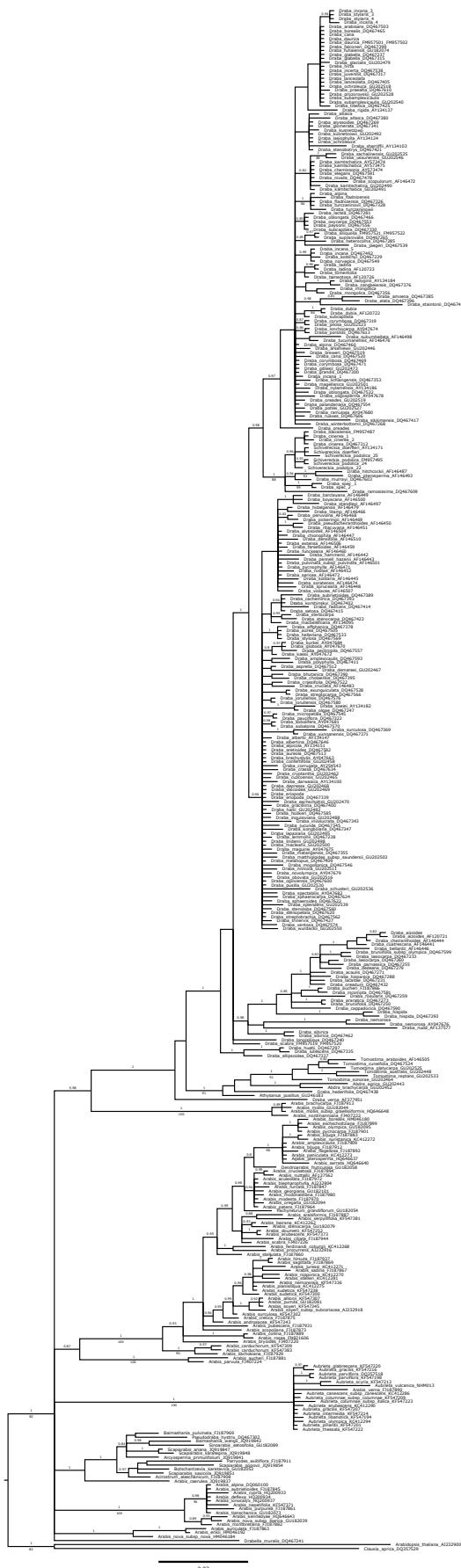


Supplement 1: Phylogenetic tree of Arabideae inferred from internal transcribed spacer locus, under the GTR+Γ substitution model.

Branch lengths are drawn to scale, with the scale bar indicating the number of nucleotide substitutions per site.

The numbers on the branches are statistical support values

(above: ML bootstrap values <80 are not shown; below: Bayesian posterior probabilities <.90 are not shown).

