# *S1 Appendix* Supplemental Material

## Evidence for Complex Life Cycle Constraints on Salamander Body Form Diversification

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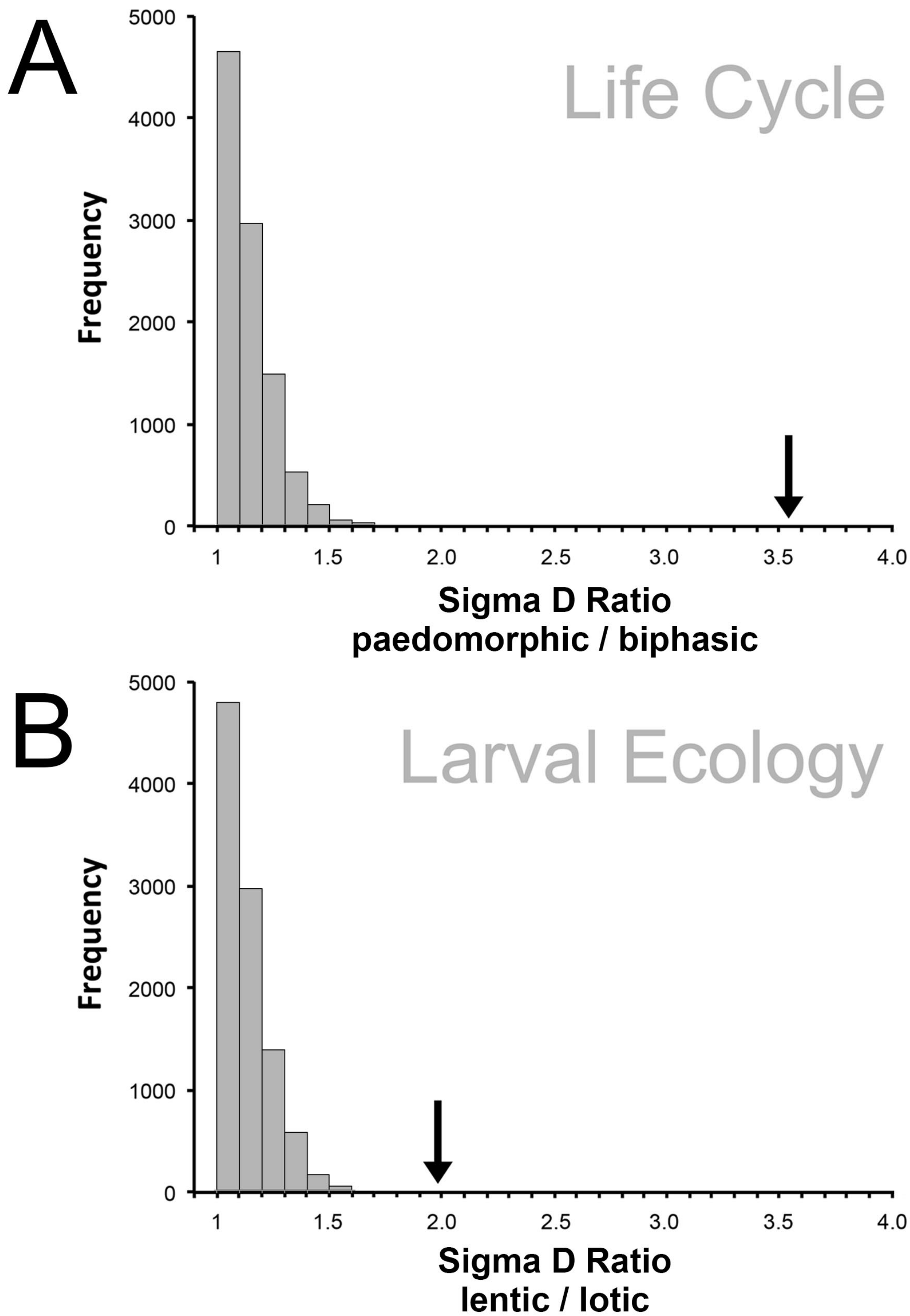
**Supplemental Table S1. Bayesian ancestral state reconstructions of salamander life cycle modes and body form metrics.** Life cycle was reconstructed using BayesTraits [S1] and the three modes were treated as ordered categorical states: paedomorphic (pd), biphasic (bi), and direct development (dd). Median *Trunk Vertebral Number* (Vert) and median *Adult Body Forms* (ABF) including 95% confidence intervals were reconstructed in StableTraits [S2]. Ancestral Vert estimates were rounded to the nearest integer. The ancestral state estimates listed below include the common ancestors of all 10 extant families and internal nodes joining families. The life cycle stage with the highest probability, and median *Trunk Vertebral Number* and *Adult Body Form* estimates are shown in Fig. 1.

| Node | pd | bi | dd | Vert Median | Vert 95% CI | ABF Median | ABF 95% CI |
|---|---|---|---|---|---|---|---|
| Living Salamanders (Root Node) | 0.13 | 0.87 | 0.00 | 17 | 15-18 | 8.8 | 6.1-11.5 |
| Cryptobranchoidea | 0.32 | 0.68 | 0.00 | 17 | 17-18 | 8.7 | 6.0-11.3 |
| Salamandroidea + Sirenoidia | 0.21 | 0.79 | 0.00 | 17 | 15-18 | 9.1 | 6.6-11.7 |
| Salamandroidea | 0.02 | 0.98 | 0.00 | 17 | 14-18 | 9.1 | 6.9-11.3 |
| Ambystomatidae + Dicamptodontidae + Salamandridae | 0.01 | 0.99 | 0.00 | 14 | 13-17 | 8.7 | 6.6-10.9 |
| Ambystomatidae + Dicamptodontidae | 0.01 | 0.99 | 0.00 | 14 | 13-15 | 7.9 | 5.6-10.2 |
| Proteidae + Rhyacotritonidae + Amphiumidae + Plethodontidae | 0.55 | 0.45 | 0.00 | 17 | 15-18 | 9.5 | 7.4-11.8 |
| Rhyacotritonidae + Amphiumidae + Plethodontidae | 0.03 | 0.88 | 0.09 | 16 | 15-17 | 9.9 | 7.7-12.1 |
| Amphiumidae + Plethodontidae | 0.14 | 0.51 | 0.35 | 16 | 15-17 | 10.3 | 8.1-12.6 |
| Cryptobranchidae | 1.00 | 0.00 | 0.00 | 17 | 17-18 | 6.8 | 4.8-9.0 |
| Hynobiidae | 0.02 | 0.98 | 0.00 | 17 | 17-17 | 8.4 | 5.7-11.1 |
| Sirenidae | 1.00 | 0.00 | 0.00 | 33 | 31-36 | 14.8 | 12.0-23.2 |
| Ambystomatidae | 0.00 | 1.00 | 0.00 | 14 | 13-15 | 7.6 | 6.0-9.0 |
| Dicamptodontidae | 0.32 | 0.68 | 0.00 | 14 | 14-14 | 6.5 | 5.9-7.2 |
| Salamandridae | 0.00 | 1.00 | 0.00 | 13 | 13-13 | 7.8 | 6.2-9.7 |
| Proteidae | 0.99 | 0.01 | 0.00 | 17 | 15-18 | 9.6 | 6.9-12.6 |
| Rhyacotritonidae | 0.00 | 1.00 | 0.00 | 16 | 15-16 | 9.4 | 8.3-10.4 |
| Amphiumidae | 1.00 | 0.00 | 0.00 | 61 | 61-61 | 17.1 | 15.6-18.4 |
| Plethodontidae | 0.00 | 0.04 | 0.96 | 16 | 15-17 | 10.6 | 9.4-11.9 |

**Considering potential discordance between Mesozoic fossils and reconstructions based on extant species:** Our ancestral life cycle reconstructions were based entirely on data from extant species, and only obligately paedomophic taxa were coded as paedomophic. The reconstruction shows support for biphasic ancestors for all salamanders, salamandroids, and cryptobranchoids. This is partially supported by several fossil salamanders from the Late Jurassic through the Early Cretaceous with a metamorphosed morphology (cryptobranchoids: *Liaoxitriton daohugouensis* [S3-S5], *Laccotriton subsolanus* [S5, S6], *Pangerpeton sinense* [S4, S5, S7], *Iridotriton hechti* [S4, S5, S8], *Nuominerpeton aquilonaris* [S9]; and a salamandroid: *Valdotriton gracilis* [S4, S5, S10]). However, there are also several other fossil salamanders from the same range of time that were likely paedomorphic (salamandroids: *Beiyanerpeton jianpingensis* [S4, S5] and *Qinglongtriton gangouensis* [S11]; and cryptobranchoids: *Sinerpeton fengshanensis* [S5, S12], *Chunerpeton tianyiensis* [S4, S5, S13], *Jeholotriton paradoxus* [S5, S14]). Furthermore, the Family Karauridae is thought to have been paedomophic (aquatic), and is often placed as sister to all extant salamanders [S4, S5, S15]. This has been used as evidence for a paedomorphic ancestor for all extant salamanders [S15]. The nature of paedomophosis (facultative vs. obligate) in fossil taxa is difficult to evaluate. Curiously though, none of these paedomophic Jurassic taxa had obviously abbarent body forms (or trunk vertebral numbers [S5]). Based on our trait analyses, this would suggest that these taxa were faculataively paedomorphic or recently evolved obligate paedomorphs. This is notion is also supported by the suggested close relationships between many paedomorphic and metamorphic Jurassic taxa [S4, S5]. Nevertheless, we find no major difference in patterns of body form evolution when we fix the basal salamander node to paedomophic (Tables S2 and S3).

