
paup> rootTrees outRoot=monophyletic;
```

```
10236 trees converted from unrooted to rooted using outgroup method
```

```
paup> contree / strict=no majRule;
```

```
50% Majority-rule consensus of 10236 trees
```



Groups found in one or more trees and frequency of occurrence:

111111112222222		
123456789012345670124567	Freq	%
.....**.....	10236	100.00%
.....***.....	10236	100.00%
.....****.....	10236	100.00%
.....**.....	10236	100.00%
.*.***.....	10236	100.00%
.*.***.....	10236	100.00%
*.***.*.*.....	10236	100.00%
**.*.*.*.*.....	10236	100.00%
*****.*.....	10236	100.00%
*****.....	10236	100.00%
*****.....	10236	100.00%
*****.....	10236	100.00%
*****.....	10236	100.00%
.....**.....	6824	66.67%
.....*.*.....	5118	50.00%
.....***.....	5118	50.00%
.....**.....	5118	50.00%
.....**.*.*.....	3960	38.69%
.....**.*.*.....	3168	30.95%
.....*.*.*.....	2916	28.49%
.....**.*.*.....	2688	26.26%
.....**.*.*.....	2688	26.26%
.....*.*.....	2532	24.74%
.....*.*.....	2532	24.74%
.....*.....	2376	23.21%
.....**.*.*.....	2376	23.21%
.....*.*.*.....	1560	15.24%
.....*.*.*.....	1560	15.24%
.....*.*.*.....	1350	13.19%
.....***.*.*.....	972	9.50%
.....*.....	972	9.50%
.....***.*.*.....	972	9.50%
.....*.....	972	9.50%
.....*.....	972	9.50%
.....*.*.....	828	8.09%
.....*.*.....	828	8.09%
.....*.*.....	828	8.09%
.....*.*.....	828	8.09%
.....*.....	792	7.74%
.....**.*.*.....	792	7.74%
.....*.....	792	7.74%
.....**.*.*.....	792	7.74%
.....*.....	468	4.57%
.....**.*.*.....	468	4.57%
.....*.*.....	468	4.57%
.....*.*.....	468	4.57%
.....***.*.*.....	324	3.17%
.....*.*.....	324	3.17%
.....*.....	324	3.17%

Bootstrap method with heuristic search:

Number of bootstrap replicates = 1000

Starting seed = generated automatically

Number of characters resampled in each replicate = 110

Optimality criterion = parsimony

Character-status summary:

Of 110 total characters:

All characters are of type 'unord'

All characters have equal weight

20 characters are constant (proportion = 0.181818)

34 variable characters are parsimony-uninformative

Number of parsimony-informative characters = 56

Gaps are treated as "missing"

Starting tree(s) obtained via stepwise addition

Addition sequence: simple (reference taxon = *Elseya* (*Pelocomastes*) *albagula*)

Number of trees held at each step = 1

