## **Science** Advances

AAAS

advances.sciencemag.org/cgi/content/full/4/5/eaao5017/DC1

## Supplementary Materials for

## Multiple origins of green blood in New Guinea lizards

Zachary B. Rodriguez, Susan L. Perkins, Christopher C. Austin

Published 16 May 2018, *Sci. Adv.* **4**, eaao5017 (2018) DOI: 10.1126/sciadv.aao5017

## This PDF file includes:

- fig. S1. ML tree for ONE-i100.
- fig. S2. Species tree for ONE-i100.
- fig. S3. ML tree for ONE-p70.
- fig. S4. Species tree for ONE-p70.
- fig. S5. ML tree for TWO-i100.
- fig. S6. Species tree for TWO-i100.
- fig. S7. Species tree for TWO-p70 data set.
- table S1. Sampling information and data processing results.
- table S2. SH test results from the SH tests for monophyly of *Prasinohaema*.
- table S3. Partial and full monophyly of *Prasinohaema*.
- table S4. Model test results for the ONE-p70 and TWO-p70 data sets.
- table S5. Results from marginal ancestral state reconstructions and stochastic character mapping using the ONE and TWO data set as input.
- table S6. Results from stochastic mapping across gene trees and posterior trees.



**fig. S1. ML tree for ONE-i100.** Maximum likelihood tree was estimated from the 100 most parsimonious informative loci from the "ONE" data set by performing unpartitioned concatenated analysis in RAxML with 20 searches for the best tree and the GTR GAMMA model of nucleotide substitution. Black circles indicate internal nodes with 100% bootstrap support. Internal nodes with bootstrap values less than 100 are shown in white circles.



**fig. S2. Species tree for ONE-i100.** A species tree was inferred from the 100 most parsimonious informative loci from the ONE data set using a summary coalescent approach. Individual gene trees were estimated in RAxML. Next, 100 multilocus bootstraps were generated by sampling loci with replacement and performing nonparametric bootstrapping by sites of each locus. The resampled data sets were used to infer species tree in ASTRAL-II. Black circles indicate internal nodes with 100% bootstrap support. Internal nodes with bootstrap values less than 100 are shown in white circles.



**fig. S3. ML tree for ONE-p70.** Maximum likelihood tree was estimated from a 70% complete sequence matrix from the "ONE" data set by performing unpartitioned concatenated analysis in RAxML with 20 searches for the best tree and the GTR GAMMA model of nucleotide substitution. Black circles indicate internal nodes with 100% bootstrap support.



**fig. S4. Species tree for ONE-p70.** A species tree was inferred from a 70% complete sequence matrix from the ONE data set using a summary coalescent approach. Individual gene trees were estimated in RAxML. Next, 100 multilocus bootstraps were generated by sampling loci with replacement and performing nonparametric bootstrapping by sites of each locus. The resampled data sets were used to infer species tree in ASTRAL-II. Black circles indicate internal nodes with 100% bootstrap support. Internal nodes with bootstrap values less than 100 are shown in white circles.



**fig. S5. ML tree for TWO-i100.** Maximum likelihood tree was estimated from the 100 most parsimonious informative loci from the "TWO" data set by performing unpartitioned concatenated analysis in RAxML with 20 searches for the best tree and the GTR GAMMA model of nucleotide substitution. Black circles indicate internal nodes with 100% bootstrap support. Internal nodes with bootstrap values less than 100 are shown in white circles.



**fig. S6. Species tree for TWO-i100.** A species tree was inferred from 100 most parsimonious informative loci from the ONE data set using a summary coalescent approach. Individual gene trees were estimated in RAxML. Next, 100 multilocus bootstraps were generated by sampling loci with replacement and performing nonparametric bootstrapping by sites of each locus. The resampled data sets were used to infer species tree in ASTRAL-II. Black circles indicate internal nodes with 100% bootstrap support. Internal nodes with bootstrap values less than 100 are shown in white circles.



**fig. S7. Species tree for TWO-p70 data set.** Unpartitioned concatenated analyses and summary coalescent approaches show highly concordant relationships. Maximum likelihood trees were estimated in RAxML with 20 searches for the best tree and the GTR GAMMA model of nucleotide substitution. For the summary coalescent approach, individual gene trees were first estimated in RAxML. Next, 100 multilocus bootstraps were generated by sampling loci with replacement and performing nonparametric bootstrapping by sites of each locus. The resampled data sets were used to infer species tree in ASTRAL-II. Black circles indicate internal nodes with 100% bootstrap support for both analyses and internal nodes with bootstrap values less than 100 are shown in white circles (support for species tree on the left and concatenated RAxML on the right).

table S1. Sampling information and data processing results. All institution codes follow Sabaj M.H. 2016. Standard symbolic codes for institutional resource collections in herpetology and ichthyology: an Online Reference. Version 6.5 (16 August 2016). Electronically accessible at http://www.asih.org/, American Society of Ichthyologists and Herpetologists, Washington, DC.