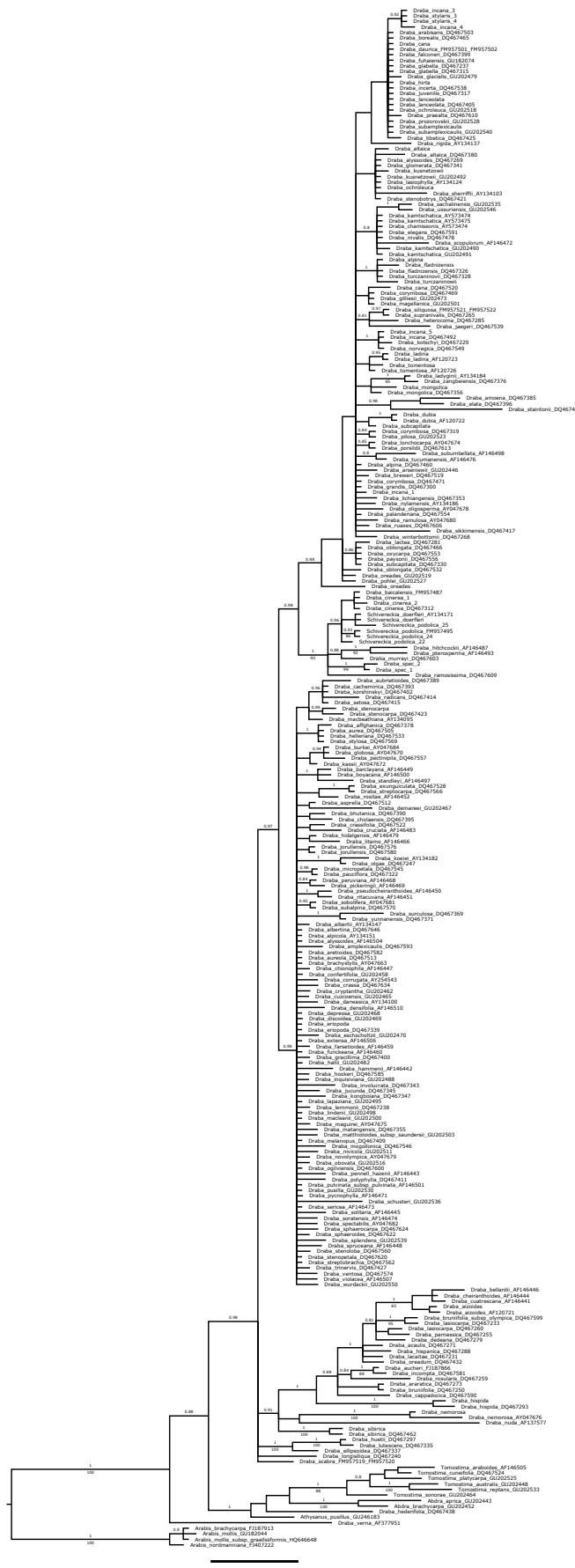


Supplement 2: Phylogenetic tree of *Draba* s.l. inferred from internal transcribed spacer locus, under the GTR+Γ substitution model.

Branch lengths are drawn to scale, with the scale bar indicating the number of nucleotide substitutions per site.

The numbers on the branches are statistical support values

(above: ML bootstrap values <80 are not shown; below: Bayesian posterior probabilities <.90 are not shown).

