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Supplemental information

Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics

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Supplemental information

Supplementary Figures

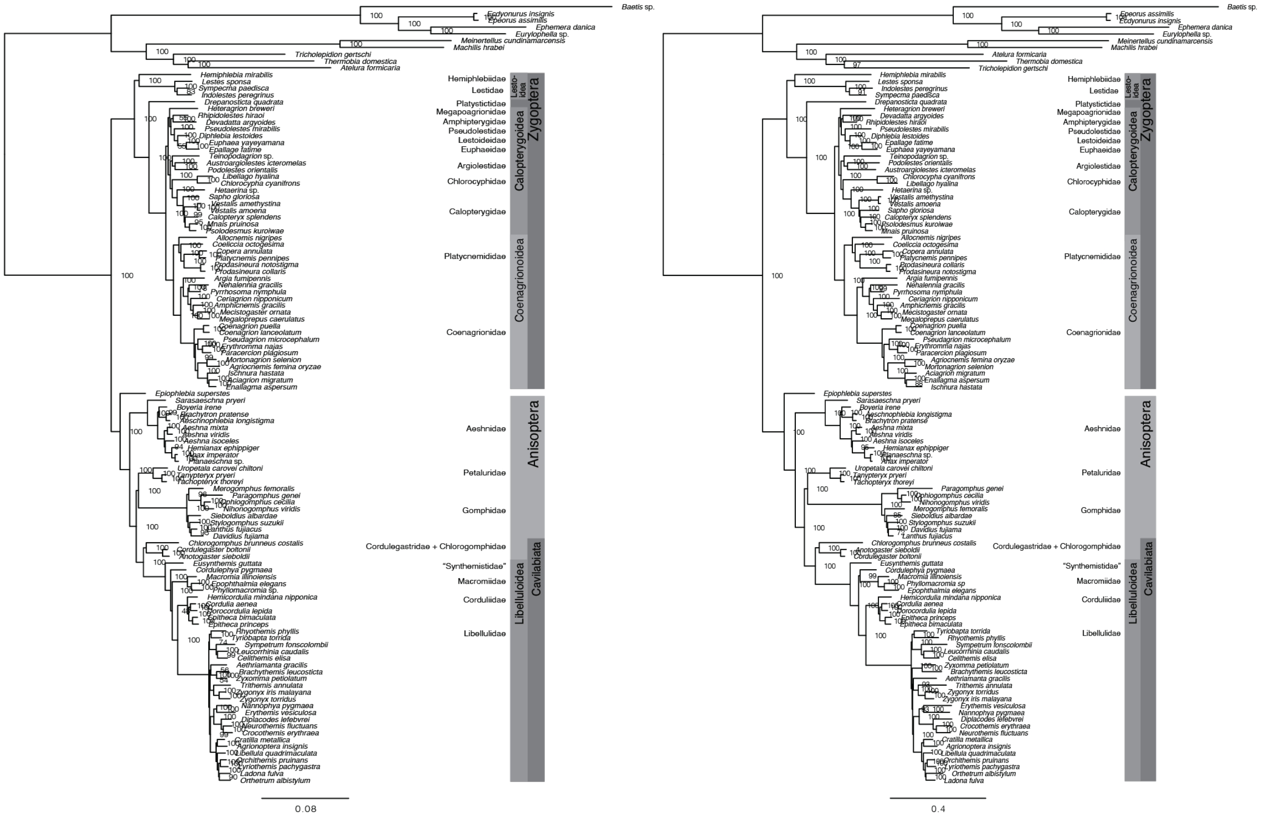


Figure S1: Phylogenetic relationships in Odonata recovered using the nucleotide dataset NT2 (right panel) and NT123 (left panel); related to figure 1.