**Considering fossil taxa in trunk vertebral number reconstructions:** Reconstructions of ancestral trunk vertebral numbers were based completely on data from extant species. However, our estimates (range 14 to 17) overlap well with counts from Late Jurassic through Early Cretaceous species assigned to the Salamandroidea and Cryptobranchoidea (range 13 to 16 [S5]). Note: Ascarrunz et al. [S5] counted all presacrals; our counts were from between the atas and the sacrum (i.e., minus the atlas).




**Supplemental Figure S1. Comparisons of rates of larval shape evolution.** Sigma D ratio calculated using the *compare.evol.rate*s function in geomorph [S16, S17] shows the differences in rates of larval body shape evolution for species partitioned by life cycle (A, paedomorphic vs. biphasic) or larval ecology (B, lentic vs. lotic). Rates of larval body shape evolution (arrows) were estimate to be 3.54 times higher for paedomorphs than biphasics, and 1.99 times higher for lentic compared to lotic dwelling larvae.

**Supplemental Table S2. Comparison of the fit of BM and OU models to salamander *Trunk Vertebral Number* with differential coding of larval ecologies and life cycles, and with alternative coding of facultatively paedomorphic taxa.** Three alternative partitions were tested: *Life Cycle* (one-part vs. two-part), *Larval Ecology* (lotic vs. lentic), and *Facultative* (facultative paedomorphs coded the same as obligate paedomorphs). Throughout this study we code facultatively paedomorphic taxa as biphasic, because we were primarily interested the consequences of long-term life cycle transitions. Fitting models with facultative paedomorphs coded the same as obligate paedomorphs allowed us to test whether our results (life cycle vs. larval ecology) were robust regardless of how we coded taxa with variable life cycles (i.e. facultative paedomorphs). It also allows us to determine whether the vertebral columns of facultative paedomorphs evolve more similar to obligate paedomorphs or biphasics. Models were fit using OUwie [S18] and parameters allowed to vary among groups included rates of evolution ($\sigma^2$) and optima ($\theta$). Model fit was based on ΔAIC and AIC Weights ($w_i$). OU-models with multiple selection parameters ($\alpha$: $OU_{\theta\alpha}$ and $OU_{\theta\sigma^2\alpha}$) were not included, because they were poorly fit or did not improve upon simpler models (based on preliminary analyses). BM-models with multiple rates and a single optimum ($BM_{\sigma^2}$) were also examined, but were never better than the best $BM_{\theta\sigma^2}$ model. Parameter estimates and 95% confidence intervals for the overall best-fit model (Life Cycle $BM_{\theta\sigma^2}$) are listed below. Life cycle models with different rates and optima for paedomorphs vs. biphasics (including facultative paedomorphs) were substantially better than all models based on larval ecology (ΔAIC > 114). Facultative paedomorphs were a better fit when combined with biphasics than with obligate paedomorphs. However, even when facultative species were coded as paedomorphic, models with rate and optimum differences separated by life cycle (facultative + obligate vs. biphasic) were still a better fit than larval ecology (ΔAIC > 49).

| Model | -lnL | AIC | ΔAIC | $w_i$ |
|---|---|---|---|---|
| Life Cycle $BM_{\theta\sigma^2}$ | -268.45 | 544.91 | 0.00 | 0.6995 |
| Life Cycle $OU_{\theta\sigma^2}$ | -268.30 | 546.60 | 1.69 | 0.3004 |
| Facultative $BM_{\theta\sigma^2}$ | -300.73 | 609.47 | 64.56 | < 0.0001 |
| Facultative $OU_{\theta\sigma^2}$ | -300.82 | 611.64 | 66.73 | < 0.0001 |
| Larval Ecol $BM_{\theta\sigma^2}$ | -326.72 | 661.44 | 116.53 | < 0.0001 |
| Larval Ecol $OU_{\theta\sigma^2}$ | -326.47 | 662.95 | 118.04 | < 0.0001 |
| Life Cycle $OU_{\theta}$ | -333.77 | 675.55 | 130.64 | < 0.0001 |
| Facultative $OU_{\theta}$ | -336.50 | 680.99 | 136.08 | < 0.0001 |
| BM1 | -339.68 | 683.36 | 138.45 | < 0.0001 |
| Larval Ecol $OU_{\theta}$ | -338.48 | 684.97 | 140.06 | < 0.0001 |
| OU1 | -339.68 | 685.36 | 140.45 | < 0.0001 |

$\theta$: bi = 15.69±0.04; pd = 40.52±0.55

$\sigma^2$: bi = 0.040±0.0005; pd = 1.994±0.108

**Outliers: Analyses performed without *Amphiuma.*** Salamanders of the Family Amphiumidae have approximately 60 trunk vertebrae (Fig. 1), which is two to four times as many as nearly all other extant salamanders. Analyses performed without the three extant species of *Amphiuma*, also recovered Life Cycle $BM_{\theta\sigma^2}$ as the best-fit model. Paedomorphic lineages still show a higher rate of trunk vertebral evolution than biphasic lineages (by >11 times; $\sigma^2$: bi = 0.041±0.0005; pd = 0.472±0.0065), but with a lower optimum ($\theta$: bi = 15.93±0.0266; pd = 29.99±0.2960). Multi-rate life cycle models were still a better fit than all models based on larval ecology (ΔAIC > 72).

**Transformation: Why we did not transform vertebral count data.** Throughout the study we did not transform vertebral count data because there was no correlation between numbers of trunk vertebrae and their variance. For example, paedomorphic clades with the highest numbers of trunk vertebrae (e.g. Amphiumidae) do not necessarily have more variation among species than paedomorphic clades with fewer trunk vertebrae (e.g. plethodontids of the genus *Eurycea* from central Texas). To evaluate this we tested for a correlation between the independent contrasts and ancestral state estimates [S19] of numbers of trunk vertebrae. These variables were not correlated ($R^2$ = 0.0570). Nevertheless, analyses performed on Log10-transformed trunk vertebral numbers yielded the same results as those presented. In the case above, Life Cycle $BM_{\theta\sigma^2}$ was still a better-fit model (ΔAIC > 68) than every model based on larval ecology. Parameter estimates for analyses of Log10-transformed data under the best-fit model (Life Cycle $BM_{\theta\sigma^2}$) were also relatively the same: a higher rate of evolution (by >13 times; $\sigma^2$: bi = 0.000033±4.13e$^{-07}$; pd = 0.00043±8.47e$^{-06}$) and optimum number of trunk vertebrae (antilog $\theta$: bi = 15.67±1.00; pd = 40.36±1.02) in paedomorphic compared to biphasic lineages.

**Ancestral Salamanders Paedomorphic?** Fossil evidence suggests that ancestral salamanders may have been paedomorphic [S15]. We set the ancestral salamander node to paedomorphic and recovered the same patterns of model fit for trunk vertebrae as when this node was metamorphic. The only difference was that the optimum vertebral number of paedomorphs was reduced (best fit model: Life Cycle $BM_{\theta\sigma^2}$; $\theta$: bi = 15.07±0.09; pd = 26.85±0.44; $\sigma^2$: bi = 0.041±0.0005; pd = 1.48±0.072).

**Supplemental Table S3. Comparison of the fit of BM and OU models to salamander *Adult Body Form* data with differential coding of larval ecologies and life cycles, and with alternative coding of facultatively paedomorphic taxa.** Three alternative partitions were tested: *Life Cycle* (one-part vs. two-part), *Larval Ecology* (lotic vs. lentic), and *Facultative* (facultative paedomorphs coded the same as obligate paedomorphs). Throughout this study we code facultatively paedomorphic taxa as biphasic, because we were primarily interested the consequences of long-term life cycle transitions. Fitting models with facultative paedomorphs coded the same as obligate paedomorphs allowed us to test whether our results (life cycle vs. larval ecology) were robust, regardless of how we coded taxa with variable life cycles (i.e. facultatively paedomorphs). It also allows us to determine whether the adult body forms of facultative paedomorphs evolve more similar to obligate paedomorphs or biphasics. Models were fit using OUwie [S18] and parameters allowed to vary among groups included rates of evolution ($\sigma^2$) and optima ($\theta$). Model fit was based on ΔAIC and AIC Weights ($w_i$). OU-models with multiple selection parameters ($\alpha$: $OU_{\theta\alpha}$ and $OU_{\theta\sigma^2\alpha}$) were not included, because they were poorly fit or did not improve upon simpler models (based on preliminary analyses). BM-models with multiple rates and a single optimum ($BM_{\sigma^2}$) were also examined, but were never better than the best $BM_{\theta\sigma^2}$ model. Parameter estimates and 95% confidence intervals for the overall best-fit model (Life Cycle $OU_{\theta\sigma^2}$) are listed below. Life cycle models with different rates and optima for paedomorphs vs. biphasics (including facultative paedomorphs) were substantially better than all models based on larval ecology (ΔAIC > 74). Facultative paedomorphs were better fit when combined with biphasics than with obligate paedomorphs. However, even when facultative species were coded as paedomorphic, models with rate differences separated by life cycle (facultative + obligate vs. biphasic) were still a better fit than larval ecology (ΔAIC > 40).