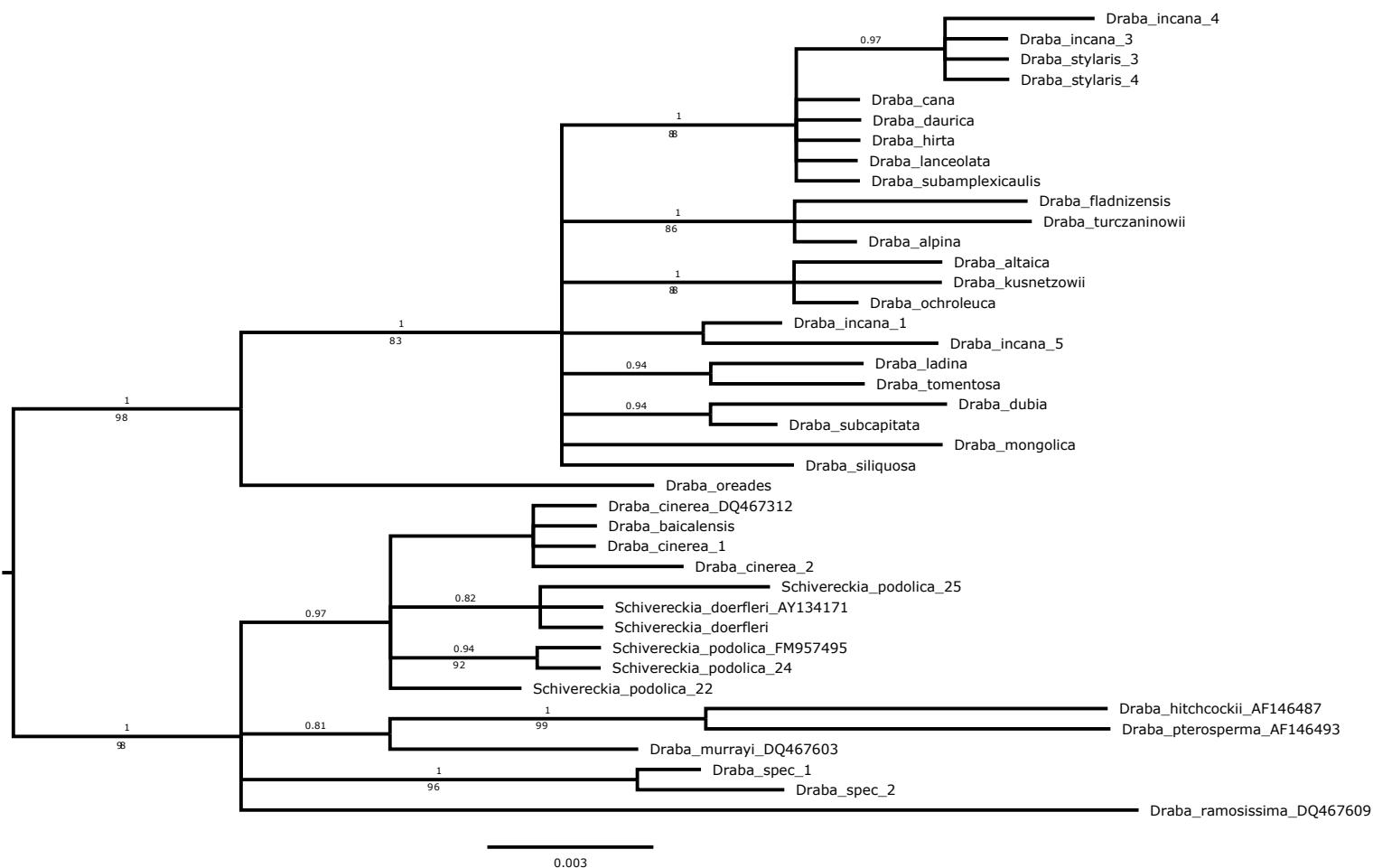


Supplement 3: Phylogenetic tree of *Schivereckia* and closely related taxa inferred from ITS, under the GTR+Γ substitution model.

Branch lengths are drawn to scale, with the scale bar indicating the number of nucleotide substitutions per site.

The numbers on the branches are statistical support values

(above: ML bootstrap values, values <80 are not shown; below: Bayesian posterior probabilities, values <.90 are not shown).