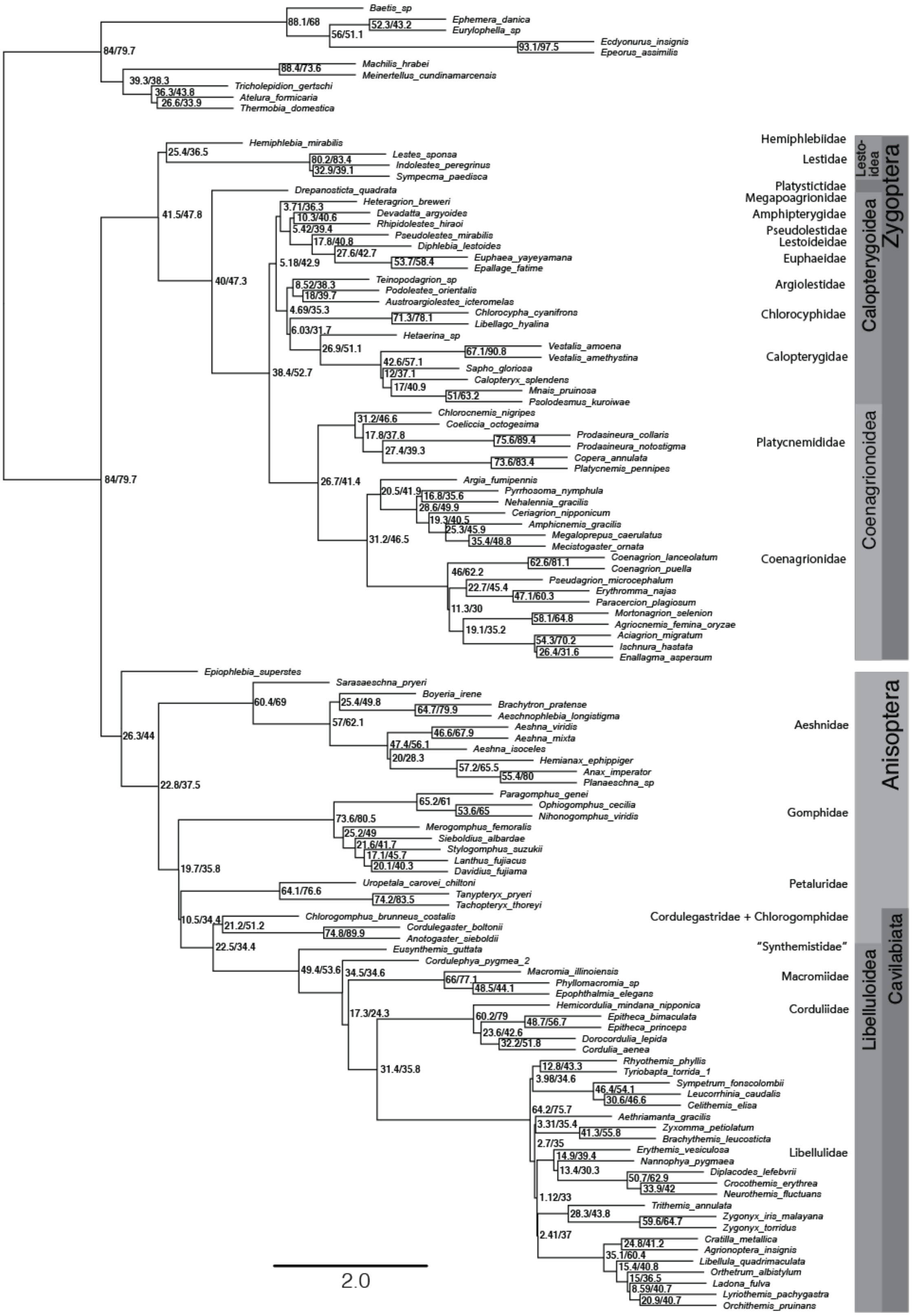


Figure S2: Phylogenetic relationships recovered using multispecies coalescence method. The numbers on the nodes show the gCF/sCF values for the branch leading to the root. Related to figure 1 and 2.