| **Model** | **-lnL** | **AIC** | **ΔAIC** | $w_i$ |
|---|---|---|---|---|
| Life Cycle $OU_{\theta\sigma^2}$ | -220.63 | 451.25 | 0.00 | 0.9888 |
| Life Cycle $BM_{\theta\sigma^2}$ | -226.11 | 460.22 | 8.97 | 0.0115 |
| Facultative $OU_{\theta\sigma^2}$ | -237.06 | 484.11 | 32.86 | < 0.0001 |
| Facultative $BM_{\theta\sigma^2}$ | -242.81 | 493.61 | 42.36 | < 0.0001 |
| Life Cycle $OU_{\theta}$ | -262.28 | 532.57 | 81.32 | < 0.0001 |
| Larval Ecol $OU_{\theta\sigma^2}$ | -262.21 | 534.42 | 83.17 | < 0.0001 |
| OU1 | -264.40 | 534.80 | 83.55 | < 0.0001 |
| Facultative $OU_{\theta}$ | -263.67 | 535.33 | 84.08 | < 0.0001 |
| BM1 | -265.92 | 535.85 | 84.33 | < 0.0001 |
| Larval Ecol $OU_{\theta}$ | -263.79 | 535.58 | 84.60 | < 0.0001 |
| Larval Ecol $BM_{\theta\sigma^2}$ | -264.01 | 536.01 | 84.76 | < 0.0001 |

$\theta$: bi = 8.27±0.01; pd = 15.57±0.09
$\sigma^2$: bi = 0.083±0.001; pd = 1.538±0.023
$\alpha$: 0.013±0.0003

**Transformation: Why we did not transform "*Adult Body Form*" data.** Our metric of *Adult Body Form* was a ratio of body length divided by body width and therefore was not log transformed.

**Outliers: Removing the most elongate salamanders from "*Adult Body Form*" analyses was unwarranted.** Numbers of trunk vertebrae are dramatically higher for one clade (Amphiumidae), and therefore we performed analyses with and without this family (see Table S2). However, even though amphiumids have over 20 more trunk vertebrae than other families, they are not equivalently more elongate than all other elongate salamanders. In fact, the salamanders with the most elongate *Adult Body Form* (highest body length to body width ratio) were actually species from four different families (Amphiumidae, Plethodontidae, Proteidae, and Sirenidae). Given the repeated evolution of extreme body elongation, it did not seem reasonable to remove all of these taxa from our analyses.

**Ancestral Salamanders Paedomorphic?** Fossil evidence suggests that ancestral salamanders may have been paedomorphic [S15]. When we set the ancestral node of salamanders to paedomorphic we recovered the same patterns of model fit for adult body form as when this node was primarily metamorphic. The only difference was that the estimated body form optima were reduced (best fit model: Life Cycle $OU_{\theta\sigma^2}$; $\theta$: bi = 7.86±0.018; pd = 13.47±0.089; $\sigma^2$: bi = 0.091±0.0014; pd = 1.44±0.017).

**Supplemental Table S4. Comparison of the fit of BM and OU models to salamander *Adult Body Form* data including direct developing lineages.** Five alternative partitions were tested: *Adult Ecology* (aquatic vs. terrestrial), *2 Life Cycles* (simple vs. complex), *3 Life Cycles* (paedomorphic, biphasic, direct development), *Partial Metamorph,* and *Larval Ecology* (lotic, lentic, direct development). For *Adult Ecology*, direct developers and biphasics were merged to create groups with terrestrial vs. aquatic (paedomorphic) adults. In the *2 Life Cycles* model, paedomorphs and direct developers were merged to create simple vs. complex (biphasic) life cycle groups. For the *Partial Metamorph* model, two families that partially metamorphose (Amphiumidae and Cryptobranchidae) were coded the same as groups that fully transform (biphasics and direct developers) vs. obligate paedomorphs (as in all other analyses). *Larval Ecology* separated taxa into three groups based on their "larval environment": lotic, lentic or direct development. Models were fit using OUwie [S18] and parameters allowed to vary among groups included rates of evolution ($\sigma^2$) and/or optima ($\theta$). Model fit was based on ΔAIC and AIC Weights ($w_i$). OU-models with multiple selection parameters ($\alpha$: $OU_{\theta\alpha}$ and $OU_{\theta\sigma^2\alpha}$) were not included, because they were poorly fit or did not improve upon simpler models (based on preliminary analyses). BM-models with multiple rates and a single optimum ($BM_{\sigma^2}$) were also examined, but were never better than the best $BM_{\theta\sigma^2}$ model. Parameter estimates and 95% confidence intervals for the best-fit model are listed below. The life cycle model with different rates and optima for paedomorphs, biphasics, and direct developers (3 Life Cycles $OU_{\theta\sigma^2}$) was substantially better than all other models. Parameters for direct developers were more similar to biphasics than paedomorphs. Consistent with this, the second best fit model based on adult ecology (Adult Ecology $OU_{\theta\sigma^2}$) treated biphasic and direct developing taxa as a single group. Partial metamorphs were better fit when combined with permanently aquatic obligate paedomorphs than with fully transformed taxa with terrestrial adults (biphasics and direct developers; compare Adult Ecology $OU_{\theta\sigma^2}$ to Partial Metamorph $OU_{\theta\sigma^2}$: ΔAIC >38). Similar to analyses without direct developers, models based on larval ecology were poorly fit compared to all multi-rate models based on life cycle, adult ecology, or partial metamorphosis.

| Model | -lnL | AIC | ΔAIC | $w_i$ |
|---|---|---|---|---|
| 3 Life Cycles $OU_{\theta\sigma^2}$ | -386.81 | 787.63 | 0.00 | 0.9578 |
| Adult Ecology $OU_{\theta\sigma^2}$ | -391.97 | 793.94 | 6.31 | 0.0408 |
| 3 Life Cycles $BM_{\theta\sigma^2}$ | -394.52 | 801.05 | 13.42 | 0.0012 |
| Adult Ecology $BM_{\theta\sigma^2}$ | -398.26 | 804.53 | 16.90 | 0.0002 |
| Partial Metamorph $OU_{\theta\sigma^2}$ | -411.13 | 832.26 | 44.63 | < 0.0001 |
| Partial Metamorph $BM_{\theta\sigma^2}$ | -414.01 | 836.02 | 48.39 | < 0.0001 |
| 2 Life Cycles $OU_{\theta\sigma^2}$ | -414.38 | 838.76 | 51.13 | < 0.0001 |
| 2 Life Cycles $BM_{\theta\sigma^2}$ | -422.17 | 852.34 | 64.71 | < 0.0001 |
| Larval Ecology $OU_{\theta\sigma^2}$ | -429.49 | 872.98 | 85.35 | < 0.0001 |
| 2 Life Cycles $OU_{\theta}$ | -434.16 | 876.32 | 88.69 | < 0.0001 |
| Larval Ecology $BM_{\theta\sigma^2}$ | -433.21 | 878.43 | 90.80 | < 0.0001 |
| Adult Ecology $OU_{\theta}$ | -436.02 | 880.04 | 92.41 | < 0.0001 |
| Partial Metamorph $OU_{\theta}$ | -436.25 | 880.51 | 92.88 | < 0.0001 |
| 3 Life Cycles $OU_{\theta}$ | -435.69 | 881.38 | 93.75 | < 0.0001 |
| OU1 | -438.61 | 883.23 | 95.60 | < 0.0001 |
| Larval Ecology $OU_{\theta}$ | -437.78 | 885.57 | 97.94 | < 0.0001 |
| BM1 | -440.82 | 885.65 | 98.02 | < 0.0001 |

$\theta$: bi = 8.17±0.02; pd = 15.39±0.08; dd = 10.64±0.04

$\sigma^2$: bi = 0.084±0.0013; pd = 1.549±0.026; dd = 0.135±0.0011

$\alpha$: 0.0138±0.0002

**Different plethodontid divergence time estimates (70 mya vs. 85 mya) produce the same results.** All direct developers are in the Family Plethodontidae. Divergence time estimates for the deepest node within the family have varied: 127 [S20], 85 [S21], and 66 [S22] mya. The analyses presented were a based on an average plethodontid divergence of 70 mya. However, we also performed this (and all) analyses with a plethodontid divergence of ~85 mya. The model ranks and patterns of significance were the same, as were the rates and optima among the 3 life cycle modes.

**Removing all bolitoglossines with 14 trunk vertebrae provides even stronger support for this analysis.** Nearly all bolitoglossines (except *Oedipina*) have 14 trunk vertebrae [S23, S24]. When these taxa were removed the 3 Life Cycles $OU_{\theta\sigma^2}$ model was an even better fit (compared to all other models, ΔAIC > 10). Parameter estimates were also similar.

**Treating ancestral plethodontids as biphasic (vs. direct developers) provides even stronger support for this analysis.** Ancestral plethodontids were likely direct developers [S25-S27]. To evaluate the influence of the ancestral plethodontid life cycle on our results, we "fixed" this node as biphasic by adding an adjacent tip with and infinitely small branch coded as biphasic. Parameter estimates were the same, and the 3 Life Cycles $OU_{\theta\sigma^2}$ model was best fit compared to all other models (ΔAIC > 18).

