

Appendix S2

We estimated rates of molecular evolution using Bayesian relaxed-clock dating with PAML 4.1 [1] and the set of programs in Multidistribute [2-4]. Methods are presented in the text, but here we expand upon the locus BFI, which had few sequences available outside of *P. kentucki*. First, we estimated the rate of evolution using a three-taxon statement, with *P. wehrlei* as the outgroup and *P. glutinosus* + *P. kentucki* as the ingroup. This is described in the main text. Because this estimate of molecular evolution was derived from limited sampling, we also estimated the rate of evolution for BFI using a phylogeny of the Salamandridae from Zhang et al.[5] in combination with sequence data on salamandrids from Sequeira et al.[6]. The outgroup was designated as *Salamandrina terdigitata*, and the ingroup included nine taxa from eight genera (Fig. B). The upper and lower limits on node ages were set based on the BEAST 2 analyses of Zhang et al. [5], including both their primary and additional calibration points (see [5] for details). For all loci, MCMC analyses included 100,000 generations of burn-in. Thereafter, the Markov chain was sampled every 100 generations until 10,000 samples were collected.

When BFI was calibrated using *Plethodon*, the estimated rate of evolution was 0.036%/myr, which is an intermediate rate among the nuclear loci. When BFI was dated using salamandrids, the estimated rate of evolution given the two different calibrations was 0.091%/myr (primary calibration) and 0.197%/myr (additional calibrations; see [7]). These rates are higher than those estimated for our other nuclear loci. For our analyses, we used the *Plethodon* calibration.

References

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Table B. Species and indention numbers of taxa and loci used in the multidivtime analysis. GenBank numbers are provided.

Species	Cyt b	ND2	tRNAs	MLC2A	GAPD	RAG1	ILF3	BFI
<i>albagula</i>	DQ994905.1	DQ018689.1	DQ018689	JN798307.1	JN798216.1	DQ995008	JN798264.1	–
<i>amplus</i>	DQ994912.1	AY874880.1	AY874880.1	JN798308.1	JN798217.1	DQ995010	JN798265.1	–
<i>angusticla</i>	DQ994913.1	DQ018676.1	DQ018676.1	–	JN798218.1	DQ995011	–	–
<i>caddoensis</i>	DQ994916.1	AY874875.1	AY874875.1	JN798311.1	JN798221.1	DQ995013	JN798268.1	–
<i>chattahooc</i>	DQ994919.1	–	–	JN798312.1	JN798222.1	DQ995014	JN798269.1	–
<i>cheoah</i>	DQ994921.1	–	–	JN798313.1	JN798223.1	DQ995015	JN798270.1	–
<i>chlorobryo</i>	DQ994923.1	–	–	JN798314.1	JN798224.1	–	JN798271.1	–
<i>cinereus</i>	AY378030	AY874875.1	AY874875.1	JN798317.1	JN798226.1	DQ995017	–	–
<i>cylindrace</i>	DQ994928.1	–	–	JN798318.1	JN798229.1	DQ995022	JN798272.1	–
<i>dorsalis</i>	AY378077.1	DQ018678.1	DQ018678.2	JN798319.1	–	DQ995023	JN798273.1	–
<i>electromor</i>	DQ994932.1	DQ018665.1	DQ018665.2	JN798320.1	JN798230.1	DQ995025	–	–
<i>elongatus</i>	AY691746.1	–	–	–	–	–	–	–
<i>fourchensi</i>	DQ994933.1	AY874876.1	AY874876.2	JN798321.1	JN798232.1	DQ995026	JN798274.1	–
<i>glutinosus</i>	–	–	–	–	–	–	–	KU841065
<i>grobmani</i>	DQ994941.1	DQ018695.1	DQ018695.2	JN798325.1	JN798236.1	DQ995028	JN798277.1	–
<i>hoffmani</i>	AY378048.1	DQ018666.1	DQ018666.2	JN798327.1	JN798238.1	DQ995029	–	–
<i>hubrichti</i>	AY378058.1	DQ018667.1	DQ018667.2	JN798328.1	JN798239.1	DQ995030	–	–
<i>idahoensis</i>	DQ994945.1	–	–	JN798329.1	–	DQ995031	–	–
<i>jordani</i>	DQ994947.1	AY874887.1	AY874887.2	JN798330.1	–	DQ995032	JN798278.1	–
<i>kentucki</i>	DQ994948.1	KU841032	KU841032	JN798331.1	JN798240.1	DQ995033	JN798279.1	KU841122
<i>kiamichi</i>	DQ994950.1	DQ018696.1	DQ018696.2	JN798332.1	JN798241.1	DQ995034	JN798280.1	–
<i>kisatchie</i>	DQ994951.1	DQ018698.1	DQ018698.2	JN798333.1	JN798242.1	DQ995035	JN798281.1	–
<i>meridianus</i>	DQ994954.1	AY874898.1	AY874898.2	JN798335.1	JN798244.1	DQ995038	JN798283.1	–
<i>metcalfi</i>	DQ994956.1	AY874903.1	AY874903.2	–	JN798245.1	DQ995040	JN798284.1	–
<i>mississipp</i>	DQ994958.1	DQ018700.1	DQ018700.2	–	JN798246.1	–	JN798285.1	–
<i>montanus</i>	DQ994961.1	AY874960.1	AY874960.2	JN798336.1	JN798247.1	DQ995042	JN798286.1	–
<i>nettingi</i>	DQ994964.1	–	–	–	JN798248.1	DQ995045	–	–