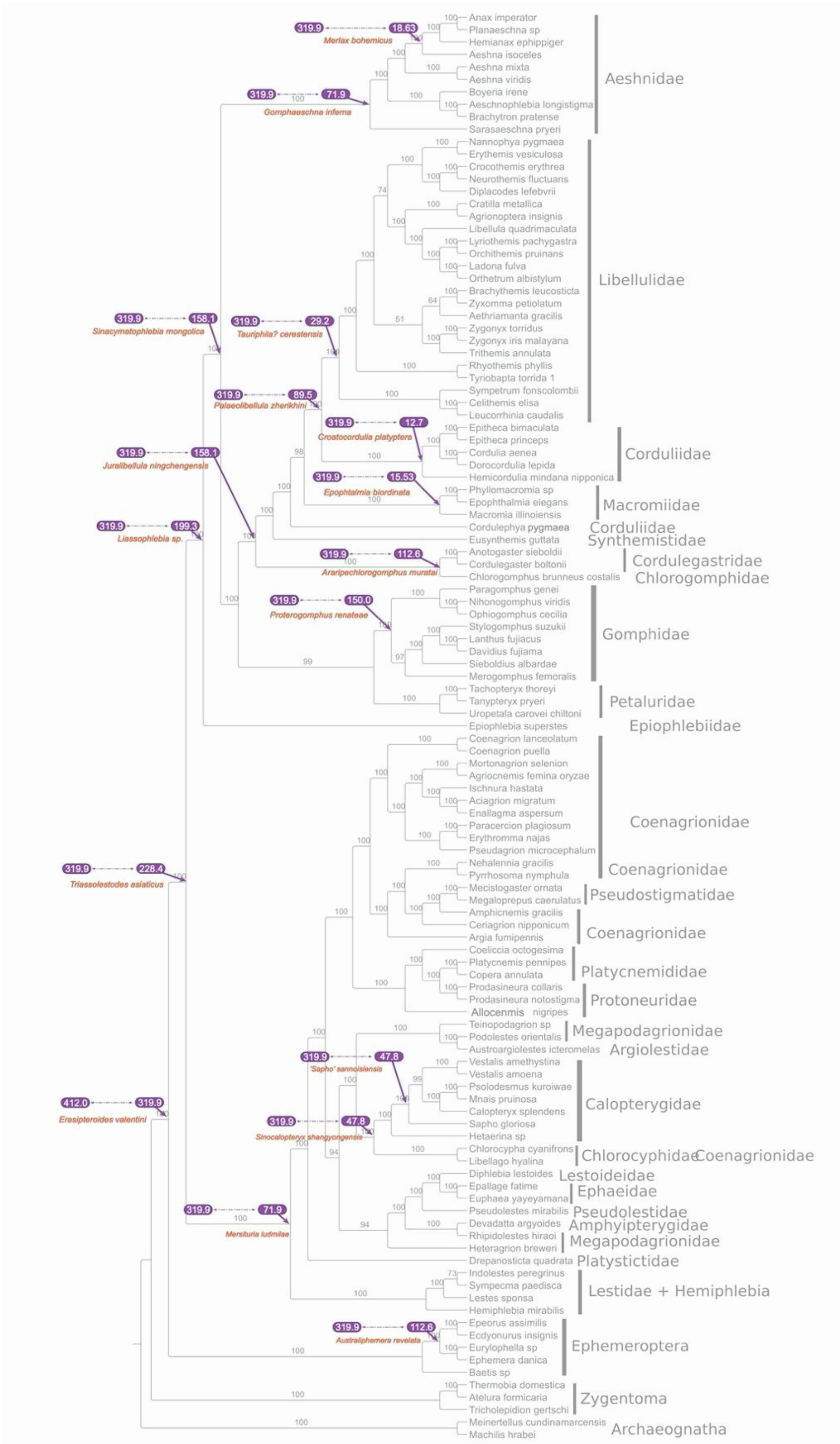


Figure S3: **Placement of the fossils** used for divergence time estimation. Fossil species are represented in orange. Purple arrows indicate the nodes fossils were placed on. The numbers in purple give the upper and lower bounds of the fossils. All fossils were modelled to have uniform distributions. Related to figure 3.