**Supplemental Table S5. Comparison of the fit of BM and OU models to salamander *Trunk Vertebral Number* including direct developing lineages.** Five alternative partitions were tested: *Adult Ecology* (aquatic vs. terrestrial), *2 Life Cycles* (simple vs. complex), and *3 Life Cycles* (paedomorphic, biphasic, direct development), *Partial Metamorph,* and *Larval Ecology* (lotic, lentic, direct development). For *Adult Ecology*, direct developers and biphasics were merged to create groups with terrestrial vs. aquatic (paedomorphic) adults. In the *2 Life Cycles* model, paedomorphs and direct developers were merged to create simple vs. complex (biphasic) life cycle groups. For the *Partial Metamorph* model, two families that partially metamorphose (Amphiumidae and Cryptobranchidae) were coded the same as groups that fully transform (biphasics and direct developers) vs. obligate paedomorphs (as in all other analyses). *Larval Ecology* separated taxa into three groups based on their "larval environment": lotic, lentic or direct development. Models were fit using OUwie [S18] and parameters allowed to vary among groups included rates of evolution ($\sigma^2$) and/or optima ($\theta$). Model fit was based on ΔAIC and AIC Weights ($w_i$). OU-models with multiple selection parameters ($\alpha$: $OU_{\theta\alpha}$ and $OU_{\theta\sigma^2\alpha}$) were not included, because they were poorly fit or did not improve upon simpler models (based on preliminary analyses). BM-models with multiple rates and a single optimum ($BM_{\sigma^2}$) were also examined, but were never better than the best $BM_{\theta\sigma^2}$ model. Parameter estimates and 95% confidence intervals for the best-fit model are listed below. Models with different rates and optima based on adult ecology or three different life cycle modes were substantially better than all other models (ΔAIC > 118). The simplest best-fit model was based on adult ecology (Adult Ecology $BM_{\theta\sigma^2}$). Partial metamorphs were better fit when combined with permanently aquatic obligate paedomorphs than with fully transformed taxa with terrestrial adults (biphasics and direct developers; compare Adult Ecology $BM_{\theta\sigma^2}$ to Partial Metamorph $OU_{\theta\sigma^2}$: ΔAIC >188). Similar to analyses without direct developers, models based on larval ecology were a poor-fit compared to all multi-rate models based on adult ecology or life cycle.

| **Model** | **-lnL** | **AIC** | **ΔAIC** | $w_i$ |
|---|---|---|---|---|
| Adult Ecology $BM_{\theta\sigma^2}$ | -466.60 | 941.20 | 0.00 | 0.5695 |
| Adult Ecology $OU_{\theta\sigma^2}$ | -466.60 | 943.20 | 2.00 | 0.2095 |
| 3 Life Cycles $BM_{\theta\sigma^2}$ | -465.85 | 943.70 | 2.50 | 0.1631 |
| 3 Life Cycles $OU_{\theta\sigma^2}$ | -465.89 | 945.78 | 4.58 | 0.0577 |
| Larval Ecology $BM_{\theta\sigma^2}$ | -526.04 | 1064.07 | 122.87 | < 0.0001 |
| Larval Ecology $OU_{\theta\sigma^2}$ | -526.82 | 1067.63 | 126.43 | < 0.0001 |
| 2 Life Cycles $BM_{\theta\sigma^2}$ | -534.06 | 1076.12 | 134.92 | < 0.0001 |
| 2 Life Cycles $OU_{\theta\sigma^2}$ | -534.06 | 1078.12 | 136.92 | < 0.0001 |
| Partial Metamorph $BM_{\theta\sigma^2}$ | -560.72 | 1129.43 | 188.23 | < 0.0001 |
| Partial Metamorph $OU_{\theta\sigma^2}$ | -560.72 | 1131.43 | 190.23 | < 0.0001 |
| 3 Life Cycles $OU_{\theta}$ | -562.33 | 1134.66 | 193.46 | < 0.0001 |
| Adult Ecology $OU_{\theta}$ | -563.53 | 1135.06 | 193.86 | < 0.0001 |
| 2 Life Cycles $OU_{\theta}$ | -568.41 | 1144.88 | 203.68 | < 0.0001 |
| Larval Ecology $OU_{\theta}$ | -569.68 | 1149.37 | 208.17 | < 0.0001 |
| BM1 | -572.92 | 1149.84 | 208.64 | < 0.0001 |
| Partial Metamorph $OU_{\theta}$ | -571.36 | 1150.71 | 209.51 | < 0.0001 |
| OU1 | -572.92 | 1151.84 | 210.64 | < 0.0001 |

$\theta$: bi+dd = 15.71±0.04; pd = 40.90±0.44
$\sigma^2$: bi+dd = 0.046±0.0026; pd = 1.948±0.0921

**Different plethodontid divergence time estimates (70 mya vs. 85 mya) produce the same results.** The analyses presented in the paper are a based on an average plethodontid divergence of 70 mya. However, we also performed this (and all) analyses with a plethodontid divergence of ~85 mya. Both divergence dates produce similar parameter estimates, and show that the Adult Ecology $BM_{\theta\sigma^2}$ and 3 Life Cycles $BM_{\theta\sigma^2}$ models are statistically the same.

**Removing all bolitoglossines with 14 trunk vertebrae has only a small (but not substantial) effect on this result.** Nearly all bolitoglossines (except *Oedipina*) have 14 trunk vertebrae [S23, S24]. When we remove these taxa the 3 Life Cycles $BM_{\theta\sigma^2}$ model was favored slightly over the Adult Ecology $BM_{\theta\sigma^2}$ model, but this was not substantial (ΔAIC = 4.5). The optimum for dd increased to 18 trunk vertebrae, but the rate differences among the three groups did not change.

**Treating ancestral plethodontids as biphasic (vs. direct developers) has no effect on this analysis.** Ancestral plethodontids were likely direct developers [S25-S27]. To evaluate the influence of the ancestral plethodontid life cycle on our results, we "fixed" this node as biphasic by adding an adjacent tip with and infinitely small branch and coded it as biphasic. Analyses with the ancestral plethodontid as biphasic produced equivalent parameters as the results shown above. The best-fit models (3 Life Cycles $BM_{\theta\sigma^2}$ and Adult Ecology $BM_{\theta\sigma^2}$) were also equivalent (ΔAIC = 0.2).

**Supplemental Tables S6, S7 and S8. Comparison of the fit of BM and/or OU models to *Trunk Vertebral Number* and *Adult Trunk Form*, or both variables for direct developers only.** These analyses test whether there are different rates of *Adult Trunk Form* and *Trunk Vertebral Number* evolution in bolitoglossines (minus *Oedipina*) compared to the rest of direct developers (other dds). Bolitoglossines are the most species rich clade of salamanders and nearly all (except the genus *Oedipina*) have 14 trunk vertebrae [S23, S24]. These analyses tests whether the fixed number of trunk vertebrae in this group is concomitant with strong constrains on the rate of evolution of adult trunk form. Alternatively, bolitoglossines may have evolved adult trunk form at a rate similar to other direct developers, despite static trunk vertebral numbers. BM bivariate evolutionary rate matrices for the two groups were compared to evaluate whether they shared common rates or common correlations (Table S6). Also, models were fit using OUwie [S18] and parameters allowed to vary among groups included rates of evolution ($\sigma^2$) and/or optima ($\theta$; Tables S7 and S8). Model fit was based on ΔAIC and AIC Weights ($w_i$). OU-models with multiple selection parameters ($\alpha$: $OU_{\theta\alpha}$ and $OU_{\theta\sigma^2\alpha}$) were not included, because they were poorly fit or did not improve upon simpler models. Below each table are parameter estimates and 95% confidence intervals for the best-fit models.

**Table S6. Bivariate evolutionary rate matrix analysis.** The best-fit model was "no common structure" between the bivariate matrices (*Trunk Vertebral Number* and *Adult Trunk Form*) of bolitoglossines (minus *Oedipina*) compared to other direct developers. Univariate and bivariate rates of the best-fit model for each trait and group are listed below. Note: evolvcv.lite will seemingly not execute if any variable is identical across all taxa. All of the bolitoglossines (minus *Oedipina*) that we included have 14 trunk vertebrae, so we arbitrarily set one taxon (*Aquiloeurycea cephalica*) to 14.001 trunk vertebrae for this analysis only.

| Model | -lnL | AIC | ΔAIC | $w_i$ |
|---|---|---|---|---|
| no common structure (between groups) | -33.09 | 82.18 | 0.00 | 0.9999 |
| different rates, common correlation | -47.99 | 109.99 | 27.81 | < 0.0001 |
| common rates, common correlation | -218.36 | 446.73 | 364.55 | < 0.0001 |
| common rates, different correlation | -217.77 | 447.56 | 365.38 | < 0.0001 |

| | bolitoglossines | other dds |
|---|---|---|
| $\sigma^2$ trunk vertebral number: | $1.00e^{-10}$±$4.59e^{-18}$ | 0.187±0.0703 |
| $\sigma^2$ adult trunk form: | 0.059±0.0071 | 0.066±0.0180 |
| $\sigma^2$ bivariate: | $4.68e^{-9}$±$4.59e^{-9}$ | 0.093±0.0355 |

**Table S7. Evolution of *Trunk Vertebral Number* for direct developers.** As expected, multi-rate models were substantially better than single rate models. The rate of trunk vertebral evolution in bolitoglossines (minus *Oedipina*) was dramatically slower than all other direct developers.

| Model | -lnL | AIC | ΔAIC | $w_i$ |
|---|---|---|---|---|
| $OU_{\theta\sigma^2}$ | 228.30 | -446.60 | 0.00 | 1.0000 |
| $BM_{\theta\sigma^2}$ | 133.08 | -258.17 | 188.43 | < 0.0001 |
| $BM_{\sigma^2}$ | 133.72 | -257.43 | 189.17 | < 0.0001 |
| $OU_{\theta}$ | -112.72 | 233.44 | 680.04 | < 0.0001 |
| BM1 | -119.00 | 242.00 | 688.60 | < 0.0001 |
| OU1 | -119.00 | 244.00 | 690.60 | < 0.0001 |