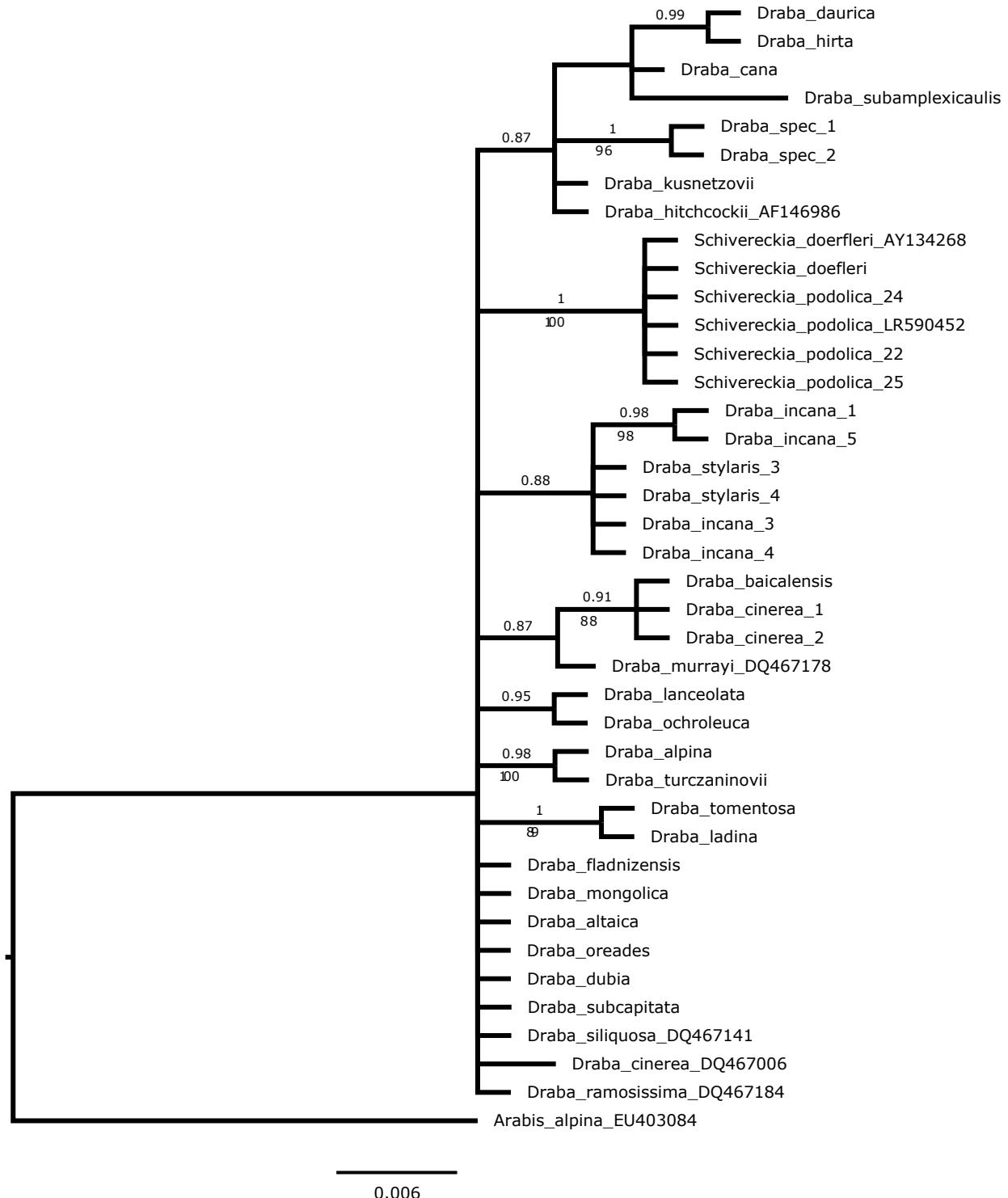


Supplement 4: Phylogenetic tree of *Schivereckia* and closely related taxa inferred from trnL-trnF, under the GTR+Γ substitution model.

Branch lengths are drawn to scale, with the scale bar indicating the number of nucleotide substitutions per site.

The numbers on the branches are statistical support values

(above: ML bootstrap values, values <80 are not shown; below: Bayesian posterior probabilities, values <.90 are not shown).



Supplement 5: Phylogenetic statistics of Arabideae, *Draba* s.l. and *Schivereckia* alignments.

Legend: bp, base pairs; PIS parsimony informative positions.

	Arabideae	<i>Draba</i> s.l.	<i>Schivereckia</i>
No. of included accessions	394	285	38
Length of the alignment (bp)	653	637	620
No. of constant characters	298	375	552
No. of variable characters	110	90	40
No. of potential PIS	245	172	28
MLoptimisation likelihood	-8817.444	-5346.499	-1424.766

Supplement 6: Ancestral area reconstruction statistics.

Process begin at 12/11/2019 2:45:45 PM

You could simply choose the model with the highest AICc_wt value as the 'Best' model,

and apply this model on your trees data set.