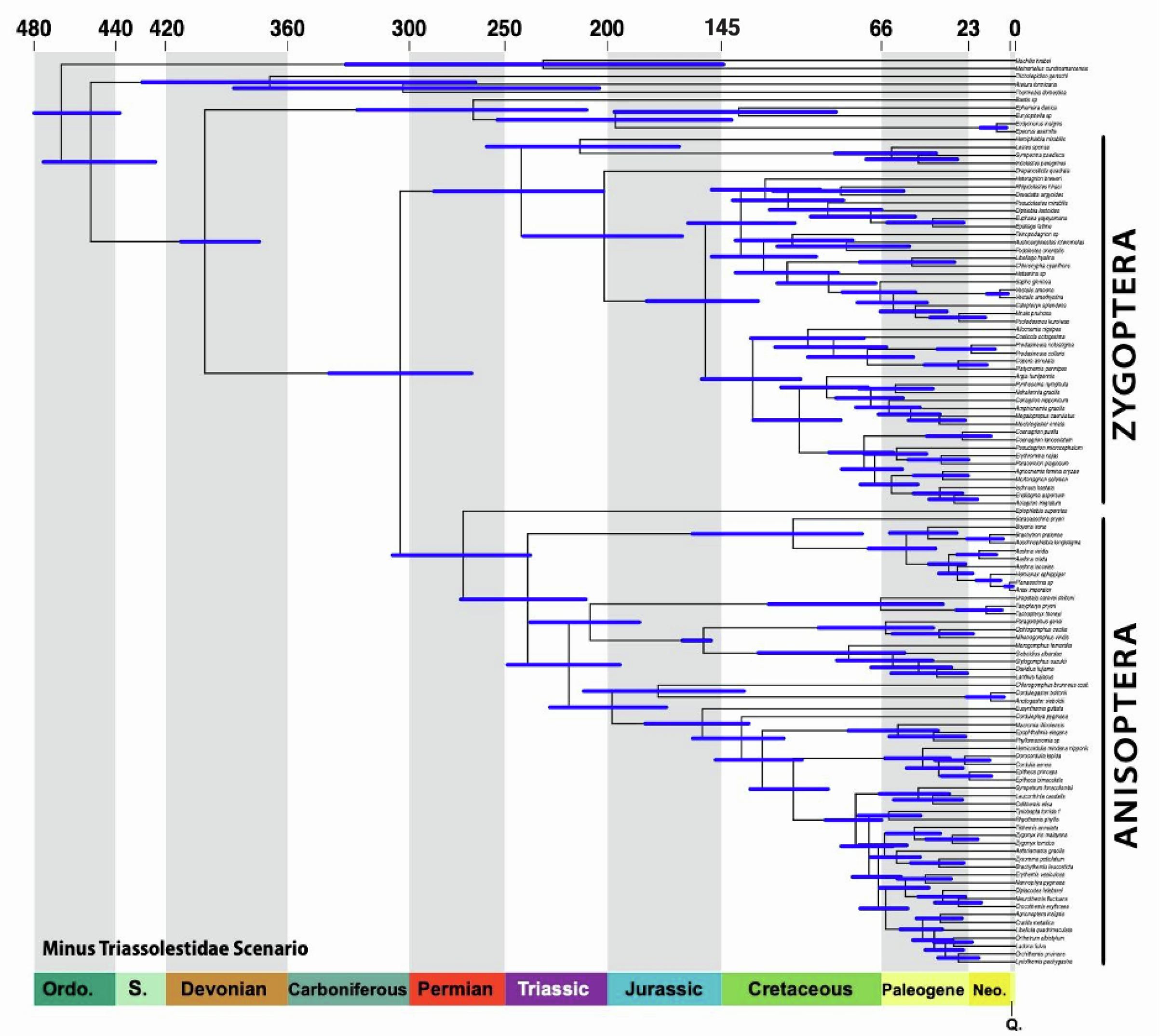
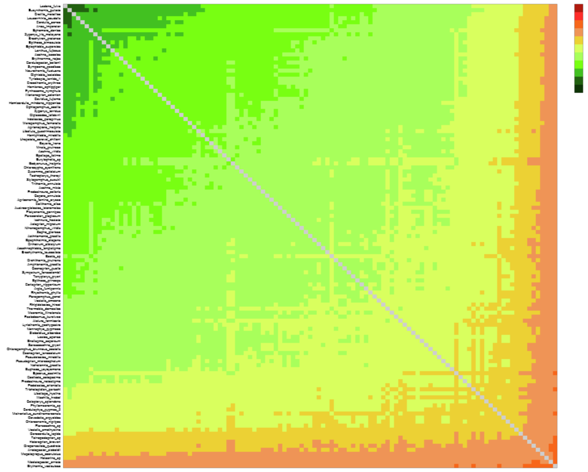
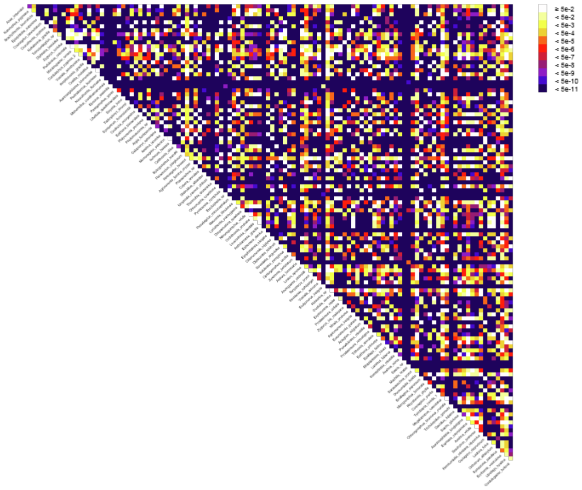


Figure S4: **Divergence time estimation results from the "Minus Triassolestidae" scenario.** For this we used all 17 chosen fossils except the fossil †*Triassolestodes asiaticus*, which was excluded from the calibration set. Blue bars around the nodes represent the confidence intervals recovered around each node. Related to figure 4.