$\theta$: bolitoglossines = 14.02±0.01; other dds = 17.51±0.03
$\sigma^2$: bolitoglossines = 0.0003±0.0001; other dds = 49.45±0.60
$\alpha$: 4.834±0.0586

**Table S8. Evolution of *Adult Trunk Form* for direct developers.** Allowing for differences in rate among the groups does not substantially improve BM or OU models. In other words, the rate of adult trunk form evolution in bolitoglossines (minus *Oedipina*) is similar to other direct developers. Albeit not substantial, the best-fit models allowed for differences in optima between the groups.

| Model | -lnL | AIC | ΔAIC | $w_i$ |
|---|---|---|---|---|
| $BM_{\theta\sigma^2}$ | -109.94 | 227.88 | 0.00 | 0.4484 |
| $OU_{\theta}$ | -110.49 | 228.98 | 1.10 | 0.2587 |
| $OU_{\theta\sigma^2}$ | -109.93 | 229.87 | 1.99 | 0.1658 |
| BM1 | -114.01 | 232.03 | 4.15 | 0.0563 |
| $BM_{\sigma^2}$ | -113.16 | 232.32 | 4.44 | 0.0487 |
| OU1 | -113.95 | 233.90 | 6.02 | 0.0221 |

$\theta$: bolitoglossines = 7.21±0.04; other dds = 10.41±0.02
$\sigma^2$: bolitoglossines = 0.065±0.0005; other dds = 0.041±0.0002

**Supplemental Table S9. Regimes, body form metrics, and Genbank accession numbers.** Alternative life cycles include: biphasic (bi), direct development (dd), and paedomorphic (pd). Only species that are obligately paedomorphic in nature were coded as paedomorphic [S28]. Facultative paedomorphs (f-bi) were coded as biphasic unless otherwise indicated (see Facultative models in the Results section). Larval ecologies were coded based on the primary habitat utilized: lotic (lo) or lentic (le). Direct developing and viviparous species do not have a free-living larval stage, so their larval ecology is listed as na. Two closely related salamandrid genera (*Lyciasalamandra* and *Salamandra*) exhibit viviparity (vi) or ovoviviparity (ovi) [S29]. These taxa may also represent simplified life cycle modes (depending on the duration of offspring retention and developmental progression), but we pruned these taxa from our analyses due to the limited phylogenetic distribution of these reproductive modes in salamanders and their lability within some taxa. Furthermore, many "newts" in the Family Salamandridae have a three-part life cycle (aquatic larva - terrestrial eft – aquatic adult). All non-viviparous and non-ovoviviparous salamandrids were coded as biphasic. This is because all of these species minimally have a larval stage and post-metamorphic stage (the latter being potentially facultative). We acknowledge that there are potentially some species that metamorphose but remain aquatic (e.g. some, but not all, species in the genus *Pachytriton* [S30]). Terrestrial juveniles are known in *Pachytriton* (e.g. *P. feii*) and their terrestrial stage may be extensive [S30-S32]. There is generally limited life history information on wild populations for most species of *Pachytriton,* especially for juvenile stages [S30, S31]. We found that these taxa had no impact on our results (when omitted or re-coded). However, fine-scale trait analyses of such groups may prove enlightening for some characteristics [S33]. *Trunk Vertebral Number* was based on modal numbers from the literature or data collected by the authors. In species with sexually dimorphic trunk vertebral numbers, an average of male and female mode numbers was used. *Adult Body Form* was snout-to-vent length divided by body width (data from Wiens and Hoverman [S34]. *Adult Trunk Form,* which was used to analyze direct developers was snout-to-vent length minus head length divided by body width, data also from Wiens and Hoverman [S34]. Taxa included in larval shape analyses are indicated with an asterisk. Genes used for the phylogeny include three mitochondrial genes: Cytochrome oxidase 1 (*Co1*), Cytochrome b (*Cytb*), NADH dehydrogenase 2 (*ND2*), and four nuclear genes: Brain Derived Neurotrophic Factor (*BDNF*), Proopiomelanocortin (*Pomc*), Recombination Activating Gene 1 (*RAG1*), Solute carrier family 8 member A3 (*Slc8a3*).

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Ambystomatidae** | | | | | | | | | | | | | |
| *Ambystoma andersoni* | pd | lo | 15 | S35 | | | AY659993 | AY659993 | AY659993 | | | | |
| *Ambystoma annulatum** | bi | le | 16 | S36 | 8.98 | | KU986254 | | KC870849 | | | | |
| *Ambystoma barbouri* | bi | lo | | | 9.25 | | NC014568 | NC014568 | NC014568 | KJ610094 | KJ610471 | | |
| *Ambystoma bishopi* | bi | le | | | 9.14 | | NC027501 | NC027501 | NC027501 | | | | |
| *Ambystoma calforniense* | bi | le | | | 6.51 | | AY659995 | AY659995 | AY659995 | | | | |
| *Ambystoma cingulatum* | bi | le | | | | | | | KC870856 | | | | |
| *Ambystoma dumerilii* | pd | le | 15 | S37 | | | AY659994 | AY659994 | AY659994 | | | | |
| *Ambystoma gracile* | f-bi | le | | | 6.54 | | | AY691729 | KC870857 | | | AY650131 | |
| *Ambystoma jeffersonianum* | bi | le | 15 | S38,S39 | 9.36 | | | EF036687 | KC870859 | KJ610128 | KJ610490 | | |
| *Ambystoma laterale* | bi | le | | | 8.58 | | AY728218 | AY728218 | AY728218 | | | | |
| *Ambystoma mabeei* | bi | le | | | 8.42 | | KU985600 | EF036632 | KC870863 | | | | |
| *Ambystoma macrodactylum* | bi | le | 15 | S38,S39 | 8.73 | | | EF036634 | KC870864 | | | | |
| *Ambystoma maculatum** | bi | le | 14 | S38,S39 | 7.80 | | | EF036637 | KC870867 | | | | |
| *Ambystoma mexicanum** | pd | le | 15 | S37 | | | AY659991 | AY659991 | AY659991 | EF195175 | | EF551561 | EF107367 |
