**Molecular phylogenetics reveals contrasting evolutionary trajectories in Trinidadian worm lizards (Amphisbaena)**
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**Table S1.** Table with *Amphisbaena alba* and *A. fuliginosa* specimens used in this study with data on vouchers, countries of origin, localities and the gene fragments.

| Species | Voucher | Country | Locality | 12S | 16S | nd2 | rag1 | c-mos | bdnf |
|---|---|---|---|---|---|---|---|---|---|
| *A. alba* | MZUSP 88618 | Brazil | Manso, MT | - | FJ441697 | FJ441940 | FJ441817 | FJ441757 | FJ441880 |
| *A. alba* | JC 795a | Brazil | Mariana, MG | - | FJ441698 | FJ441941 | FJ441818 | FJ441758 | FJ441881 |
| *A. alba* | MTR 5502a | Brazil | Uruçuí-Una, PI | - | FJ441699 | FJ441942 | FJ441819 | FJ441759 | FJ441882 |
| *A. alba* | CHUNB 12795 | Brazil | Vilhena, RO | - | FJ441700 | FJ441943 | FJ441820 | FJ441760 | FJ441883 |
| *A. alba* | MZUSP 94813 | Brazil | Lajeado, TO | - | FJ441701 | FJ441944 | FJ441821 | FJ441761 | FJ441884 |
| *A. alba* | UFMT 3476 | Brazil | Campo Novo dos Parecis, MT | - | FJ441702 | FJ441945 | FJ441822 | FJ441762 | FJ441885 |
| *A. alba* | CHUNB 30678 | Brazil | Jalapão, TO | - | FJ441705 | FJ441948 | FJ441825 | FJ441765 | FJ441888 |
| *A. alba* | UFMT 3468 | Brazil | Guarantã do Norte, MT | - | FJ441706 | FJ441949 | FJ441826 | FJ441766 | FJ441889 |
| *A. alba* | CHUNB 430 | Brazil | Minaçu, GO | - | FJ441703 | FJ441946 | FJ441823 | FJ441763 | FJ441886 |
| *A. alba* | CHUNB 435 | Brazil | Minaçu, GO | - | FJ441704 | FJ441947 | FJ441824 | FJ441764 | FJ441887 |
| *A. alba* | SBH266671 | Peru | Madre de Dios, 15 km E Puerto Maldonado | EU203644 | EU203644 | - | - | - | - |
| *A. alba* | 103 KGRC-2022 | Brazil | Araraquara, SP | - | JQ627277 | - | - | - | - |
| *A. alba* | ITV42434 | Brazil | Sao Geraldo do Araguaia, PA | - | PQ733157 | - | - | - | - |
| *A. alba* | MLS 1904 | Colombia | Paz de Ariporo, Casanare | - | - | MT433762 | - | - | - |
| *A. alba* | UWIZM.2016.12.3 | Trinidad | Lopinot Road, Arouca, Trinidad | QB133898 | QB133892 | QB134343 | QB134353 | QB134357 | QB134348 |
| *A. alba* | UWIZM.2016.12.4 | Trinidad | Mt Catherine in the northwest peninsula | QB133899 | QB133893 | QB134344 | QB134354 | QB134358 | QB134349 |
| *A. fuliginosa* | CH9395 | Panama | Calle del Mamoni, abecera de Rio Madrono | - | MH140476 | - | - | - | - |
| *A. fuliginosa* | USNMFS254015 | Panama | El Cope | - | MH140475 | - | - | - | - |
| *A. fuliginosa* | MZUSP103746 | Brazil | São Paulo | OK523347 | OK523353 | - | OK523367 | OK523362 | OK523357 |
| *A. fuliginosa* | MTR3177 | Brazil | Manso, MT | - | FJ441683 | FJ441926 | FJ441803 | FJ441743 | FJ441866 |
| *A. fuliginosa* | MZUSP82798 | Brazil | Aripuanã, MT | OK523341 | FJ441684 | FJ441927 | FJ441804 | FJ441744 | FJ441867 |
| *A. fuliginosa* | KU222189 | Peru | San Jacinto Loreto | - | FJ441682 | FJ441925 | FJ441802 | FJ441742 | FJ441865 |
| *A. fuliginosa* | MLS 1903 | Colombia | San Martín, Meta | - | - | MT433765 | - | - | - |
| *A. fuliginosa* | UIS-R 3181 | Colombia | Bucaramanga, Santander | - | - | MT433764 | - | - | - |
| *A. fuliginosa* | UIS-R 3724 | Colombia | Girón, Santander | - | - | MT433766 | - | - | - |
| *A. fuliginosa* | 7111 | Guyana | Dubulay Ranch | - | QB133894 | QB134345 | - | QB134359 | QB134350 |
| *A. fuliginosa* | 7009 | Guyana | Dubulay Ranch | QB133900 | QB133895 | QB134346 | QB134355 | QB134360 | QB134351 |
| *A. fuliginosa* | UWIZM.2014.13 | Trinidad | St. Augustine, St. George | QB133902 | QB133897 | - | - | - | - |
| *A. fuliginosa* | UWIZM.2012.38.1 | Trinidad | Cocal, Manzanilla | QB133901 | QB133896 | QB134347 | QB134356 | QB134361 | QB134352 |