Genus	Species	Voucher Number	Field Number	Country	No. cleaned reads	No. of UCE contigs	Average UCE length (bp)
Emoia	obscura	LSUMZ 98711	CCA 17259	Papua New Guinea	4,598,611	2,584	400
Eugongylus	albofasciolatus	LSUMZ 93632	CCA 02575	Papua New Guinea	13,625,188	4,176	1,045
Eugongylus	rufescens	LSUMZ 94256	CCA 04766	Papua New Guinea	22,471,656	3,909	1,125
Eugongylus	rufescens	LSUMZ 98638	CCA 17074	Papua New Guinea	12,656,885	4,072	1,122
Fojia	bumui	LSUMZ 98355	CCA 15812	Papua New Guinea	5,334,894	3,475	464
Fojia	bumui	LSUMZ 98364	CCA 15922	Papua New Guinea	5,848,684	3,733	592
Insulasaurus	arborens	KU	RMB 306	Philippines	2,895,278	1,753	647
Insulasaurus	arborens	TNHC 62465	RMB 3306	Philippines	9,819,743	3,583	1,042
Lipinia	albodorsale	LSUMZ 92018	CCA 03500	Papua New Guinea	2,893,570	2,192	357
Lipinia	inexpectata	ZRC	ID 7190	Malaysia	4,148,732	1,898	316
Lipinia	infralineolata	TNHC 59519	JAM 2291	Indonesia	8,111,621	4,011	628
Lipinia	leptosoma	CAS 248067	FS 230287	Palau (Republic of)	2,919,004	3,529	571
Lipinia	leptosoma	SAMA R47992	CCA 01349	Palau (Republic of)	2,523,009	2,757	389
Lipinia	longiceps	LSUMZ 98389	CCA 15866	Papua New Guinea	3,599,113	3,208	428
Lipinia	longiceps	THNM 51284	CCA 00452	Papua New Guinea	33,643,353	2,949	1,013
Lipinia	longiceps	THNM 51285	CCA 00483	Papua New Guinea	381,344	935	286
Lipinia	noctua	CAS 248878	FS 230869	Palau (Republic of)	1,617,582	554	318
Lipinia	noctua	LSUMZ 93980	CCA 01554	Papua New Guinea	3,024,403	1,682	377
Lipinia	noctua	LSUMZ 94094	CCA 01618	Papua New Guinea	4,377,671	2,769	500
Lipinia	noctua	LSUMZ 94103	CCA 02074	Papua New Guinea	12,354,224	3,940	914
Lipinia	noctua	LSUMZ 94105	CCA 02111	Papua New Guinea	4,418,386	3,043	472
Lipinia	noctua	LSUMZ 94433	CCA 04648	Papua New Guinea	4,071,929	3,249	430
Lipinia	noctua	LSUMZ 94435	CCA 05566	Papua New Guinea	1,253,271	285	285
Lipinia	noctua	LSUMZ 96954	CCA 16818	Papua New Guinea	2,403,783	463	297
Lipinia	noctua	LSUMZ 96955	CCA 16819	Papua New Guinea	9,989,037	3,906	617
Lipinia	pulchella	TNHC 55036	JAM 735	Philippines	50,434,940	4,095	1,178
Lipinia	pulchella	TNHC 56378	RMB 1078	Philippines	7,272,864	3,312	438
Lipinia	pulchella	TNHC 56379	RMB 1079	Philippines	2,199,007	823	312
Lipinia	pulchra	LSUMZ 92277	CCA 03201	Papua New Guinea	5,873,260	2,675	414
Lipinia	pulchra	LSUMZ 92283	CCA 03518	Papua New Guinea	9,835,002	3,976	996
Lipinia	pulchra	LSUMZ 94102	CCA 02526	Papua New Guinea	2,780,663	1,041	327
Lipinia	quadrivittata	SAMA R48633	CCA 01269	Philippines	3,152,114	2,497	474
Lipinia	rouxi	THNM 51429	CCA 00692	Papua New Guinea	20,340,489	3,934	1,196
Lipinia	rouxi	THNM 51432	CCA 00708	Papua New Guinea	3,399,524	3,545	903
Lipinia	rouxi	THNM 51437	CCA 00715	Papua New Guinea	6,385,611	1,639	503
Lipinia	sp.	SAMA R57046	JCUNQ 2404	Papua New Guinea	4,482,059	3,482	491
Lipinia	vittigera	CAS 229605	JBS 19651	Myanmar	6,546,005	3,323	477
Lipinia	vittigera	CAS 243723	MHS 28158	Myanmar	6,931,390	2,574	362
Lipinia	vittigera	DSM 1404L	KU 328481	Indonesia	2,044,101	762	313
Lipinia	vittigera	FMNH 261861	HKV 64673	Cambodia	3,686,400	804	304
Lipinia	vittigera	ZRC 2.4677	-	Bhutan	5,865,272	1,201	326
Lobulia	alpina	SAM 12594	-	Papua New Guinea	9,305,563	3,840	1,064