#Results of Model Test#

LnL	numparams	d	e	j	AICc	AICc_wt
DEC	-57.03	2	0.14	0.13	0	118.4
DEC+J	-39.35	3	1.0e-12	1.0e-12	0.019	85.37
DIVALIKE	-46.44	2	0.044	1.0e-12	0	97.2
DIVALIKE+J	-39.57	3	1.0e-12	1.0e-12	0.020	85.8
BAYAREALIKE	-70.91	2	0.040	0.40	0	146.1
BAYAREALIKE+J	-41.4	3	1.0e-07	1.0e-07	0.022	89.47
						0.066

Use the AICc to select the best model

The p-value of the LRT (Likelihood Ratio Test) tells you whether or not you can reject

the null hypothesis that without J and +J confer equal likelihoods on the data.

alt	null	LnLalt	LnLnull	DFalt	DFnull	DF	Dstatistic	pval	test	tail	AIC1	AIC2
		AICwt1	AICwt2	AICweight_ratio_model1		AICweight_ratio_model2						
DEC+J	DEC	-39.35	-57.03	3	2	1	35.36	2.7e-09	chi-squared			one-tailed
		84.71	118.1	1.00	5.7e-08	1.75e+07	5.7e-08					
DIVALIKE+J	DIVALIKE	-39.57	-46.44	3	2	1	13.74	0.0002	chi-squared			
	one-tailed	85.13	96.87	1.00	0.0028	354.1	0.0028					
BAYAREALIKE+J	BAYAREALIKE	-41.4	-70.91	3	2	1	59.01	1.6e-14	chi-squared			
squared	one-tailed	88.81	145.8	1.00	4.2e-13	2.39e+12	4.2e-13					

Process end at 12/11/2019 2:46:44 PM

Open [Graphic->Tree View] to see the result

NODE41:
EVENT MATRIX:
Dispersal:0
Vicariance:0
Extinction:0
Event Route:
B->B^B->B|B
PROBABILITY:
0.9970

NODE42:
EVENT MATRIX:
Dispersal:0
Vicariance:0
Extinction:0
Event Route:
B->B^B->B|B
PROBABILITY:
0.9974

NODE43:
EVENT MATRIX:
Dispersal:0
Vicariance:0
Extinction:0
Event Route:
B->B^B->B|B
PROBABILITY:
0.9923

NODE54:
EVENT MATRIX:
Dispersal:0
Vicariance:0
Extinction:0
Event Route:
B->B^B->B|B
PROBABILITY:
0.9994

NODE55:
EVENT MATRIX:
Dispersal:0
Vicariance:0
Extinction:0
Event Route:
B->B^B->B|B
PROBABILITY:
0.9997

NODE56:
EVENT MATRIX:
Dispersal:0
Vicariance:0
Extinction:0
Event Route:
B->B^B->B|B
PROBABILITY:
0.9979

NODE67:
EVENT MATRIX:
Dispersal:2
Vicariance:1
Extinction:0
Event Route:
DG->DEFG->DE|FG
PROBABILITY:
0.3327

NODE68:
EVENT MATRIX:
Dispersal:0
Vicariance:1
Extinction:0
Event Route:
BH->H|B
PROBABILITY:
0.9885

NODE69:
EVENT MATRIX:
Dispersal:1
Vicariance:0
Extinction:0
Event Route:
B->B^B->BH^B->B|BH
PROBABILITY:
0.8207