**Table S2.** Tracer summary statistics for selected parameters from the final BEAST2 divergence-time analysis. Values are shown for the posterior, likelihood, prior, partition-specific likelihoods, relaxed-clock parameters, birth-Death tree prior parameters, and calibrated MRCA ages. ESS values were calculated in Tracer after burn-in removal. All parameters showed ESS values > 200.

| Parameter | Mean | 95% HPD interval | ESS |
|---|---|---|---|
| posterior | –59375.22 | [–59413.8171, –59333.5179] | 1703 |
| likelihood | –58953.114 | [–58993.1992, –58914.5133] | 1756 |
| prior | –422.1058 | [–432.2725, –411.8946] | 1686 |
| Tree.height | 88.3843 | [84.612, 92.345] | 5032 |
| Tree.treeLength | 1577.4676 | [1482.608, 1673.2332] | 1189 |
| treeLikelihood.12S | –13058.051 | [–13072.4883, –13043.57] | 1145 |
| treeLikelihood.16S | –9323.9341 | [–9346.4218, –9300.2903] | 692,4 |
| treeLikelihood.ND2 | –25819.965 | [–25843.0071, –25800.3294] | 423,9 |
| treeLikelihood.bdnf | –2304.5977 | [–2319.1752, –2290.1157] | 689,5 |
| treeLikelihood.cmos | –5177.7026 | [–5195.1057, –5160.947] | 1679 |
| treeLikelihood.rag1 | –3268.8635 | [–3284.9571, –3252.0654] | 1512 |
| ucldMean.12S | 0.0102 | [8.5432E-3, 0.0119] | 863,7 |
| ucldMean.16S | 0.0073 | [5.8003E-3, 9.0249E-3] | 783,8 |
| ucldMean.ND2 | 0.0165 | [0.0143, 0.0188] | 495,5 |
| ucldMean.bdnf | 0.0003 | [2.2124E-4, 3.626E-4] | 2390 |
| ucldMean.cmos | 0.0005 | [4.1557E-4, 5.603E-4] | 2421 |
| ucldMean.rag1 | 0.0006 | [4.9639E-4, 7.2079E-4] | 2170 |
| ucldStdev.12S | 0.4221 | [0.3082, 0.5496] | 356,6 |
| ucldStdev.16S | 0.6764 | [0.5199, 0.8272] | 471,8 |
| ucldStdev.ND2 | 0.4092 | [0.3153, 0.5099] | 362,1 |
| ucldStdev.bdnf | 0.4582 | [0.1857, 0.7404] | 2061 |
| ucldStdev.cmos | 0.3616 | [0.193, 0.538] | 1639 |
| ucldStdev.rag1 | 0.4386 | [0.2413, 0.6445] | 1680 |
| BirthDeath | –382.8557 | [–389.643, –375.2873] | 1151 |
| BDBirthRate | 0.0465 | [0.0239, 0.0692] | 336,9 |
| BDDeathRate | 0.4635 | [0.0871, 0.8245] | 372,6 |
| mrca.age(Amphisbaenia) | 88.3843 | [84.612, 92.345] | 5032 |
| mrca.age(Amphisbaeniformes) | 63.7348 | [60.4223, 66.9589] | 3389 |
| mrca.age(Amphisbaenoidea) | 58.3051 | [55.1111, 61.4933] | 4967 |
| mrca.age(Trogo_Amphis) | 46.635 | [43.5662, 49.5281] | 2518 |
| mrca.age(grupo_ridley_fulig) | 23.0763 | [20.5905, 25.4315] | 1679 |
| mrca.age(ridleyi_group) | 14.2417 | [11.9544, 16.5677] | 1077 |