Lobulia	brongersmai	LSUMZ 92260	CCA 03073	Papua New Guinea	7,052,356	3,261	702
Lobulia	brongersmai	LSUMZ 92264	CCA 03482	Papua New Guinea	5,492,468	3,831	485
Lobulia	brongersmai	PNGNMAG	CCA 01784	Papua New Guinea	2,642,618	3,299	458
Lobulia	elegans	LSUMZ 93986	CCA 01639	Papua New Guinea	5,601,454	2,422	372
Lobulia	elegans	LSUMZ 98702	CCA 17485	Papua New Guinea	3,974,026	2,691	380
Lobulia	elegans	PNGNMAG	CCA 01789	Papua New Guinea	4,202,842	2,279	441
Lygosoma	sp.	KU	ACD 7390	Philippines	16,199,602	3,876	1,200
Lygosoma	sp.	KU	ACD 7391	Philippines	9,824,952	4,013	1,111
Lygosoma	sp.	KU	ACD 7392	Philippines	18,782,309	4,038	1,258
Papuascincus	sp. nov.	LSUMZ 95112	CCA 05980	Papua New Guinea	7,104,282	3,654	882
Papuascincus	stanleyanus	LSUMZ 93741	CCA 01636	Papua New Guinea	2,113,773	3,313	453
Papuascincus	stanleyanus	LSUMZ 93746	CCA 02482	Papua New Guinea	3,103,738	3,783	504
Papuascincus	stanleyanus	LSUMZ 93747	CCA 02483	Papua New Guinea	3,369,715	2,225	348
Papuascincus	stanleyanus	LSUMZ 93749	CCA 02485	Papua New Guinea	17,335,489	3,301	435
Papuascincus	stanleyanus	LSUMZ 93754	CCA 02542	Papua New Guinea	3,226,482	2,370	413
Papuascincus	stanleyanus	LSUMZ 98684	CCA 17235	Papua New Guinea	3,416,612	1,162	330
Papuascincus	stanleyanus	LSUMZ 98685	CCA 17489	Papua New Guinea	2,817,250	2,082	329
Papuascincus	stanleyanus	PNGNMAG	CCA 01787	Papua New Guinea	5,080,825	3,191	441
Papuascincus	stanleyanus	THNM 51351	CCA 00795	Papua New Guinea	5,338,734	3,703	634
Papuascincus	stanleyanus	THNM 51352	CCA 00799	Papua New Guinea	3,428,954	3,099	440
Prasinohaema	flavipes	LSUMZ 93719	CCA 01658	Papua New Guinea	2,752,292	2,699	374
Prasinohaema	flavipes	LSUMZ 98629	CCA 17083	Papua New Guinea	3,477,740	3,364	512
Prasinohaema	flavipes	LSUMZ 98637	CCA 17482	Papua New Guinea	3,096,405	1,049	326
Prasinohaema	prehensicauda	LSUMZ 93691	CCA 01684	Papua New Guinea	6,310,448	2,574	473
Prasinohaema	prehensicauda	LSUMZ 98647	CCA 17143	Papua New Guinea	6,017,648	3,475	936
Prasinohaema	prehensicauda	LSUMZ 98658	CCA 17222	Papua New Guinea	10,312,650	3,849	1,057
Prasinohaema	prehensicauda	LSUMZ 98660	CCA 17245	Papua New Guinea	4,712,608	3,394	542
Prasinohaema	prehensicauda	LSUMZ 98937	CCA 17244	Papua New Guinea	6,294,482	3,693	573
Prasinohaema	prehensicauda	PNGNMAG	CCA 01788	Papua New Guinea	11,856,117	3,213	706
Prasinohaema	semoni	LSUMZ 94437	CCA 04475	Papua New Guinea	4,081,238	2,908	383
Prasinohaema	semoni	THNM 51281	CCA 00481	Papua New Guinea	14,896,847	2,315	732
Prasinohaema	semoni	THNM 51532	CCA 00899	Papua New Guinea	8,030,456	1,118	637
Prasinohaema	semoni	THNM 51533	CCA 00900	Papua New Guinea	57,525,450	4,031	1,317
Prasinohaema	sp. nov.	LSUMZ 87781	CCA 01623	Papua New Guinea	4,374,208	2,813	383
Prasinohaema	sp. nov.	SAMA	U15	Papua New Guinea	5,283,969	2,315	355
Prasinohaema	sp. nov.	SAMA	W25	Papua New Guinea	8,126,474	2,380	316
Prasinohaema	sp. nov.	THNM 53464	CCA 01005	Papua New Guinea	19,888,897	3,889	900
Prasinohaema	virens	LSUMZ 92258	CCA 03105	Papua New Guinea	2,412,663	576	306
Prasinohaema	virens	LSUMZ 93644	CCA 02265	Papua New Guinea	5,711,291	486	291
Prasinohaema	virens	LSUMZ 93647	CCA 02347	Papua New Guinea	5,757,549	2,703	395
Prasinohaema	virens	LSUMZ 93654	CCA 02503	Papua New Guinea	2,914,553	281	283
Prasinohaema	virens	LSUMZ 93656	CCA 02661	Papua New Guinea	3,504,326	3,655	504
Prasinohaema	virens	LSUMZ 94105	CCA 02234	Papua New Guinea	2,835,274	2,330	445
Prasinohaema	virens	LSUMZ 94487	CCA 15387	Papua New Guinea	6,272,070	2,987	583
Prasinohaema	virens	LSUMZ 97808	CCA 15615	Papua New Guinea	615,711	96	286