Branch-swapping algorithm: tree-bisection-reconnection (TBR) with reconnection limit = 8

Steepest descent option not in effect

'Maxtrees' setting = 40000 (will not be increased)

Branches collapsed (creating polytomies) if maximum branch length is zero

'Multrees' option in effect

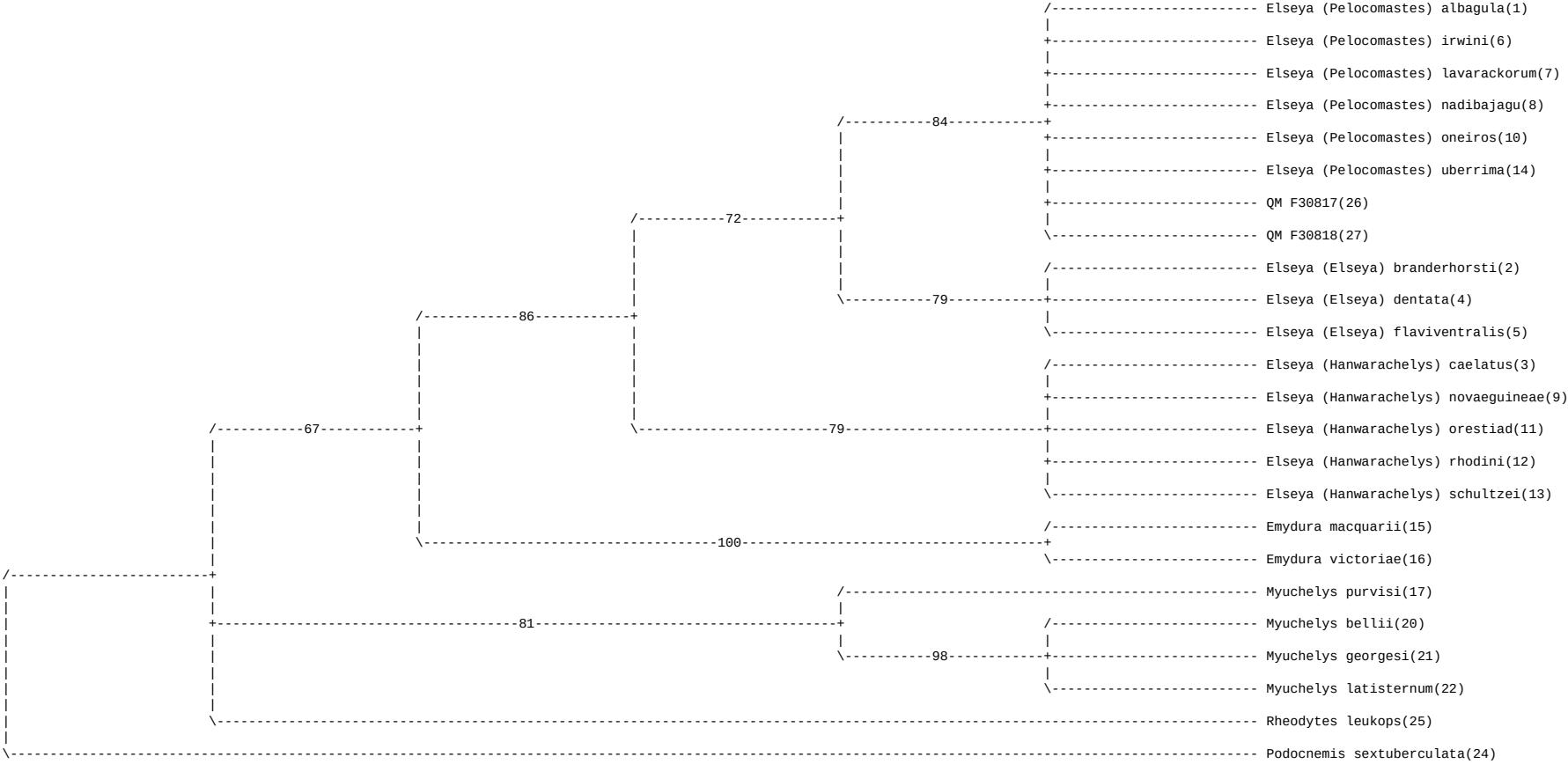
No topological constraints in effect

Trees are unrooted

1000 bootstrap replicates completed

Time used = 13:43:49 (CPU time = 13:43:22.6)

Bootstrap 50% majority-rule consensus tree



Bipartitions found in one or more trees and frequency of occurrence (bootstrap support values):

1111111122222222		
123456789012345670124567	Freq	%
.....**.....	999.45	99.95%
.....***.....	979.87	97.99%
.....*****..	861.80	86.18%
.****.*.***.*****.	837.43	83.74%
.....****.....	807.22	80.72%
..*.....	786.98	78.70%
..*.....	786.22	78.62%
..*.....	716.63	71.66%
.....*****.	671.96	67.20%
..*.....	484.82	48.48%
.....**.....	476.81	47.68%
.....**.....	412.35	41.23%
.....*****.	361.02	36.10%
..*.....	333.47	33.35%
.....**.*.*.....	317.02	31.70%
.....*****.	305.08	30.51%
.....**.....	299.17	29.92%
..*.....	244.54	24.45%
.....*.*.....	214.48	21.45%
*****.*.*.*.*.*.*.*.*.	197.40	19.74%
.....**.*.*.....	171.26	17.13%
*****.*.*.*.*.*.*.*.*.	160.96	16.10%
.....**.*.*.....	152.52	15.25%
.....**.*.*.....	152.45	15.25%
.....**.....	139.68	13.97%
.....**.*.*.....	133.64	13.36%
.....*.*.*.....	131.28	13.13%
.....*.*.....	129.67	12.97%
.....*.*.....	129.16	12.92%
*****.*.*.*.*.*.*.*.*.	128.17	12.82%
*****.*.*.*.*.*.*.*.*.	124.96	12.50%
.....*****.*.	124.83	12.48%
.....*.*.*.*.*.*.*.*.	122.02	12.20%
.....*.*.....	116.37	11.64%
*****.*.*.*.*.*.*.*.*.	91.31	9.13%
*****.*.*.*.*.*.*.*.*.	90.93	9.09%
*****.*.*.*.*.*.*.*.*.	81.61	8.16%
*****.*.*.*.*.*.*.*.*.	75.01	7.50%
.....*****.	74.49	7.45%
*****.*.*.*.*.*.*.*.*.	74.23	7.42%
*****.*.*.*.*.*.*.*.*.	70.75	7.08%
*****.*.*.*.....	62.62	6.26%
.....*.*.*.*.....	62.13	6.21%
.....*.*.*.*.....	62.09	6.21%
.....*.*.*.*.....	59.26	5.93%
.....*.*.*.*.....	57.90	5.79%
.....*.*.*.*.....	57.02	5.70%
*****.*.*.*.*.*.*.*.*.	55.81	5.58%
*****.*.*.*.*.*.*.*.*.	55.27	5.53%
.....*.*.*.*.....	51.63	5.16%
.....*.*.*.*.....	50.52	5.05%
.....*.*.*.*.....	50.41	5.04%

912 groups at (relative) frequency less than 5% not shown