**Table S3.** Posterior and prior-only estimates for calibrated MRCA ages used in the BEAST2 divergence-time analyses. Posterior estimates were calculated from the final BEAST2 analysis after removing 25% burn-in, whereas prior-only estimates were calculated from an analysis using the same calibration scheme, tree prior, and clock models but sampling from the prior without incorporating the sequence likelihood, after removing 50% burn-in. ESS values were assessed in Tracer. The prior-only analysis was used to evaluate the behaviour of the temporal calibration priors.

| Node | Calibration mean (Ma) | Posterior mean (Ma) | Posterior 95% HPD (Ma) | Posterior ESS | Prior-only mean (Ma) | Prior-only 95% HPD (Ma) | Prior-only ESS |
|---|---|---|---|---|---|---|---|
| Amphisbaenia | 88 | 88,38 | 84.61-92.35 | 4768 | 87,85 | 84.07-91.77 | 4704 |
| Amphisbaeniformes | 66 | 63,73 | 60.41-66.96 | 3145 | 62,91 | 60.09-65.59 | 2930 |
| Amphisbaenoidea | 60 | 58,31 | 55.11-61.50 | 4558 | 62,9 | 60.05-65.56 | 2930 |
| Trogonophidae + Amphisbaenidae | 44 | 46,63 | 43.57-49.53 | 2317 | 43,86 | 40.06-47.96 | 1139 |
| *A. fuliginosa* + *A. ridleyi* group | 21 | 23,07 | 20.59-25.43 | 1877 | 20,49 | 16.10-24.77 | 2706 |
| *A. ridleyi* group | 13 | 14,22 | 11.93-16.55 | 1121 | 13,86 | 9.84-18.38 | 3971 |

**Table S4.** Comparative values of AICc (Akaike Information Criterion with correction) for the models tested in the TSDM scenario implemented in BioGeoBEARS.

| | LnL | Npar | d | e | j | AICc | AICc_wt |
|---|---|---|---|---|---|---|---|
| DEC | –179.5 | 2 | 0.0053 | 0.0010 | 0 | 363.2 | 3.7e-06 |
| DEC+J | –166 | 3 | 0.0032 | 0.0008 | 0.026 | 338.2 | 0.99 |
| DIVALIKE | –191.8 | 2 | 0.0073 | 0.0023 | 0 | 387.6 | 1.8e-11 |
| DIVALIKE+J | –175 | 3 | 0.0039 | 0.0013 | 0.028 | 356.1 | 0.0001 |
| BAYAREALIKE | –223.3 | 2 | 0.0046 | 0.027 | 0 | 450.8 | 3.5e-25 |
| BAYAREALIKE+J | –170.9 | 3 | 0.0024 | 0.0015 | 0.034 | 348 | 0.0073 |

**Table S5.** Comparative values of AICc (Akaike Information Criterion with correction) for the models tested in the TSDM scenario implemented in RASP (reconstruct ancestral state in phylogenies).

| | LnL | Npar | d | e | j | AICc | AICc_wt |
|---|---|---|---|---|---|---|---|
| DEC | –160 | 2 | 0.013 | 0.19 | 0 | 324.2 | 0.0036 |
| DEC+J | –156.6 | 3 | 0.0099 | 0.15 | 0.015 | 319.5 | 0.038 |
| DIVALIKE | –163.3 | 2 | 0.014 | 0.22 | 0 | 330.8 | 0.0001 |
| DIVALIKE+J | –160.4 | 3 | 0.011 | 0.25 | 0.012 | 327 | 0.0009 |
| BAYAREALIKE | –162.6 | 2 | 0.013 | 0.29 | 0 | 329.4 | 0.0003 |
| BAYAREALIKE+J | –153.4 | 3 | 0.0099 | 0.28 | 0.010 | 313.1 | 0.96 |