Table S2: Diagnostics of the final dataset including results obtained from MARE, AliStat and SymTest. related to STAR methods.

		AMINO ACID
		Basis: original supermatrix IC0 excluded
	MATRIX	SOS (MARE default)
	# taxa	115
	# data blocks	2890
	# aa sites	824783
MARE	IC	74.20%
	saturation	91.40%
	# partitions with IC=0	none
AliStat	Ca	65.49%
	Cr_max	91.62%
	Cr_min	28.06%
SymTest	% tests p < 0.05	91.27%
	% tests p < 0.0005	78.89%
	% tests p < 0.000005	69.57%
	AliStat Heat Map	
	SymTest Heat Map	

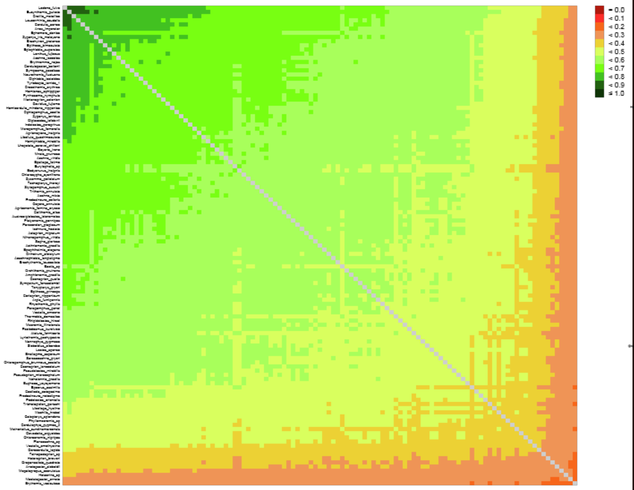
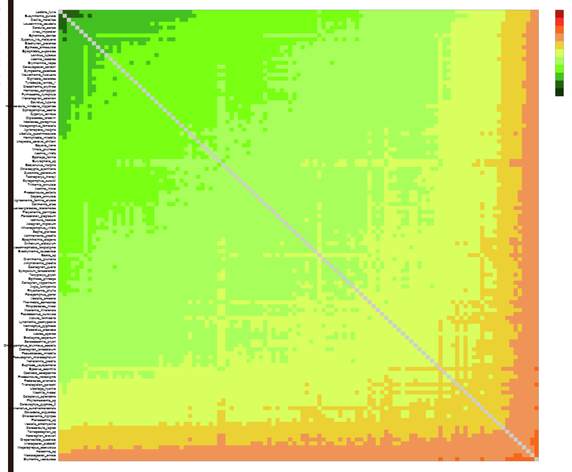
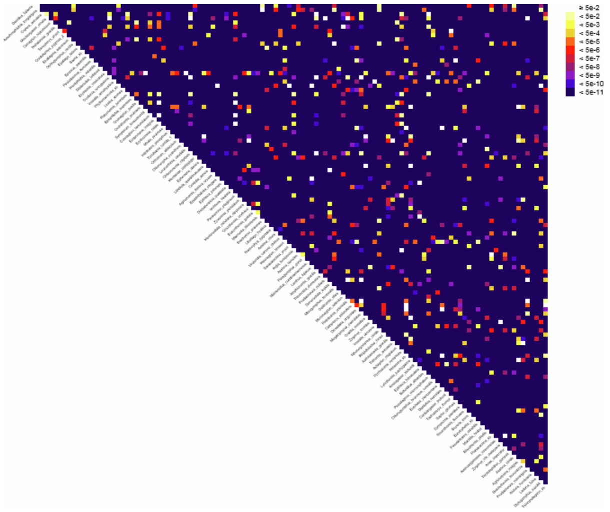
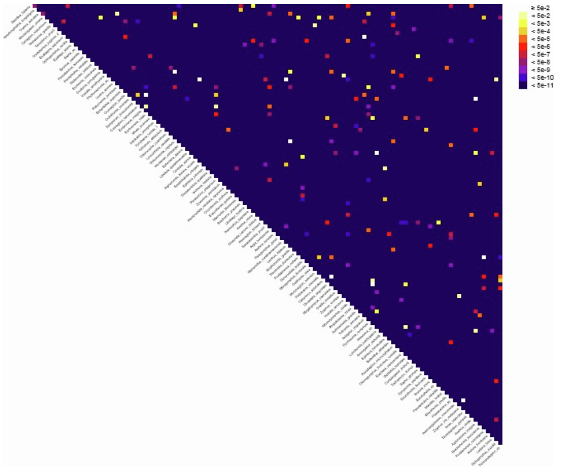
SOS supermatrix on NUCLEOTIDE	SOS supermatrix on NUCLEOTIDE
Basis: original supermatrix IC0 excluded	Basis: original supermatrix IC0 excluded
SOS supermatrix 2^{nd} codon position	SOS supermatrix all 3 codon position
115	115
2890	2890
824783	2474349
65.49%	65.49%
91.62%	91.62%
28.06%	28.06%
99.05%	99.82%
97.15%	99.42%
95.26%	98.90%
	