Prasinohaema	virens	THNM 51507	CCA 00859	Papua New Guinea	3,040,181	3,119	498
Prasinohaema	virens	THNM 51508	CCA 00860	Papua New Guinea	3,477,862	2,643	447
Scincella	lateralis	LSUMZ 99203	CCA 17499	USA	2,712,540	934	325
Scincella	lateralis	LSUMZ 99209	CCA 21483	USA	302,468	2,049	363
Scincella	lateralis	LSUMZ 99210	CCA 21484	USA	404,182	672	293
Scincella	potanini	CAS 214905	JBS 16021	China	13,161,225	3,721	1,094
Scincella	potanini	CAS 242132	GLGS 3384	China	4,601,790	3,835	551
Scincella	punctatolineata	CAS 221870	JBS 8047	Myanmar	15,121,680	3,912	1,201
Scincella	punctatolineata	CAS 234733	JBS 24553	Myanmar	2,070,513	3,309	436
Scincella	reevesi	CAS 214133	JBS 4241	Myanmar	3,884,971	3,886	516
Scincella	reevesi	CAS 216298	JBS 7105	Myanmar	3,098,088	483	301
Scincella	rufocaudata	FMNH 263355	HKV 33072	Cambodia	1,874,839	3,255	435
Scincella	rufocaudata	FMNH 263356	HKV 33088	Cambodia	3,058,103	3,559	608
Scincella	sikkimensis	CAS177478	RM 8379	China	2,266,337	970	298
Scincella	victoriana	CAS 220628	JBS 8014	Myanmar	7,883,350	3,763	580
Scincella	victoriana	CAS 240154	JBS 21858	Myanmar	2,559,214	712	310
Sphenomorphus	concinnatus	LSUMZ 93701	CCA 02720	Papua New Guinea	27,040,215	3,882	1,218
Sphenomorphus	darlingtoni	LSUMZ 93394	CCA 02541	Papua New Guinea	2,707,732	3,423	466
Sphenomorphus	forbesi	LSUMZ 93407	CCA 04800	Papua New Guinea	1,852,569	496	302
Sphenomorphus	granulatus	LSUMZ 97803	CCA 15482	Papua New Guinea	2,288,882	548	299
Sphenomorphus	jobiense	LSUMZ 98764	CCA 17224	Papua New Guinea	7,337,254	3,858	1,078
Sphenomorphus	jobiense	LSUMZ 98765	CCA 17225	Papua New Guinea	12,081,209	4,125	1,155
Sphenomorphus	leptofasciatus	LSUMZ 98749	CCA 17101	Papua New Guinea	119,426,985	4,241	1,396
Sphenomorphus	mulleri	LSUMZ 94461	CCA 05888	Papua New Guinea	9,409,597	3,535	1,041
Sphenomorphus	nigrolineatus	LSUMZ 94671	CCA 05422	Papua New Guinea	14,877,687	3,855	1,222
Sphenomorphus	pratti	LSUMZ 91881	CCA 03288	Papua New Guinea	4,081,719	3,052	415
Sphenomorphus	simus	LSUMZ 94619	CCA 05749	Papua New Guinea	670,003	123	282
Sphenomorphus	solomonis	LSUMZ 93431	CCA 02659	Papua New Guinea	4,409,768	2,605	389
Sphenomorphus	sp.	LSUMZ 94140	CCA 02640	Papua New Guinea	60,343,429	4,097	1,085
Tropidophorus	berdmorei	CAS 204900	JBS 1150	Myanmar	2,881,225	306	289
Tropidophorus	cocincinensis	FMNH 258754	HKV 63793	Laos	3,102,574	1,717	364
Tropidophorus	robinsoni	CAS 228558	JBS 15922	Myanmar	3,319,029	3,453	495

**table S2. SH test results from the SH tests for monophyly of** *Prasinohaema*. Tests were performed on the ONE and TWO concatenated data sets in RAxML. For each test, the best maximum likelihood estimate tree was compared to the best tree with a constrained topology using 20 searches for the best tree. All trees that constrained *Prasinohaema* to be monophyletic were significantly worse than any unconstrained topology at the 5%, 2% and 1% intervals.