**Table S6.** Event matrix for nodes 1-3 indicated in Fig. S3.

| Node | Dispersal | Vicariance | Extinction | RASP route | Probability |
|---|---|---|---|---|---|
| 1 | 1 | 1 | 1 | DC->->^AM->AM^AM->AM\|AM | 0.7155 |
| 2 | 1 | 1 | 0 | AM->AMTA->AM\|TA | 0.9979 |
| 3 | 2 | 1 | 0 | AM->AMDCAF->AM\|DCAF | 0.9988 |

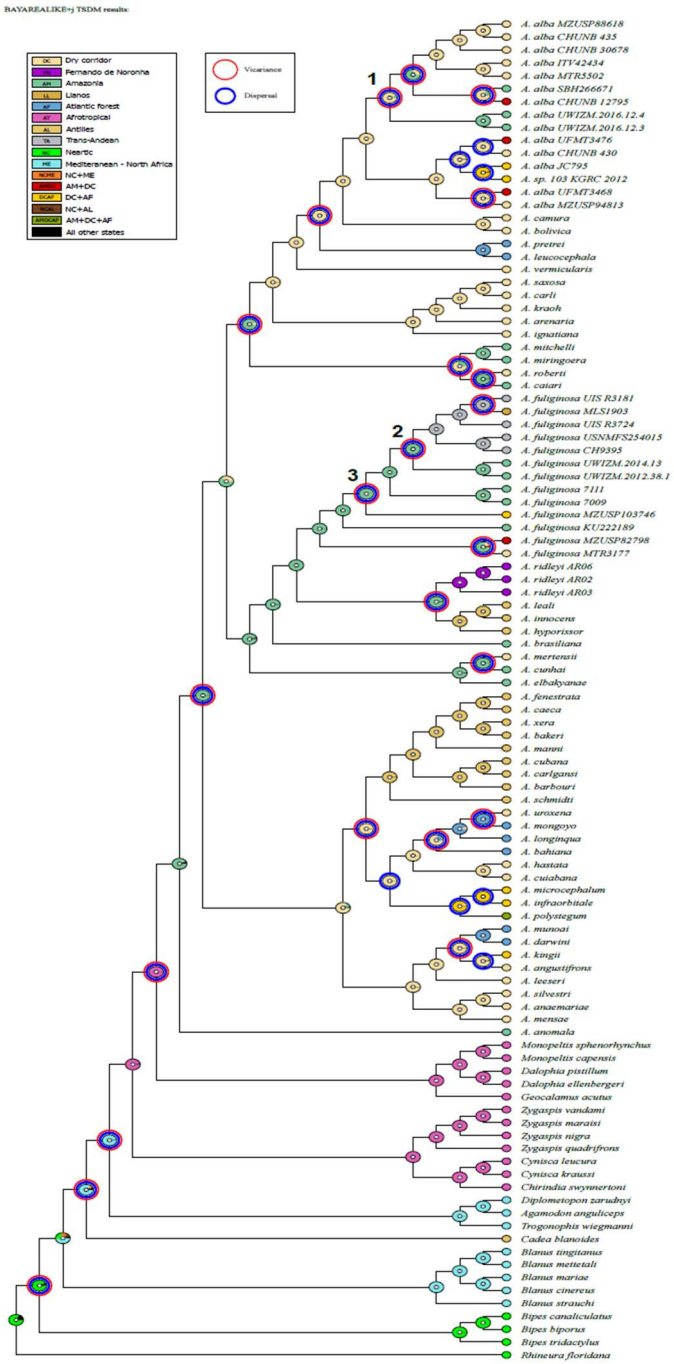



**Fig. S1.** Bayesian phylogeny of amphisbaenians and reconstruction of ancestral geographic ranges under the BAYAREALIKE+J model and TSDM scenario implemented in RASP (reconstruct ancestral state in phylogenies). Pie charts indicate the relative probabilities of the ancestral ranges inferred at each node.