Species	Cyt b	ND2	tRNAs	MLC2A	GAPD	RAG1	ILF3	BFI
<i>ocmulgee</i>	DQ994967.1	DQ018702.1	DQ018702.2	JN798338.1	JN798250.1	DQ995048	JN798288.1	–
<i>ouachitae</i>	Y691747.1	AY874877.1	AY874877.2	–	JN798251.1	–	JN798289.1	–
<i>petraeus</i>	DQ994973.1	AY874878.1	AY874878.2	JN798339.1	JN798252.1	DQ995049	JN798290.1	–
<i>punctatus</i>	AY378078.1	DQ018685.1	DQ018685.2	–	JN798253.1	DQ995050	JN798291.1	–
<i>richmondi</i>	AY378070.1	DQ018670.1	DQ018670.2	JN798340.1	JN798254.1	DQ995051	–	–
<i>savannah</i>	DQ994978.1	–	–	JN798341.1	JN798255.1	DQ995055	JN798292.1	–
<i>sequoyah</i>	DQ994979.1	DQ018705.1	–	JN798342.1	–	DQ995056	JN798293.1	–
<i>serratus</i>	AY378073.1	DQ018671.1	DQ018671.2	JN798343.1	JN798256.1	DQ995057	–	–
<i>shenandoah</i>	AY378043.1	DQ018674.1	DQ018674.2	JN798345.1	JN798257.1	DQ995062	–	–
<i>teyahalee</i>	DQ994990.1	–	–	JN798347.1	–	DQ995068	JN798295.1	–
<i>vandykei</i>	AY691759.1	–	–	–	JN798260.1	–	–	–
<i>variolatus</i>	DQ994991.1	–	–	JN798348.1	–	DQ995069	JN798296.1	–
<i>vehiculum</i>	AY691760.1	DQ018661.1	DQ018661.2	JN798349.1	–	–	–	–
<i>ventralis</i>	DQ994993.1	DQ018680.1	DQ018680.2	JN798350.1	JN798261.1	DQ995071	JN798297.1	–
<i>virginia</i>	AY378049.1	DQ018675.1	DQ018675.2	JN798351.1	–	DQ995072	JN798298.1	–
<i>websteri</i>	AY378076.1	–	–	JN798352.1	–	DQ995073	JN798299.1	–
<i>wehrlei</i>	AY378079.1	DQ018686.1	DQ018686.2	JN798353.1	–	DQ995075	JN798300.1	KU863657
<i>welleri</i>	AY691761.1	–	–	–	JN798262.1	–	JN798301.1	–
<i>yonahlosse</i>	AY378075.1	AY874879.1	AY874879.2	JN798354.1	JN798263.1	DQ995078	JN798302.1	–