	

Table S3: FCLM analysis results for the five relationships tested. Related to STAR methods.

Hypothesis 1: Sister group relationship between Petaluridae and Gomphidae

	Original	Permutation I:	Permutation II:	Permutation III:
T1	11.70%	36.30%	30.40%	34.00%
T2	10.10%	31.60%	27.30%	29.10%
T3	78.20%	32.10%	36.00%	36.90%

Hypothesis 2: Sister group relationship between Cordulegastroidea and Libelluloidea

	Original	Permutation I:	Permutation II:	Permutation III:
T1	95.70%	37.90%	37.60%	33.20%
T2	0.00%	28.20%	24.30%	30.70%
T3	4.30%	33.90%	38.10%	36.10%

Hypothesis 3: Aeshnidae is sister group to all remaining Anisoptera

	Original	Permutation I:	Permutation II:	Permutation III:
T1	100%	51.80%	41.50%	36.40%
T2	0.00%	22.30%	32.50%	33.60%
T3	0.00%	23.60%	26.00%	30.00%

Hypothesis 4: Corduliidae is sister group to Libellulidae

	Original	Permutation I:	Permutation II:	Permutation III:
T1	100%	38.70%	42.10%	39.10%
T2	0.00%	36.30%	29.70%	31.20%
T3	0.00%	25.00%	28.20%	29.70%

Hypothesis 5: Status of Synthemistidae s.l. (sensu Letsch et al., 2016, i.e., GSI-Complex sensu Ware et al., 2007)

	Original	Permutation I:	Permutation II:	Permutation III:
T1	1.10%	9.70%	26.90%	66.70%
T2	0.00%	55.90%	57.00%	12.90%
T3	98.90%	34.40%	16.10%	20.40%

Table S4: Fossil calibrations and results of the divergence time estimation under three different scenarios. Related to STAR methods, figure 3 and figure 4.

Tree Node	Fossil species	Fossil Age/ Prior lower bound	Prior upper bound	Resul	
				Mean	CI Lower bound
Root			484.5	470.28	440.66
Paleoptera	*Erasipteroides valentini*	319.9	412	399.2	372.08
Odonata	*Triassolestodes asiaticus*	228.4	319.9	297.36	266.15
Epiprocta	*Liassophlebia sp.*	199.3	319.9	267.35	237.49
Anisoptera	*Sinacymatophlebia mongoli*	158.1	319.9	237.01	210.46
Zygoptera	*Mersituria ludmilae*	71.9	319.9	239.62	200.94
Aeshnidae	*Gomphaeschna inferna*	71.9	319.9	108.86	75.36
Aeschna isoceles + Hemianax, etc.	*Merlax bohemicus*	18.6	319.9	28.3	21.07
Gomphidae	*Proterogomphus renateae*	150	319.9	153.74	150.09
Gomphidae + Petaluridae	*Proterogomphus renateae*	150	319.9	207.32	184.57
Petaluridea				65.62	35.62
Cavilabiata	*Juralibellula ningchengensis*	158.1	319.9	196.71	171.37
Chlorogomphidae + Cordulegasteridae	*Araripechlorogomphus mur*	112.6	319.9	174.51	133.75
Libellulidae	*Tauriphila? cerestensis*	29.2	319.9	78.16	65.97
Cordullidae	*Croatocordulia platyptera*	12.7	319.9	45.01	32.02
Libellulidae + Cordullidae	*Palaeolibellula zherikhini*	89.5	319.9	108.69	92.25
Macromiidae	*Epophtalmia biordinata*	15.5	319.9	57.54	37.9
Lestoidea				211.12	163.39
Calopterygoidea				133.55	107.37
Coenagrionoidea				127.93	105.27
Ephemroptera - Baetis sp.	*Australiphemera revelata*	112.6	319.9	197.66	139.48
Ephemroptera				267.14	209.39
Calopterygidae + Chlorocyphidae	*Sinocalopteryx shangyonger*	47.8	319.9	110.88	86.15
S-gloria+Sistergroup	*'Sapho' sannoisiensis*	23	319.9	66.06	49.01