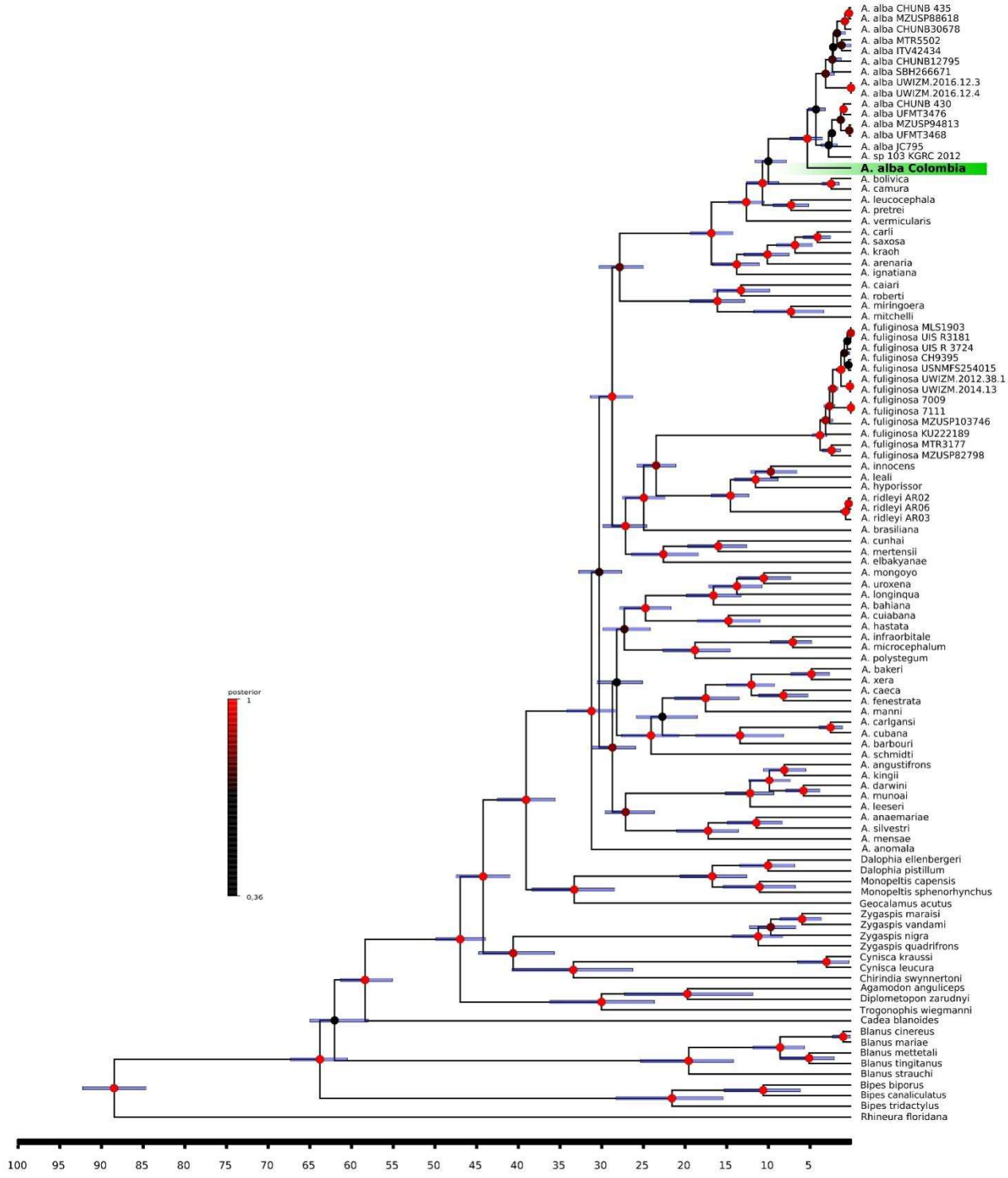



**Fig. S2.** Divergence time estimates from representative *Amphisbaena* samples, including the Colombian *Amphisbaena alba* nd2 short fragment (in green). Inference was based on the combined mtDNA and nDNA data.