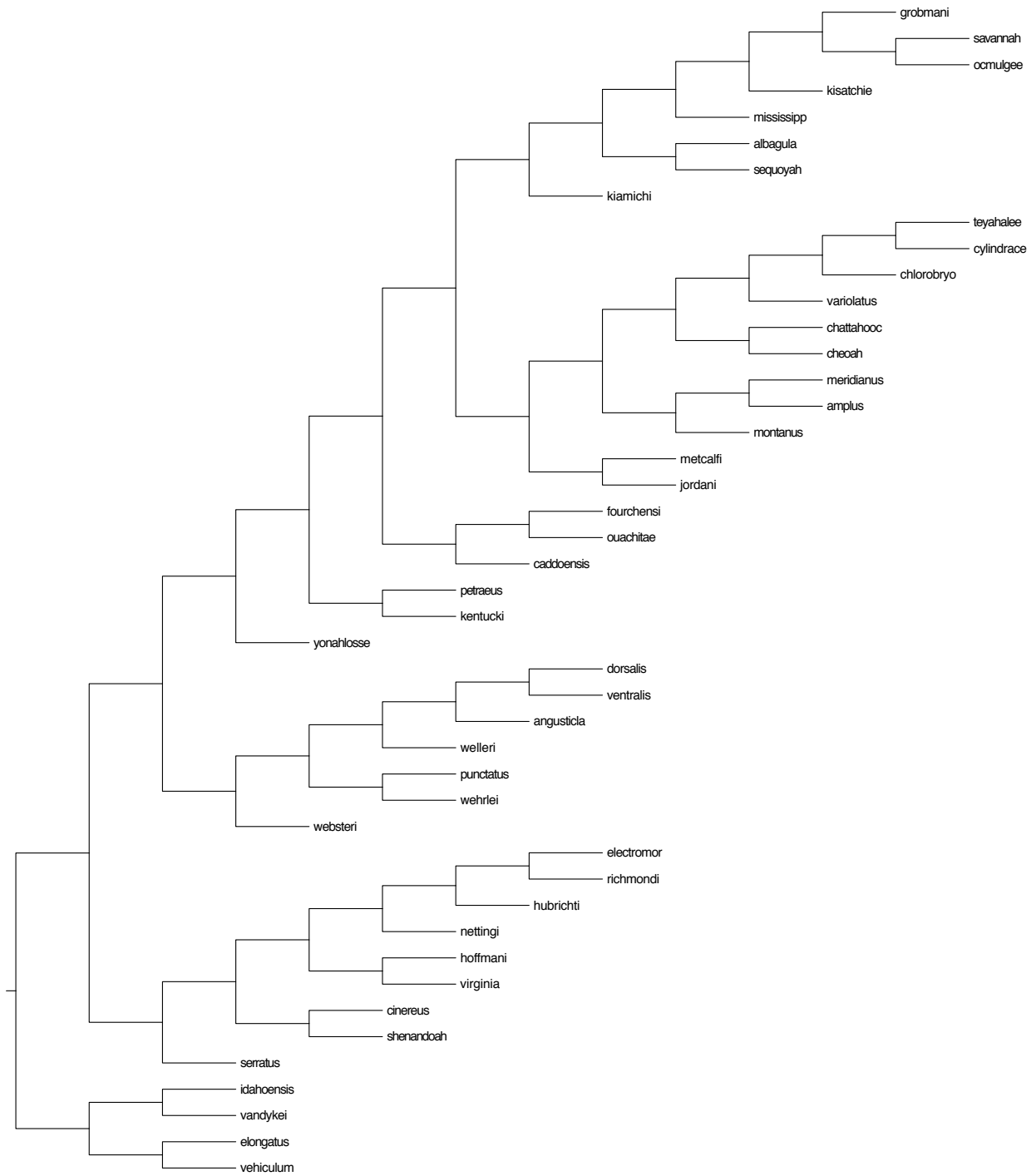


Figure A. Phylogeny of *Plethodon* used in the Multidivtime analyses. See text for details.