ts: Primary Tree			Results: Minus Triassolestidae					Results	
CI Upper Bound	CI Length	rates/100 mya	Mean	CI Lower bound	CI Upper Bound	CI Length	rates/100 mya	Mean	CI Lower bound
484.05	43.39	NA	470.71	441.86	484.06	42.2	NA	469.9	439.94
411.58	39.5	0.0935	399.85	373.09	411.62	38.53	0.0924	396.96	366.15
318.53	52.38	0.226	303.59	268.33	338.64	70.31	0.2431	263.4	235.14
294.12	56.63	0.0739	272.48	239.36	307.24	67.88	0.0718	232.16	207.7
264.62	54.16	0.0766	240.56	211.9	273.54	61.64	0.0731	201.07	183.28
277.16	76.22	0.0547	243.78	203.35	286.8	83.45	0.0534	206.35	176.08
155.8	80.44	0.0256	109.72	75.67	159.39	83.72	0.0251	95.2	73.02
37.53	16.46	0.0507	28.59	21.17	37.69	16.52	0.0502	23.97	19.22
163.78	13.69	0.136	153.87	150.1	164.24	14.14	0.1308	72.3	56.5
233.45	48.88	0.0521	209.86	185.54	239.33	53.79	0.051	172.74	156.68
118.27	82.65	0.0177	66.51	35.79	121.71	85.92	0.0175	55.14	31.95
223.72	52.35	0.0668	198.97	172.28	229.61	57.33	0.0651	165.87	158.34
207.73	73.98	0.038	176.28	133.88	212.84	78.96	0.0374	146.53	125.2
93.04	27.07	0.205	78.81	66.12	93.74	27.62	0.2042	66.99	58.13
62.93	30.91	0.0341	45.65	32.38	64.35	31.97	0.034	36.56	27.37
129.48	37.23	0.0843	109.56	92.47	130.77	38.3	0.084	96.52	89.79
82.06	44.16	0.0488	58	38.25	82.42	44.17	0.0485	49	34.08
252.29	88.9	0.0435	214.84	165.94	260.76	94.82	0.0431	183.12	150.61
158.14	50.77	0.0427	135.47	108.87	161.42	52.55	0.0427	112.33	93.8
152.19	46.92	0.0702	129.58	105.92	154.71	48.79	0.0694	107.26	89.98
249.52	110.04	0.0899	197.29	140.02	255.57	115.55	0.0893	192.04	134.29
318.09	108.7	0.1695	267.44	211.56	324.68	113.12	0.1703	260.47	200.93
135.04	48.89	0.0581	112.52	87.48	137.96	50.48	0.0573	93.74	76.38
83.83	34.82	0.0691	66.71	49.34	85.37	36.03	0.0676	56.63	43.58

: Stem Placement

CI Upper Bound	CI Length	rates/100 mya
484.03	44.09	NA
411.5	45.35	0.0894
297.35	62.21	0.1717
263.31	55.61	0.07
226.59	43.31	0.0738
243.22	67.14	0.0544
131.33	58.31	0.0308
30.53	11.31	0.0613
92.85	36.35	0.0697
194.05	37.37	0.0549
93.65	61.7	0.0211
183.87	25.53	0.081
168.55	43.35	0.0402
77.33	19.2	0.2057
49.2	21.83	0.0357
109.33	19.54	0.0988
67.18	33.1	0.0531
221.01	70.4	0.0507
133.88	40.08	0.0487
127.43	37.45	0.0798
249.45	115.16	0.09
315.58	114.65	0.1638
114.23	37.85	0.0679
70.61	27.03	0.0794