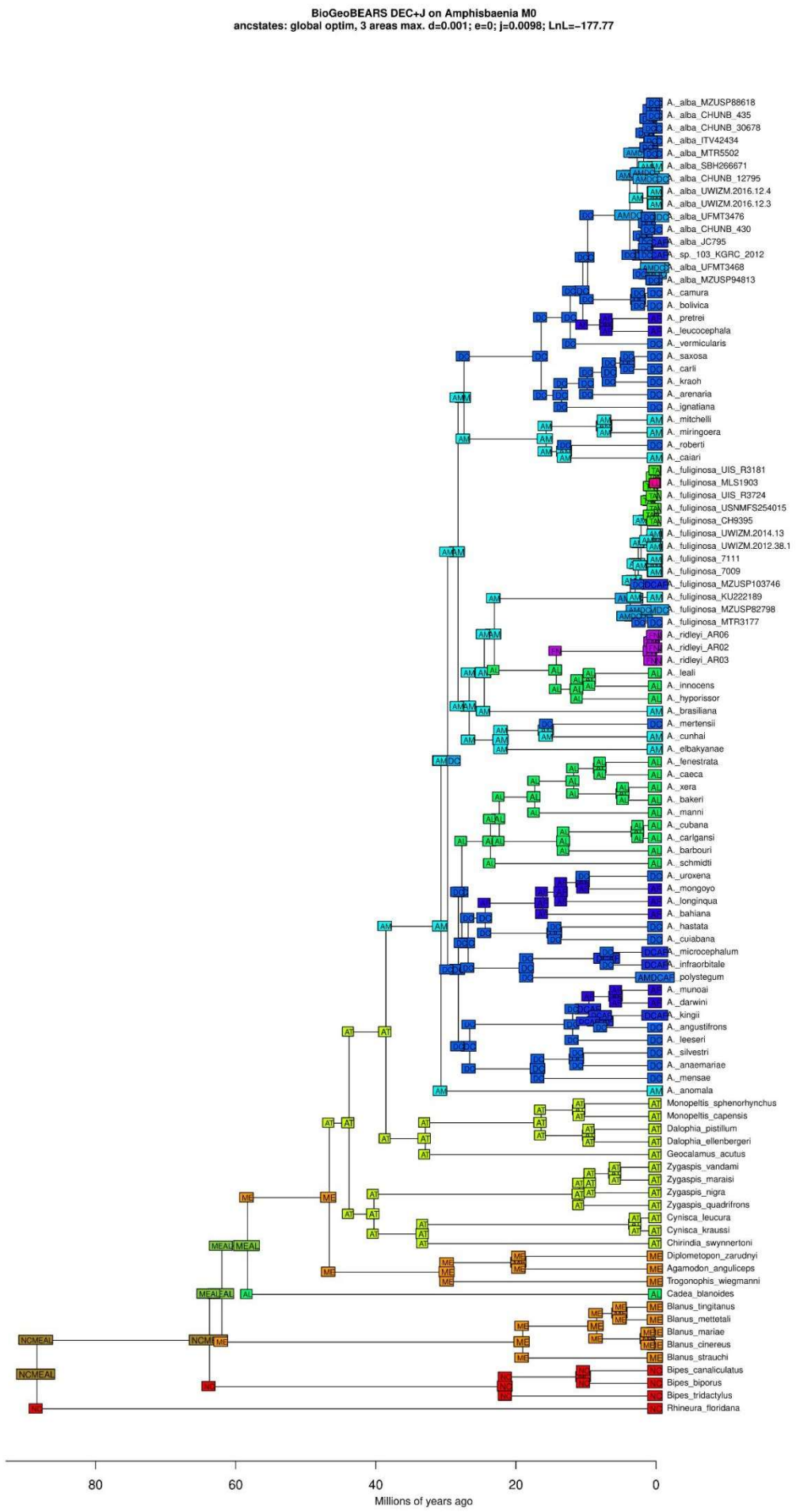



**Fig. S3.** Historical biogeographic reconstruction under the best model (DEC+J) selected when implementing the scenario NTS (no time strata) in BioGeoBEARS.