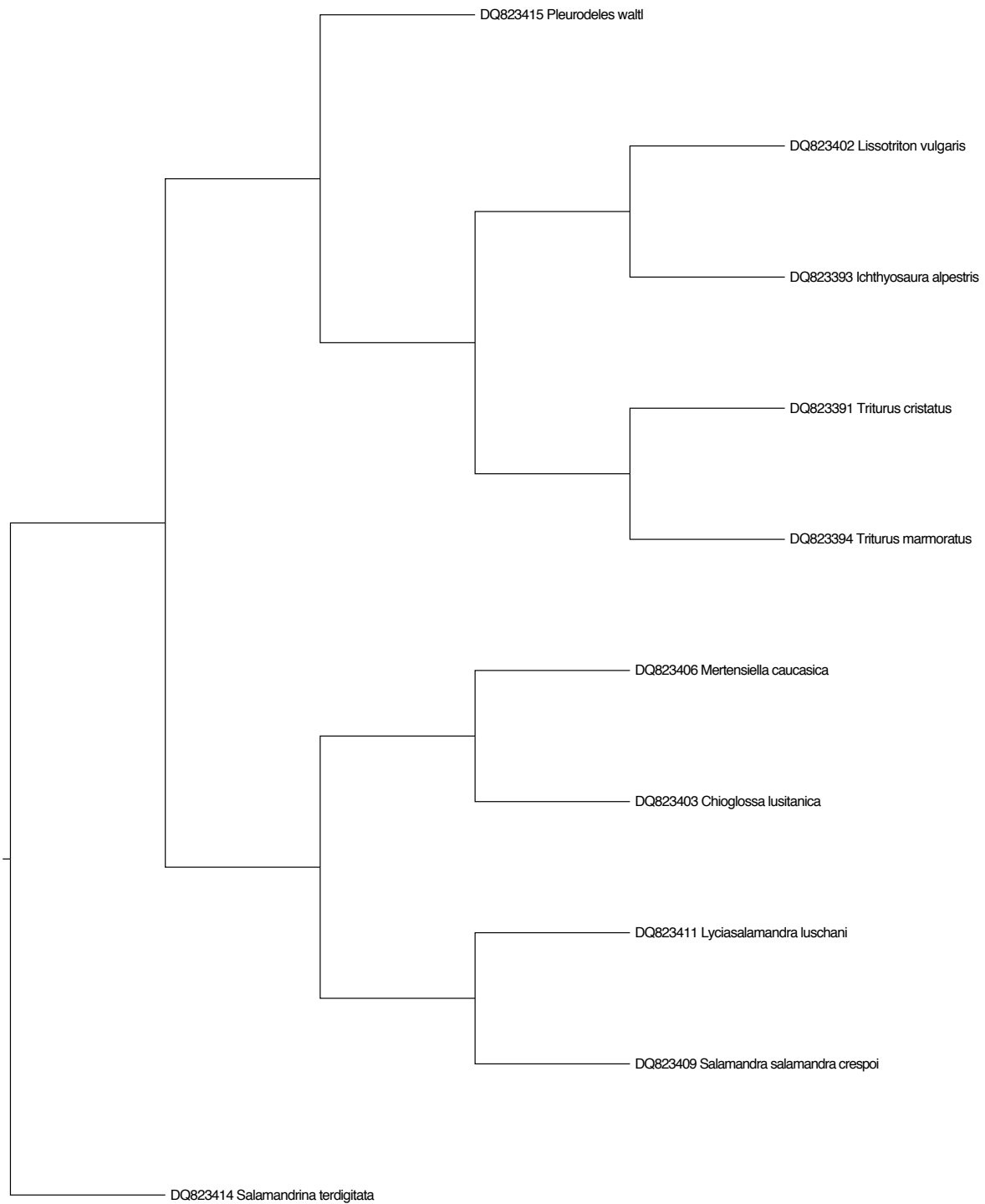


Figure B. Phylogeny of Salamandridae used in the Multidivtime analyses. See text for details.