Data set	Likelihood	D(LH)	SD	Sigr	nificantly W	orse
ONE-i100	-134389.1779	-308.503314	37.899959	Yes (5%)	Yes (2%)	Yes (1%)
ONE-i250	-362505.45	-850.733672	64.164921	Yes (5%)	Yes (2%)	Yes (1%)
ONE-i500	-723520.0991	-1815.53703	94.103811	Yes (5%)	Yes (2%)	Yes (1%)
ONE-i750	-1053469.387	-2784.121336	116.614108	Yes (5%)	Yes (2%)	Yes (1%)
ONE-p50	-5360055.024	-13932.18534	266.395891	Yes (5%)	Yes (2%)	Yes (1%)
ONE-p60	-5096029.524	-13589.69216	262.925118	Yes (5%)	Yes (2%)	Yes (1%)
ONE-p70	-4222920.33	-11575.99492	243.195332	Yes (5%)	Yes (2%)	Yes (1%)
ONE-p80	-2591828.913	-7171.189922	193.180006	Yes (5%)	Yes (2%)	Yes (1%)
TWO-i100	-171079.8313	-524.351471	52.490455	Yes (5%)	Yes (2%)	Yes (1%)
TWO-i250	-383988.2156	-1240.633917	78.837606	Yes (5%)	Yes (2%)	Yes (1%)
TWO-i500	-751806.035	-2463.986577	110.538604	Yes (5%)	Yes (2%)	Yes (1%)
TWO-i750	-1090463.88	-3638.180898	135.366651	Yes (5%)	Yes (2%)	Yes (1%)
TWO-p50	-5295336.998	-16563.54494	292.057112	Yes (5%)	Yes (2%)	Yes (1%)
TWO-p60	-4960403.411	-15755.90509	284.709641	Yes (5%)	Yes (2%)	Yes (1%)
TWO-p70	-3921918.587	-12684.61291	254.915164	Yes (5%)	Yes (2%)	Yes (1%)
TWO-p80	-1795286.542	-5786.942382	173.071221	Yes (5%)	Yes (2%)	Yes (1%)

table S3. Partial and full monophyly of *Prasinohaema*. To test for partial monophyly of *Prasinohaema*, we iterated over all individually estimated gene trees for each data set listed using the is.monophyletic function in the R package ape. Numbers represent decimal percent of gene trees that support monophyly of 18 aberrant relationships within *Prasinohaema*. Fewer than 30 trees (<0.1%) supported full *Prasinohaema*monophyly, which were visually confirmed to be the result of large multifurcations or the exclusion of red-blooded taxa. Lower-case letters represent five *Prasinohaema* species: P. flavipes (p), P. sp. nov. (n), P. prehensicauda (p), P. semoni (s), P. virens (v).