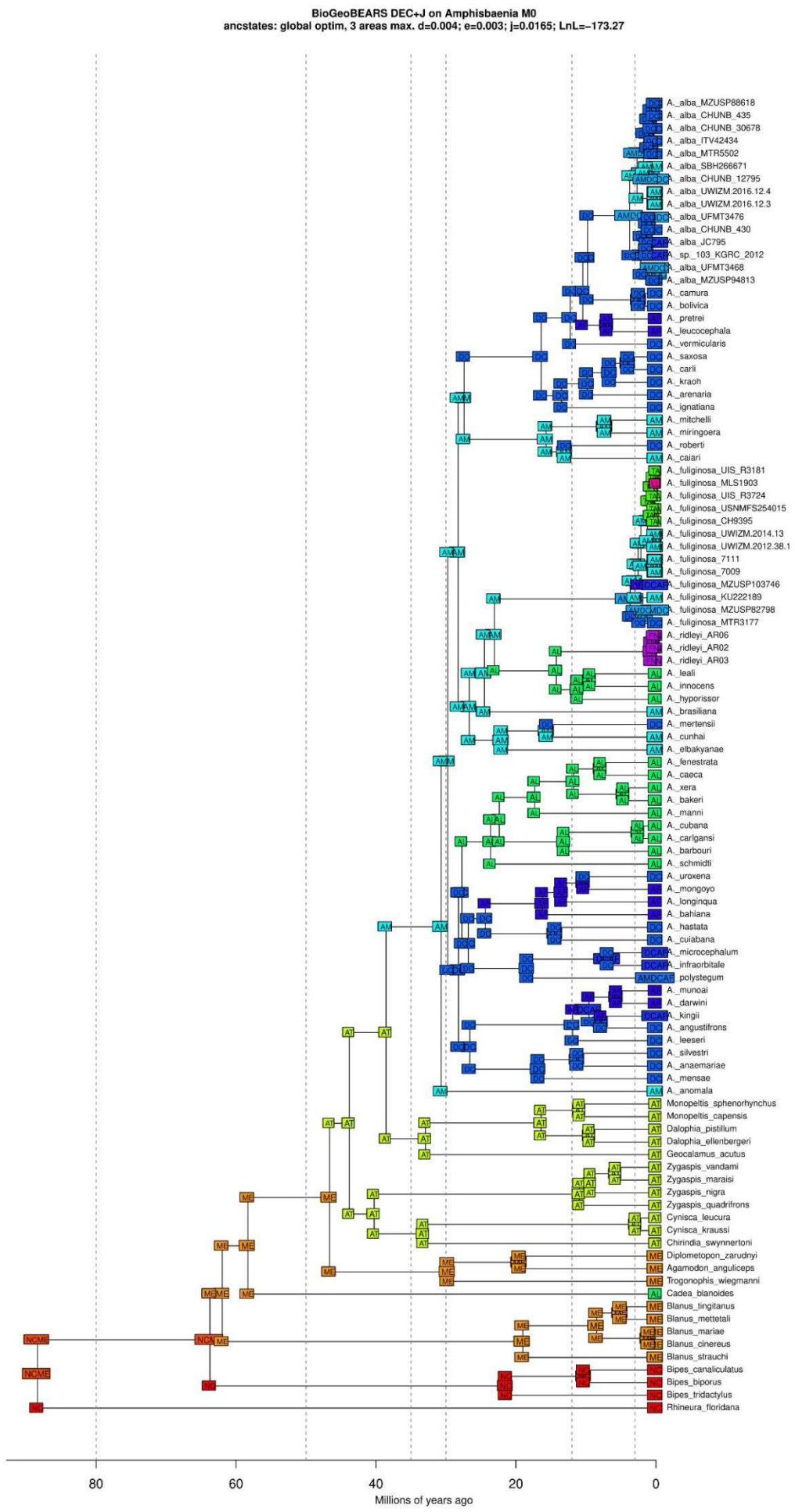



**Fig. S4.** Historical biogeographic reconstruction under the best model (DEC+J) selected when implementing the scenario TSDMA (time stratified – dispersal matrix – allowed areas) in BioGeoBEARS.