| *Ambystoma opacum* | bi | le | 14 | S38,S39 | 7.02 | | KU986081 | AY691730 | KC870871 | | | AY650130 | |
| *Ambystoma ordinarium* | f-bi | lo | | | 5.32 | | | | KC870872 | | | AY583345 | |
| *Ambystoma rosaceum* | f-bi | lo | | | | | | | | EU275887 | EU275841 | | |
| *Ambystoma talpoideum* | f-bi | le | 13 | S39 | 5.93 | | KU985959 | EF036640 | KC870874 | | | | |
| *Ambystoma texanum** | bi | le | 16 | S39 | 8.04 | | GU078471 | GU078471 | GU078471 | KJ610104 | KJ610445 | | |
| *Ambystoma tigrinum* | f-bi | le | 15 | S38,S39 | 5.88 | | AY659992 | AY659992 | AY659992 | | | | |
| **Amphiumidae** | | | | | | | | | | | | | |
| *Amphiuma means* | pd | le | 61 | S36,S37 | 17.43 | | FJ951301 | AY691722 | AY916037 | | FJ951366 | AY650127 | JX145021 |
| *Amphiuma pholeter* | pd | le | 60 | S36 | 25.25 | | FJ951302 | AY691723 | AY916035 | | FJ951367 | AY650128 | JX145022 |
| *Amphiuma tridactylum** | pd | le | 61 | S36 | 17.03 | | FJ951300 | FJ951359 | AY916036 | EU275863 | FJ951368 | FJ951369 | JX145023 |
| **Cryptobranchidae** | | | | | | | | | | | | | |
| *Andrias davidianus* | pd | lo | 17 | S36 | 6.85 | | NC004926 | NC004926 | NC004926 | EU275889 | EU275843 | AY650142 | AY948911 |
| *Andrias japonicus* | pd | lo | | | | | AB208679 | AB208679 | AB208679 | | | AY583346 | |
| *Cryptobranchus alleganiensis** | pd | lo | 18 | S36,S37 | 6.18 | | GQ368662 | GQ368662 | GQ368662 | | | AY650141 | |
| **Dicamptodontidae** | | | | | | | | | | | | | |
| *Dicamptodon copei** | pd | lo | 15 | S36 | 7.30 | | | AY734609 | | | KC295575 | AY691695 | JX145020 |
| *Dicamptodon ensatus* | f-bi | lo | 14 | S36 | 6.36 | | KU985936 | AY734622 | | | | EF107335 | |
| *Dicamptodon tenebrosus** | f-bi | lo | 14 | S36 | 6.15 | | | AY734613 | AY916018 | EU275870 | EU275824 | AY650132 | |
| **Hynobiidae** | | | | | | | | | | | | | |
| *Batrachuperus karlschmidti* | bi | lo | | | | | KF748919 | KF748917 | KF748919 | | | KJ715360 | |
| *Batrachuperus longdongensis* | bi | lo | | | | | DQ333809 | DQ333809 | DQ333809 | HM037737 | HM037762 | HM037712 | |
| *Batrachuperus pinchonii* | bi | lo | 17 | S40 | 6.87 | | DQ333815 | DQ333815 | DQ333815 | HM037738 | HM037763 | HM037713 | EF107362 |
| *Batrachuperus tibetanus* | bi | lo | | | | | DQ333817 | DQ333817 | DQ333817 | HM037739 | HM037764 | HM037714 | |
| *Batrachuperus yenyuanensis* | bi | lo | | | 7.05 | | DQ333818 | DQ333818 | DQ333818 | HM037740 | HM037765 | HQ902535 | |
| *Hynobius abei* | bi | le | | | 7.16 | | | | AY915939 | | | | |
| *Hynobius amjiensis* | bi | le | | | | | DQ333808 | DQ333808 | DQ333808 | HM037741 | HM037766 | HM037716 | |
| *Hynobius boulengeri* | bi | lo | | | | | | | AY915936 | | | | |
| *Hynobius chinensis* | bi | le | | | | | DQ333819 | DQ333819 | DQ333819 | HM037742 | HM037767 | HM037717 | |
| *Hynobius dunni* | bi | le | | | 7.88 | | | LC003308 | AY915926 | | | | |
| *Hynobius formosanus* | bi | lo | | | | | DQ333816 | DQ333816 | DQ333816 | | | DQ347285 | EF107400 |
| *Hynobius guabangshanensis* | bi | le | | | | | GU384690 | GU384690 | GU384690 | HM037743 | HM037768 | HM037718 | |
| *Hynobius hidamontanus* | bi | le | | | | | JQ929919 | JQ929919 | JQ929919 | | | | |
| *Hynobius kimurae* | bi | lo | | | | | JQ929920 | JQ929920 | JQ929920 | | | KJ715369 | |
| *Hynobius leechii** | bi | le | 16 | S40 | 7.30 | | DQ333811 | DQ333811 | DQ333811 | HM037744 | HM037769 | HM037719 | |
| *Hynobius lichenatus* | bi | le | | | 7.64 | | JQ929921 | JQ929921 | JQ929921 | | | | |
| *Hynobius maoershanensis* | bi | le | | | | | NC023789 | NC023789 | NC023789 | HM037745 | HM037770 | HM037720 | |
| *Hynobius naevius* | bi | lo | 17 | S40 | 7.48 | | | AB266672 | AY915937 | | | | |
| *Hynobius nebulosus* | bi | le | 16 | S40 | 7.96 | | HM036356 | HM036356 | HM036356 | HM037746 | HM037771 | AY650144 | |
| *Hynobius nigrescens* | bi | le | 15 | S40 | 7.39 | | JQ929922 | JQ929922 | JQ929922 | | | KJ715356 | |
| *Hynobius quelpaertensis* | bi | lo | | | | | EF201847 | EF201847 | EF201847 | HM037747 | HM037772 | HM037722 | |
| *Hynobius retardatus* | f-bi | le | | | | | HM036351 | HM036351 | HM036351 | HM037748 | HM037773 | HM037723 | |
| *Hynobius sonani* | bi | lo | | | | | | | AY915945 | EU275864 | EU275818 | | |
| *Hynobius stejnegeri* | bi | lo | | | 8.87 | | | AB921162 | AY915938 | | | | |
| *Hynobius takedai* | bi | le | | | | | | | AY915942 | | | | |
| *Hynobius tokyoensis* | bi | le | | | | | HM036357 | HM036357 | HM036357 | HM037749 | HM037774 | HM037724 | |
| *Hynobius tsuensis* | bi | le | | | 7.61 | | JQ929923 | JQ929923 | JQ929923 | | | | |
| *Hynobius yangi* | bi | lo | | | | | JN415127 | JN415127 | JN415127 | | | | |
| *Hynobius yiwuensis* | bi | le | | | | | HM036354 | HM036354 | HM036354 | HM037750 | HM037775 | HM037725 | |
| *Liua shihi* | bi | lo | 16.5 | S40,S41 | 7.13 | | DQ333810 | DQ333810 | DQ333810 | HM037751 | HM037776 | HM037726 | |
| *Liua tsinpaensis* | bi | lo | | | | | KP233806 | KP233806 | KP233806 | HM037752 | HM037777 | HM037727 | |
| *Onychodactylus fischeri** | bi | lo | 20 | S40 | | | DQ333820 | DQ333820 | DQ333820 | HM037753 | HM037778 | KC165594 | |
| *Onychodactylus japonicus* | bi | lo | 18 | S40 | 9.21 | | JX158189 | AB452955 | AY915923 | | | AY650143 | |
| *Onychodactylus zhangyapingi* | bi | lo | | | | | NC026853 | NC026853 | NC026853 | | | KJ715373 | |