<p>NODE44: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9975</p> <p>NODE45: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9944</p> <p>NODE46: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9940</p> <p>NODE47: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9991</p> <p>NODE48: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9953</p> <p>NODE49: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9933</p> <p>NODE50: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9983</p>	<p>NODE57: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9999</p> <p>NODE58: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9996</p> <p>NODE59: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9984</p> <p>NODE60: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9939</p> <p>NODE61: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9860</p> <p>NODE62: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9702</p> <p>NODE63: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.9104</p>	<p>NODE70: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: B->B^B->B B PROBABILITY: 0.7674</p> <p>NODE71: EVENT MATRIX: Dispersal:1 Vicariance:1 Extinction:1 Event Route: BD->B->BE->E B PROBABILITY: 0.8529</p> <p>NODE72: EVENT MATRIX: Dispersal:2 Vicariance:0 Extinction:0 Event Route: BD->BD^D->BDG^D->BD DG PROBABILITY: 0.2516</p> <p>NODE73: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: C->C^C->C C PROBABILITY: 0.8841</p> <p>NODE74: EVENT MATRIX: Dispersal:1 Vicariance:1 Extinction:0 Event Route: BD->BCD->C BD PROBABILITY: 0.3439</p> <p>NODE75: EVENT MATRIX: Dispersal:1 Vicariance:1 Extinction:0 Event Route: BD->ABD->A BD PROBABILITY: 0.2629</p> <p>NODE76: EVENT MATRIX: Dispersal:0 Vicariance:0 Extinction:0 Event Route: A->A^A->A A PROBABILITY: 0.9189</p>
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NODE51:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:0
 Extinction:0
 Event Route:
 $B \rightarrow B^A B \rightarrow B|B$
 PROBABILITY:
 0.9927

NODE64:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:0
 Extinction:0
 Event Route:
 $G \rightarrow G^A G \rightarrow G|G$
 PROBABILITY:
 0.9755

NODE77:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:1
 Extinction:0
 Event Route:
 $AB \rightarrow B|A$
 PROBABILITY:
 0.7450

NODE52:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:0
 Extinction:0
 Event Route:
 $B \rightarrow B^A B \rightarrow B|B$
 PROBABILITY:
 0.9870

NODE65:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:1
 Extinction:0
 Event Route:
 $FG \rightarrow F|G$
 PROBABILITY:
 0.7630

NODE78:
 EVENT MATRIX:
 Dispersal:2
 Vicariance:0
 Extinction:0
 Event Route:
 $AB \rightarrow AB^A B \rightarrow ABD^A B \rightarrow AB|BD$
 PROBABILITY:
 0.1534

NODE53:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:0
 Extinction:0
 Event Route:
 $B \rightarrow B^A B \rightarrow B|B$
 PROBABILITY:
 0.9999

NODE66:
 EVENT MATRIX:
 Dispersal:0
 Vicariance:1
 Extinction:0
 Event Route:
 $DE \rightarrow E|D$
 PROBABILITY:
 0.9938

NODE79:
 EVENT MATRIX:
 Dispersal:1
 Vicariance:0
 Extinction:0
 Event Route:
 $B \rightarrow B^A B \rightarrow AB^A B \rightarrow AB|B$
 PROBABILITY:
 0.2012

Dispersal Between Areas:
 $A \rightarrow D: 0.5$
 $B \rightarrow A: 1.5$
 $B \rightarrow C: 0.5$
 $B \rightarrow D: 0.5$
 $B \rightarrow E: 0.5$
 $B \rightarrow G: 0.5$
 $B \rightarrow H: 1$
 $D \rightarrow A: 0.5$
 $D \rightarrow C: 0.5$
 $D \rightarrow E: 1$
 $D \rightarrow F: 0.5$
 $D \rightarrow G: 0.5$
 $G \rightarrow E: 0.5$
 $G \rightarrow F: 0.5$

Dispersal Table:

	from	to	within
A	0.50	2.00	1
B	4.50	0.00	27
C	0.00	1.00	1
D	3.00	1.00	1
E	0.00	2.00	0
F	0.00	1.00	0
G	1.00	1.00	1
H	0.00	1.00	0

Global Cost:
 Global Dispersal: 11
 Global Vicariance: 8
 Global Extinction: 1

Speciation Within Areas:
 A:1
 B:27
 C:1
 D:1
 G:1

Supplement 7. Mantel-Test results for geographical versus RAPD Distance of Schivereckia.