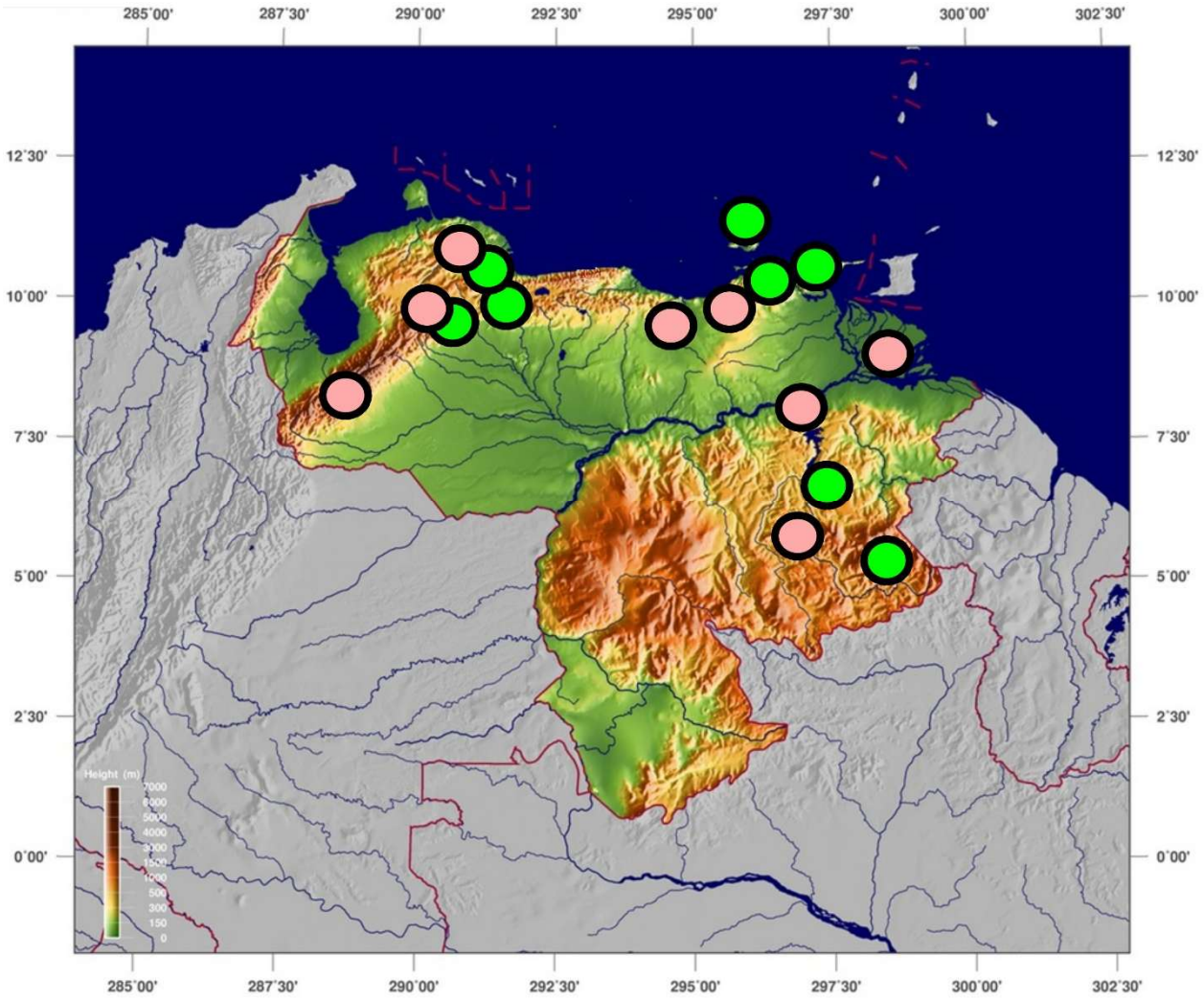



**Fig. S5.** Map showing the distribution of *Amphisbaena alba* and *A. fuliginosa* in Venezuela.