Data set	f+v	p+v	p+n	f+n	f+p+n	f+p+v	v+n	S+V	s+v+n	p+v+n	f+v+n	s+n	f+s	p+s	f+p+s	f+p+s+n	s+f+p+v	f+p+s+v+n
ONE-i100	0.0	0.0	0.0	0.0	0.0	0.0	5.0	5.0	0.0	0.0	2.0	1.0	0.0	1.0	2.0	0.0	0.0	0.0
ONE-i250	1.2	1.6	0.0	0.0	0.0	0.0	2.4	3.2	0.0	0.0	0.8	0.8	1.6	1.6	3.2	0.0	0.0	0.0
ONE-i500	1.0	0.6	0.2	0.8	0.4	0.2	4.2	2.4	0.2	0.2	1.4	0.8	1.6	2.4	2.4	0.0	0.2	0.0
ONE-i750	0.8	0.7	0.1	0.5	0.4	0.0	5.2	2.4	0.4	0.1	1.2	0.9	2.1	3.1	2.9	0.0	0.1	0.0
ONE-p50	0.9	1.2	0.6	0.7	0.3	0.8	6.1	2.6	0.3	0.0	1.0	1.5	2.5	2.1	2.2	0.0	0.1	0.0
ONE-p60	0.9	1.1	0.7	0.7	0.5	0.7	6.2	2.7	0.4	0.0	1.1	1.5	2.1	2.5	2.3	0.0	0.1	0.0
ONE-p70	0.7	1.1	0.6	0.6	0.5	0.5	7.1	2.9	0.4	0.1	1.3	1.9	2.2	2.3	2.4	0.0	0.0	0.0
ONE-p80	0.7	0.9	0.8	0.6	0.8	0.5	8.3	2.9	0.2	0.2	1.2	1.9	1.9	2.3	2.3	0.0	0.1	0.1
TWO-i100	0.0	1.0	1.0	0.0	0.0	0.0	4.0	1.0	0.0	1.0	1.0	3.0	0.0	1.0	3.0	0.0	0.0	0.0
TWO-i250	0.0	0.4	0.4	0.4	0.8	0.4	5.2	1.2	0.4	0.4	0.8	2.0	1.2	1.6	2.8	0.0	0.0	0.0
TWO-i500	0.2	0.4	0.6	0.6	0.4	0.4	6.4	1.4	0.2	0.2	0.4	1.4	0.8	1.8	3.2	0.0	0.0	0.0
TWO-i750	0.3	0.7	0.5	0.3	0.4	0.5	5.5	1.5	0.1	0.1	0.3	1.3	1.3	1.9	2.7	0.0	0.0	0.0
TWO-p50	0.6	0.7	0.6	0.3	0.5	0.5	5.1	2.1	0.1	0.1	0.3	1.2	1.2	1.5	1.6	0.0	0.0	0.0
TWO-p60	0.5	0.7	0.6	0.3	0.5	0.6	5.6	1.9	0.1	0.1	0.3	1.2	1.2	1.6	1.5	0.0	0.1	0.0
TWO-p70	0.6	0.7	0.7	0.3	0.5	0.6	5.7	1.6	0.1	0.1	0.3	1.5	1.1	1.5	1.7	0.0	0.0	0.0
TWO-p80	0.4	0.5	0.6	0.2	0.7	0.5	6.7	1.2	0.1	0.1	0.5	1.7	0.9	1.5	1.4	0.0	0.1	0.1

**table S4. Model test results for the ONE-p70 and TWO-p70 data sets.** Comparison of model tests among three transition rate models (ARD, ER, and IR) on our ONE-p70 and TWO-p70 data sets. The weighted AIC scores (AICw) were used to determine number (out of 1000) of simulations to perform under each model for the "MIXED" model. Results for each model also include the forward (qRG) and reverse (qGR) rates, the likelihood score (lnL), the corrected AIC scores (AICc), and the number of estimated parameters (k). Transition rate matrices and alignments are described in the main text.

Alignment	Model	qrg	qgr	lnL	AICc	AICw	Nsim	k	p-value
	ARD	10.6	140.5	-14.4	33.0	0.255	255	2	1.00
ONE-p70	ER	12.3	12.3	-15.0	32.2	0.394	394	1	0.25
	IR	11.4	0.0	-15.1	32.4	0.351	351	1	0.21
	ARD	7.9	124.5	-15.6	35.3	0.176	176	2	1.00
TWO-p70	ER	10.9	10.9	-15.8	33.6	0.417	417	1	0.52
	IR	10.5	0.0	-15.8	33.7	0.407	407	1	0.50

table S5. Results from marginal ancestral state reconstructions and stochastic character mapping using the ONE and TWO data set as input. Model fitting results include the forward (qRG) and reverse (qGR) rates, standated error for the estimated rates (SE), the Akaike information criteria score (AIC), the weighted AIC scores (wAIC), and the likelihood scores (lnL). During stochastic character mapping, the transition rate matrix was either fixed at its maximum likelihood estimate for all simulations (Q = fixed), or a new transistion rate matrix was sampled by bayesian mcmc for each simulation (Q = mcmc). Results from the stochastic character include the number (average, minimum, maximum) and type (forward, reverse) of transitions between green and red blood for New Guinea lizards estimated from 1000 stochastic mappings. Alignments and models used are described in the main text.