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Pachyhynobius shangchengensis* | bi | lo | | | 7.46 | | DQ333812 | DQ333812 | DQ333812 | HM037754 | HM037779 | HM037729 | |
| *Paradactylodon gorganensis* | bi | lo | | | | | DQ333822 | DQ333822 | DQ333822 | HM037755 | HM037780 | HM037730 | |
| *Paradactylodon mustersi* | bi | lo | 17 | S40 | 6.87 | | DQ333821 | DQ333821 | DQ333821 | HM037756 | HM037781 | HM037731 | |
| *Pseudohynobius flavomaculatus* | bi | lo | | | | | NC020635 | NC020635 | NC020635 | HM037758 | HM037783 | HM037733 | |
| *Pseudohynobius jinfo* | bi | le | | | | | NC026698 | NC026698 | NC026698 | | | | |
| *Pseudohynobius puxiongensis* | bi | lo | 17 | S42 | | | NC020634 | NC020634 | NC020634 | HM037757 | HM037782 | HM037732 | |
| *Pseudohynobius shuichengensis* | bi | le | | | | | NC021001 | NC021001 | NC021001 | HM037759 | HM037784 | HM037734 | |
| *Ranodon sibiricus* | bi | lo | 15 | S40 | 7.40 | | NC004021 | NC004021 | NC004021 | HM037760 | HM037785 | HM037735 | |
| *Salamandrella keyserlingii* | bi | le | 17 | S40 | 6.92 | | DQ333814 | DQ333814 | DQ333814 | HM037761 | HM037786 | AY650145 | |
| *Salamandrella tridactyla* | bi | le | | | | | NC021106 | NC021106 | NC_021106 | KJ855094 | | KJ855096 | |
| **Plethodontidae** | | | | | | | | | | | | | |
| *Aneides aeneus* | dd | na | 16 | S36 | 9.95 | 7.8 | | AY691742 | | EU275890 | EU275844 | AY691701 | |
| *Aneides ferreus* | dd | na | 17 | S36 | | | DQ105339 | KF781793 | DQ105339 | EU275891 | EU275845 | EU275805 | |
| *Aneides flavipunctatus* | dd | na | 16 | S36 | 9.89 | 7.9 | AY728214 | AY728214 | AY728214 | EU275894 | EU275848 | EU275809 | |
| *Aneides hardii* | dd | na | 16 | S36 | 9.89 | 8 | AY728226 | AY728226 | AY728226 | EU275857 | EU275811 | EU275780 | |
| *Aneides lugubris* | dd | na | 16 | S36 | 7.41 | 5.8 | DQ105329 | AY691758 | | EU275893 | EU275847 | AY650118 | |
| *Aneides vagrans* | dd | na | | | 10.51 | | DQ105343 | KF781800 | | EU275892 | EU275846 | EU275806 | |
| *Aquiloeurycea cephalica* | dd | na | 14 | S23 | 9.68 | 7.7 | KP886919 | KP900066 | | | KP900108 | KP900152 | KP900198 |
| *Aquiloeurycea galeanae* | dd | na | | | 8.88 | | KP886904 | KP900051 | | | KP900093 | KP900137 | KP900184 |
| *Aquiloeurycea quetzalanensis* | dd | na | | | | | | KP900055 | | | KP900097 | KP900141 | KP900188 |
| *Batrachoseps altasierrae* | dd | na | 18.5 | S43 | | | | KM203060 | | | KM202828 | KM203006 | |
| *Batrachoseps attenuatus* | dd | na | | | 13.77 | | EU117188 | | EU117188 | JF449372 | KM202699 | KM202873 | KP900217 |
| *Batrachoseps bramei* | dd | na | 18.5 | S43 | | | | JQ035768 | | | KM202847 | KM203025 | |
| *Batrachoseps campi* | dd | na | 18 | S44 | | | EU117193 | KM203094 | EU117193 | | KM202860 | KM203039 | |
| *Batrachoseps diabolicus* | dd | na | 20 | S44,S45 | | | EU117190 | KM203054 | EU117190 | | KM202783 | KM202961 | |
| *Batrachoseps gabrieli* | dd | na | 20 | S44,S46 | | | EU117195 | KM203056 | EU117195 | | KM202763 | KM202941 | |
| *Batrachoseps gavilanensis* | dd | na | 20 | S44,S47 | | | EU117191 | KM203065 | EU117191 | | KM202725 | KM202901 | |
| *Batrachoseps gregarius* | dd | na | 21 | S44,S45 | | | EU117192 | KM203079 | EU117192 | | KM202790 | KM202968 | |
| *Batrachoseps incognitus* | dd | na | | | | | | KM203058 | | | KM202737 | KM202913 | |
| *Batrachoseps kawia* | dd | na | 20 | S44,S45 | | | | KM203066 | | | KM202822 | KM203000 | |
| *Batrachoseps luciae* | dd | na | | | | | | KM203053 | | | KM202713 | KM202889 | |
| *Batrachoseps major* | dd | na | 20.5 | S44 | 14.72 | 12.7 | EU117194 | JQ250228 | EU117194 | EU275901 | KM202771 | KM202949 | |
| *Batrachoseps minor* | dd | na | | | | | | JQ250327 | | | KM202738 | KM202914 | |
| *Batrachoseps nigriventris* | dd | na | 21 | S44 | | | NC028184 | NC028184 | NC028184 | | KM202745 | KM202927 | |
| *Batrachoseps pacificus* | dd | na | | | | | | JQ250330 | | | KM202758 | KM202935 | |
| *Batrachoseps pacificus* | dd | na | 20 | S44 | | | | JQ250330 | | | KM202758 | KM202935 | |
| *Batrachoseps regius* | dd | na | 19.5 | S44,S45 | | | | KM203071 | | | KM202811 | KM202989 | |
| *Batrachoseps relictus* | dd | na | 18.5 | S44 | | | | KM203093 | | | KM202852 | KM203030 | |
| *Batrachoseps robustus* | dd | na | | | | | | KM203064 | | | KM202862 | KM203040 | |
| *Batrachoseps simatus* | dd | na | 20.5 | S43 | | | | JQ035754 | | | KM202851 | KM203029 | |
| *Batrachoseps wrighti* | dd | na | 17 | S44 | | | | KM203062 | | JF449369 | KM202865 | KM203043 | |
| *Batrachoseps wrightorum* | dd | na | | | | | AY728221 | AY728221 | AY728221 | | | EU020165 | |
| *Bolitoglossa adspersa* | dd | na | 14 | S44,S45 | 9.82 | 8.1 | | AF212984 | | | | | |
| *Bolitoglossa alberchi* | dd | na | | | | | KP886900 | KP735278 | | KP735258 | KP735288 | KP735306 | KP735323 |
| *Bolitoglossa alvaradoi* | dd | na | | | | | | AY526194 | | | | | |
| *Bolitoglossa aureogularis* | dd | na | | | | | | JQ899182 | | | | | |
| *Bolitoglossa biseriata* | dd | na | | | | | KM527317 | AY526161 | | | | KC614436 | |
| *Bolitoglossa borburata* | dd | na | | | | | | | | | | | |
| *Bolitoglossa bramei* | dd | na | | | | | | JQ899189 | | | | | |
| *Bolitoglossa carri* | dd | na | | | | | | AY526176 | | | | KC614458 | |
| *Bolitoglossa cataguana* | dd | na | | | | | | KJ628090 | | | | | |
| *Bolitoglossa celaque* | dd | na | | | | | | AY526177 | | | | | |
| *Bolitoglossa cerroensis* | dd | na | 14 | S23 | | | | AF212096 | | | | KC614459 | |
| *Bolitoglossa chinanteca* | dd | na | | | | | | KC288079 | | | KC288041 | | |
| *Bolitoglossa chucantiensis* | dd | na | | | | | KM527308 | | | | | | |
| *Bolitoglossa colonnea* | dd | na | 14 | S23 | | | FJ766578 | AY526162 | | | | | |
| *Bolitoglossa compacta* | dd | na | | | | | | JQ899193 | | | | | |
| *Bolitoglossa conanti* | dd | na | | | | | | GU725458 | | | | KC699924 | |
| *Bolitoglossa cuchumatana* | dd | na | | | | | | GU725467 | | | | | |
| *Bolitoglossa cuna* | dd | na | | | | | KM527307 | | | | | | |
| *Bolitoglossa decora* | dd | na | | | | | | AY526180 | | | | | |
| *Bolitoglossa diaphora* | dd | na | | | | | | GU725460 | | | | | |
| *Bolitoglossa dofleini* | dd | na | 14 | S36 | 6.67 | 5.5 | | KP900047 | | | KP900089 | KP900133 | KP900180 |
| *Bolitoglossa dunni* | dd | na | 14 | S23 | | | | GU725459 | | | | KC614438 | |
| *Bolitoglossa engelhardti* | dd | na | 14 | S23 | 10.89 | 8.6 | | GU725461 | | | | KC699925 | |
| *Bolitoglossa epimela* | dd | na | | | | | | AF212097 | | | | | |
| *Bolitoglossa equitoriana* | dd | na | | | | | | DQ353842 | | | | KC614451 | |
| *Bolitoglossa eremia* | dd | na | | | | | | HQ009998 | | | | | |
| *Bolitoglossa flavimembris* | dd | na | | | | | | GU725462 | | | KP900087 | KP900132 | KP900178 |
| *Bolitoglossa flaviventris* | dd | na | 14 | S23 | | | | AF212983 | | | | | |
| *Bolitoglossa franklini* | dd | na | | | | | | AY526184 | | | | KC614439 | |
| *Bolitoglossa gomezi* | dd | na | | | | | | JQ899171 | | | | | |
| *Bolitoglossa gracilis* | dd | na | | | | | | AF212067 | | | | | |
| *Bolitoglossa hartwegi* | dd | na | | | | | KP886897 | KC288103 | | | KC288057 | KP900131 | |
| *Bolitoglossa heiroreias* | dd | na | | | | | | HQ010010 | | | | | |
| *Bolitoglossa helmrichi* | dd | na | 14 | S23 | | | | AY691755 | | | | AY650124 | |
| *Bolitoglossa hermosa* | dd | na | | | | | | AF416678 | | | | | |
| *Bolitoglossa kamuk* | dd | na | | | | | | JQ899175 | | | | | |
| *Bolitoglossa kaqchikelorum* | dd | na | | | | | | HQ010020 | | | | | |
| *Bolitoglossa lincolni* | dd | na | | | | | | GU725464 | | | | KC614440 | |
| *Bolitoglossa longissima* | dd | na | | | | | | AY526186 | | | | KC614441 | |
| *Bolitoglossa macrinii* | dd | na | | | | | | AF416679 | | | | | |
| *Bolitoglossa marmorea* | dd | na | 14 | S23 | | | | U89627 | | | | | |
| *Bolitoglossa medemi* | dd | na | | | | | KM527309 | AY526163 | | | | KC614437 | |
| *Bolitoglossa meliana* | dd | na | | | | | | KJ175105 | | | | | |
| *Bolitoglossa mexicana* | dd | na | 14 | S23 | 10.49 | 8.6 | | KC288104 | | | KC288058 | EF018055 | EF107384 |
| *Bolitoglossa minutula* | dd | na | | | | | | AF212098 | | | | KC614434 | |
| *Bolitoglossa mombachoensis* | dd | na | | | | | | AY133485 | | | | | |
| *Bolitoglossa morio* | dd | na | 14 | S23,S36 | 8.13 | 6.6 | | KJ787752 | | | | KC699926 | |
| *Bolitoglossa mucuyensis* | dd | na | | | | | JQ665278 | JQ665282 | | | | | |
| *Bolitoglossa mulleri* | dd | na | | | 9.52 | | | HQ010012 | | | | | |
| *Bolitoglossa nigrescens* | dd | na | 14 | S23 | | | | JQ899194 | | | | | |
| *Bolitoglossa nympha* | dd | na | | | | | KP886896 | KC288068 | | | KC288021 | KP900130 | KP900176 |
| *Bolitoglossa oaxacensis* | dd | na | | | | | | AF416681 | | | KP900088 | | KP900179 |
| *Bolitoglossa occidentalis* | dd | na | 14 | S23 | 10.40 | 8.1 | | AY526158 | | | KC288030 | KC614435 | |
| *Bolitoglossa odonnelli* | dd | na | | | | | | HQ009993 | | | | KC699922 | |
| *Bolitoglossa orestes* | dd | na | 14 | S23 | | | | JQ665281 | | | | | |
| *Bolitoglossa pacaya* | dd | na | | | | | | KJ787751 | | | | | |
| *Bolitoglossa palmata* | dd | na | | | 9.38 | | | AY526164 | | | | | |
| *Bolitoglossa paraensis* | dd | na | | | | | | AY526166 | | | | | |
| *Bolitoglossa peruviana* | dd | na | | | | | | DQ353815 | | | | KC614443 | |