Alignment Model			Par	ameters for	· Ancestral	State I	Reconstr	uction		Number of Transitions (Q = Fixed)			Number of Transitions (Q = MCMC)		
Alignment	Niodei	qrg	qgr	SE(qrg)	SE(q <sub>GR</sub> )	AIC	dAIC	wAIC	ln(L)	mean (min - max)	gains	reversals	mean (min - max)	gains	reversals
	ARD	6.2	88.6	5.5	27.4	32.2	0.0	0.406	-14.1	12.146 (4 - 28)	3.1	9.1	4.057 (4 - 8)	4.0	0.1
ONE-i100	ER	7.6	7.6	2.9	2.9	32.7	0.5	0.317	-15.3	4.581 (4 - 12)	4.2	0.4	4.144 (4 - 8)	4.0	0.2
	IR	7.1	0.0	2.5	0.0	32.9	0.8	0.277	-15.5	4.03 (4 - 6)	4.0	0.0	4.015 (4 - 6)	4.0	0.0
	ARD	7.2	86.1	6.3	28.5	32.4	0.0	0.355	-14.2	13.243 (4 - 33)	4.0	9.3	4.057 (4 - 8)	4.0	0.1
ONE-i250	ER	7.2	7.2	2.8	2.8	32.5	0.1	0.341	-15.3	4.661 (4 - 10)	4.2	0.4	4.175 (4 - 8)	4.0	0.2
	IR	6.6	0.0	2.4	0.0	32.8	0.3	0.303	-15.4	4.027 (4 - 6)	4.0	0.0	4.017 (4 - 5)	4.0	0.0
	ARD	6.7	86.7	6.0	28.1	32.1	0.0	0.412	-14.1	12.482 (4 - 27)	3.6	8.9	4.052 (4 - 8)	4.0	0.1
ONE-i500	ER	7.4	7.4	2.9	2.9	32.6	0.5	0.316	-15.3	4.724 (4 - 10)	4.3	0.5	4.197 (4 - 10)	4.0	0.2
	IR	6.7	0.0	2.4	0.0	32.9	0.8	0.272	-15.5	4.036 (4 - 5)	4.0	0.0	4.017 (4 - 5)	4.0	0.0
	ARD	7.2	93.8	6.4	30.3	32.1	0.0	0.434	-14.0	12.661 (4 - 30)	3.6	9.0	4.057 (4 - 9)	4.0	0.1
ONE-i750	ER	7.9	7.9	3.1	3.1	32.8	0.7	0.306	-15.4	4.71 (4 - 10)	4.2	0.5	4.175 (4 - 9)	4.0	0.2
	IR	7.2	0.0	2.6	0.0	33.1	1.0	0.260	-15.6	4.036 (4 - 6)	4.0	0.0	4.011 (4 - 5)	4.0	0.0
	ARD	11.6	134.0	10.2	45.4	32.2	0.0	0.376	-14.1	12.885 (4 - 31)	4.0	8.9	4.031 (4 - 7)	4.0	0.1
ONE-p50	ER	11.6	11.6	4.5	4.5	32.5	0.2	0.337	-15.2	4.813 (4 - 13)	4.3	0.5	4.062 (4 - 8)	3.9	0.1
	IR	10.5	0.0	3.7	0.0	32.8	0.5	0.287	-15.4	4.033 (4 - 5)	4.0	0.0	4.01 (4 - 5)	4.0	0.0
	ARD	11.6	134.7	10.2	45.4	32.2	0.0	0.381	-14.1	12.796 (4 - 29)	3.9	8.9	4.029 (4 - 6)	4.0	0.0
ONE-p60	ER	11.6	11.6	4.5	4.5	32.5	0.3	0.335	-15.2	4.683 (4 - 12)	4.2	0.5	4.092 (4 - 8)	4.0	0.1
	IR	10.5	0.0	3.7	0.0	32.8	0.6	0.285	-15.4	4.029 (4 - 6)	4.0	0.0	4.014 (4 - 5)	4.0	0.0
	ARD	11.7	137.2	10.3	45.8	32.2	0.0	0.386	-14.1	12.919 (4 - 30)	4.0	9.0	4.027 (4 - 6)	4.0	0.0
ONE-p70	ER	11.8	11.8	4.6	4.6	32.5	0.3	0.332	-15.3	4.681 (4 - 10)	4.2	0.5	4.078 (4 - 7)	4.0	0.1
	IR	10.6	0.0	3.8	0.0	32.8	0.6	0.282	-15.4	4.039 (4 - 6)	4.0	0.0	4.009 (4 - 5)	4.0	0.0
	ARD	11.9	151.8	10.7	48.7	32.1	0.0	0.428	-14.1	12.564 (4 - 29)	3.6	8.9	4.05 (4 - 7)	4.0	0.0
ONE-p80	ER	12.9	12.9	5.0	5.0	32.8	0.6	0.312	-15.4	4.704 (4 - 12)	4.2	0.5	4.078 (4 - 7)	3.9	0.1
	IR	11.5	0.0	4.1	0.0	33.1	1.0	0.260	-15.6	4.032 (4 - 6)	4.0	0.0	4.008 (4 - 5)	4.0	0.0
TWO ;100	ARD	4.0	74.0	3.3	21.2	32.2	0.0	0.519	-14.1	11.666 (4 - 27)	2.5	9.2	4.059 (4 - 7)	4.0	0.1
1 WO-1100	ER	6.1	6.1	2.3	2.3	33.6	1.4	0.257	-15.8	4.601 (4 - 12)	4.1	0.5	4.146 (4 - 8)	4.0	0.2

	IR	5.6	0.0	2.0	0.0	33.8	1.7	0.224	-15.9	4.018 (4 - 6)	4.0	0.0	4.005 (4 - 5)	4.0	0.0
	ARD	5.0	87.0	4.2	25.7	32.9	0.0	0.449	-14.4	11.637 (4 - 28)	2.5	9.1	4.045 (4 - 6)	4.0	0.1
TWO-i250	ER	7.5	7.5	2.9	2.9	33.7	0.8	0.294	-15.9	4.657 (4 - 11)	4.2	0.5	4.135 (4 - 8)	4.0	0.2
	IR	6.9	0.0	2.4	0.0	34.0	1.1	0.257	-16.0	4.02 (4 - 5)	4.0	0.0	4.018 (4 - 5)	4.0	0.0
	ARD	5.3	86.7	4.5	26.1	33.3	0.0	0.376	-14.7	11.817 (4 - 30)	2.6	9.2	4.054 (4 - 7)	4.0	0.1
TWO-i500	ER	7.7	7.7	3.0	3.0	33.6	0.3	0.329	-15.8	4.629 (4 - 10)	4.2	0.4	4.152 (4 - 9)	4.0	0.2
	IR	7.1	0.0	2.5	0.0	33.8	0.5	0.295	-15.9	4.035 (4 - 6)	4.0	0.0	4.014 (4 - 5)	4.0	0.0
	ARD	5.4	88.0	4.6	26.8	33.3	0.0	0.368	-14.6	11.547 (4 - 28)	2.6	8.9	4.032 (4 - 6)	4.0	0.1
TWO-i750	ER	7.9	7.9	3.0	3.0	33.5	0.2	0.331	-15.7	4.606 (4 - 10)	4.2	0.5	4.146 (4 - 8)	4.0	0.2
	IR	7.3	0.0	2.6	0.0	33.7	0.4	0.301	-15.8	4.024 (4 - 5)	4.0	0.0	4.014 (4 - 5)	4.0	0.0
	ARD	8.0	123.3	7.1	39.2	33.7	0.3	0.313	-14.9	11.161 (4 - 28)	2.8	8.3	4.029 (4 - 6)	4.0	0.0
TWO-p50	ER	11.1	11.1	4.3	4.3	33.4	0.0	0.357	-15.7	4.518 (4 - 9)	4.1	0.4	4.091 (4 - 8)	4.0	0.1
	IR	10.4	0.0	3.7	0.0	33.6	0.2	0.329	-15.8	4.024 (4 - 5)	4.0	0.0	4.01 (4 - 5)	4.0	0.0
	ARD	8.0	124.1	7.0	39.3	33.7	0.2	0.317	-14.8	11.052 (4 - 24)	2.8	8.3	4.021 (4 - 6)	4.0	0.0
TWO-p60	ER	11.2	11.2	4.3	4.3	33.5	0.0	0.355	-15.7	4.566 (4 - 9)	4.2	0.4	4.067 (4 - 8)	3.9	0.1
	IR	10.4	0.0	3.7	0.0	33.6	0.2	0.327	-15.8	4.029 (4 - 6)	4.0	0.0	4.01 (4 - 5)	4.0	0.0
	ARD	8.1	126.5	7.0	39.5	33.6	0.1	0.326	-14.8	11.236 (4 - 29)	2.8	8.4	4.028 (4 - 7)	4.0	0.0
TWO-p70	ER	11.2	11.2	4.3	4.3	33.5	0.0	0.351	-15.7	4.644 (4 - 11)	4.2	0.4	4.08 (4 - 7)	4.0	0.1
	IR	10.5	0.0	3.7	0.0	33.7	0.2	0.323	-15.8	4.024 (4 - 6)	4.0	0.0	4.017 (4 - 5)	4.0	0.0
	ARD	8.6	147.3	7.3	44.6	33.4	0.0	0.389	-14.7	11.686 (4 - 26)	2.6	9.1	4.02 (4 - 6)	4.0	0.0
TWO-p80	ER	12.9	12.9	5.0	5.0	33.7	0.4	0.322	-15.9	4.675 (4 - 11)	4.2	0.5	4.055 (4 - 6)	3.9	0.1
	IR	11.9	0.0	4.2	0.0	33.9	0.6	0.290	-16.0	4.027 (4 - 6)	4.0	0.0	4.005 (4 - 5)	4.0	0.0

**table S6. Results from stochastic mapping across gene trees and posterior trees.** Random samples of 1000 trees from either the set of gene trees (GT) or posterior probability (PP) trees were taken and one character map was simulated for each tree. GTs were individually estimated in RAxML and PP trees were obtained in exabayes using the concatenated data set. As there are different topologies among trees within a set, results cannot be reconciled onto a single topology. Mean (minimum - maximum) number of transitions are shown.

ONE-p70	<b>Total No. Transitions</b>	R→G	R←G
Gene Trees	4.26 (1 - 10)	3.59 (1 - 7)	0.67 (0 - 9)
Posterior Probability Trees	4.03 (4 - 6)	4.00 (3 - 5)	0.03 (0 - 1)