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Bolitoglossa pesrubra* | dd | na | | | | | | AF212070 | | | | | |
| *Bolitoglossa platydactyla* | dd | na | 14 | S23 | 8.93 | 7.4 | | AY133484 | | | | KC699923 | |
| *Bolitoglossa porrasorum* | dd | na | | | | | | AY526188 | | | | | |
| *Bolitoglossa riletti* | dd | na | | | | | | AF416682 | | | | | |
| *Bolitoglossa robinsoni* | dd | na | | | | | | JQ899191 | | | | | |
| *Bolitoglossa robusta* | dd | na | 14 | S23 | 8.04 | 6.7 | | EU448110 | | | | | |
| *Bolitoglossa rostrata* | dd | na | 14 | S23,S36 | 10.52 | 8.6 | | KJ175107 | | | | | |
| *Bolitoglossa rufescens* | dd | na | 14 | S23 | 8.77 | 7.1 | KR736078 | KC288065 | | | KC288019 | KF911887 | |
| *Bolitoglossa schizodactyla* | dd | na | 14 | S23 | | | FJ766579 | AY526171 | | | | | |
| *Bolitoglossa sombra* | dd | na | | | | | | | | EU275897 | EU275851 | | KP900181 |
| *Bolitoglossa splendida* | dd | na | | | | | | JQ899181 | | | | | |
| *Bolitoglossa subpalmata* | dd | na | 14 | S23,S36 | 8.80 | 7.3 | | AF212092 | | | | | |
| *Bolitoglossa suchitanensis* | dd | na | | | | | | HQ010001 | | | | | |
| *Bolitoglossa synoria* | dd | na | | | | | | AY526193 | | | | | |
| *Bolitoglossa tica* | dd | na | | | | | | JQ899192 | | | | | |
| *Bolitoglossa yucatana* | dd | na | | | 9.98 | | | AF212980 | | | | | |
| *Bolitoglossa zapoteca* | dd | na | | | | | | AF416683 | | | | | |
| *Bradytriton silus* | dd | na | 14 | S48 | 7.75 | 6.3 | KP886934 | KP337342 | | KP735274 | KP735303 | KP735308 | KP735326 |
| *Chiropterotriton arboreus* | dd | na | 14 | S23 | | | | KP900083 | | | KP900124 | KP900170 | KP900212 |
| *Chiropterotriton chondrostega* | dd | na | | | 10.93 | | | KT820699 | | | | | |
| *Chiropterotriton cracens* | dd | na | | | | | | KT820700 | | | | | |
| *Chiropterotriton dimidiatus* | dd | na | 14 | S23 | 11.95 | 9.5 | | KT820701 | | | | | |
| *Chiropterotriton lavae* | dd | na | | | 11.54 | | | KT820702 | | | | | |
| *Chiropterotriton magnipes* | dd | na | | | | | | KP900085 | | | KP900126 | KP900172 | KP900214 |
| *Chiropterotriton miquihuanus* | dd | na | | | | | | KT820713 | | | | | |
| *Chiropterotriton mosaueri* | dd | na | | | | | | KT820703 | | | | | |
| *Chiropterotriton multidentatus* | dd | na | 14 | S23,S36 | 12.33 | 9.6 | | KT820704 | | | | | |
| *Chiropterotriton priscus* | dd | na | 14 | S23 | 9.39 | 7.6 | | KT820707 | | | | | |
| *Cryptotriton alvarezdeltoroi* | dd | na | | | | | | KP735279 | | KP735269 | KP735293 | KP735318 | KP735332 |
| *Cryptotriton monzoni* | dd | na | | | | | | KJ547609 | | KP735262 | KP735290 | KP735314 | KP735328 |
| *Cryptotriton nasalis* | dd | na | 14 | S24 | 10.96 | 8.7 | KP886935 | KJ563294 | | KP735264 | KP735291 | KP735310 | KP735335 |
| *Cryptotriton necopinus* | dd | na | | | | | | KJ547610 | | KP735268 | KP735296 | KP735309 | |
| *Cryptotriton sierraminensis* | dd | na | | | | | | KJ547605 | | KP735267 | KP735295 | KP735312 | KP735336 |
| *Cryptotriton varaepacis* | dd | na | | | | | | KJ547606 | | KP735266 | KP735297 | KP735317 | KP735329 |
| *Dendrotriton bromeliacius* | dd | na | 14 | S48 | | | KP886939 | JN559990 | | KP735259 | JN560007 | JN560024 | JN560041 |
| *Dendrotriton chujorum* | dd | na | | | | | | JN559993 | | | JN560010 | JN560026 | JN560044 |
| *Dendrotriton cuchumatanus* | dd | na | 14 | S48 | | | | JN559995 | | | JN560012 | JN560028 | JN560046 |
| *Dendrotriton kekchiorum* | dd | na | | | | | | JN559996 | | | JN560013 | JN560030 | JN560047 |
| *Dendrotriton megarhinus* | dd | na | 14 | S48 | | | | JN559998 | | | JN560015 | JN560031 | JN560049 |
| *Dendrotriton rabbi* | dd | na | 14 | S48 | | | | AF199194 | | | JN560016 | JN560033 | JN560050 |
| *Dendrotriton sanctibarbarus* | dd | na | | | | | KP886940 | JN560000 | | | JN560017 | JN560034 | JN560051 |
| *Dendrotriton xolocalcae* | dd | na | 14 | S23 | 12.92 | 10.1 | | JN560004 | | | JN560021 | JN560037 | JN560055 |
| *Desmognathus abditus* | bi | lo | | | | | | | KR732330 | | KR732341 | KR732365 | |
| *Desmognathus aeneus* | dd | na | 15 | S23 | 10.07 | 8 | KU985866 | AY691736 | AY612342 | | KR732342 | AY691696 | |
| *Desmognathus apalachicolae* | bi | lo | | | | | EU311666 | | AY612373 | | KR732343 | KR732367 | |
| *Desmognathus auriculatus* | bi | le | 15 | S23 | 9.35 | | EU311650 | | AY612414 | | KR732344 | KR732368 | |
| *Desmognathus brimleyorum** | bi | lo | 15 | S36 | 8.34 | | KU986036 | AY691737 | AY612422 | EU275865 | EU275819 | AY691697 | |
| *Desmognathus carolinensis* | bi | lo | 15 | S36 | | | EU311642 | AF442540 | AY612368 | | KR732345 | KR732369 | |
| *Desmognathus conanti* | bi | lo | | | | | EU311667 | KF242415 | AY612383 | | KR732346 | KR732370 | |
| *Desmognathus folkertsi* | bi | lo | | | | | EU311714 | | AY612351 | | KR732347 | KM107913 | |
| *Desmognathus fuscus* | bi | lo | 15 | S23 | 8.03 | | AY728227 | AY728227 | AY728227 | EU275858 | EU275812 | KR827007 | |
| *Desmognathus imitator* | bi | lo | | | 9.60 | | AF437504 | | AY612343 | | KR732349 | KR732373 | |
| *Desmognathus marmoratus* | bi | lo | 15 | S23,S36 | 7.73 | | EU311718 | | AY612344 | | KR732350 | KR732374 | |
| *Desmognathus monticola* | bi | lo | 15 | S23,S36 | 7.70 | | | AY691738 | AY612374 | | KR732352 | AY691698 | EF107391 |
| *Desmognathus ochrophaeus* | bi | lo | 15 | S23 | 8.91 | | KU986074 | AF442525 | AY612366 | | KR732353 | KR732377 | |
| *Desmognathus ocoee* | bi | lo | 15 | S23,S36 | | | | AF442541 | AY612352 | | KR732354 | KR827010 | |
| *Desmognathus orestes* | bi | lo | | | | | EU311703 | AF442536 | AY612363 | | KR732356 | KR827015 | |
| *Desmognathus organi* | dd | na | | | | | | KF242417 | KR827001 | | KR732357 | KR732381 | |
| *Desmognathus planiceps* | bi | lo | | | | | | EF028646 | KR732337 | | KR732358 | KR732382 | |
| *Desmognathus quadramaculatus** | bi | lo | 15 | S23,S36 | 7.08 | | EU311700 | AY691739 | AY612347 | | KR732359 | AY650117 | |
| *Desmognathus santeetlah* | bi | lo | | | | | EU311676 | KF242410 | AY612391 | | KR732360 | KR732384 | |
| *Desmognathus welteri* | bi | lo | | | 8.47 | | EU311675 | | AY612416 | | KR732362 | KR732386 | |
| *Desmognathus wrighti* | dd | na | 15 | S23 | 10.71 | 8.5 | KU986239 | AY691740 | KR732339 | | KR732363 | AY691699 | |
| *Ensatina eschscholtzii* | dd | na | 14 | S36 | 9.17 | 7.4 | AY728216 | AY728216 | | EU275862 | EU275816 | AY650119 | EF107441 |
| *Eurycea aquatica* | bi | lo | | | | | | KF562543 | FJ785624 | | | KF562645 | |
| *Eurycea bislineata** | bi | lo | 15 | S36 | 11.13 | | AY728217 | AY528402 | JQ920804 | EU275861 | EU275815 | AY691706 | |
| *Eurycea chamberlaini* | bi | le | 17 | S36 | | | | KF562544 | JQ920881 | | JQ920752 | KF562646 | |
| *Eurycea chisholmensis* | pd | lo | 18 | S36 | | | | KF562545 | | | | KF562647 | |
| *Eurycea cirrigera* | f-bi | lo | 15 | S36 | 11.04 | | | KF562548 | DQ018556 | | JQ920728 | KF562650 | |
| *Eurycea guttolineata* | bi | lo | 15 | S36 | | | | KF562549 | DQ018388 | | JQ920731 | KF562651 | |
| *Eurycea junaluska* | bi | lo | | | 10.05 | | | KF562550 | DQ018655 | | | FJ750246 | |
| *Eurycea latitans* | pd | lo | 18 | S36 | 9.23 | | | KF562551 | JQ920812 | | | KF562652 | |
| *Eurycea longicauda* | bi | lo | 15 | S36 | 10.84 | | | AY528403 | DQ018386 | | JQ920730 | AY650121 | |
| *Eurycea longicauda melanopleura* | bi | lo | 15 | S36 | | | | KF562552 | FJ866452 | | | KF562653 | |
| *Eurycea lucifuga* | bi | lo | 15 | S36 | 9.86 | | | KF562553 | JQ920807 | | JQ920729 | KF562654 | |
| *Eurycea multiplicata* | bi | lo | 20 | S36 | 12.49 | | | AY528339 | JQ920803 | | JQ920725 | AY691707 | |
| *Eurycea nana* | pd | lo | 17 | S36 | 12.75 | | | KF562554 | JQ920814 | | JQ920735 | KF562656 | |
| *Eurycea naufragia* | pd | lo | 17 | S36 | | | | KF562555 | JQ920811 | | JQ920733 | KF562657 | |
| *Eurycea neotenes** | pd | lo | 17 | S36 | 10.87 | | | AY528400 | JQ920817 | | | AY650122 | |
| *Eurycea paludicola** | bi | le | 17 | S36 | 12.62 | | | AY528401 | JQ920823 | | JQ920740 | KF562662 | |
| *Eurycea pterophila* | pd | lo | 17 | S36 | | | | KF562556 | JQ920816 | | | KF562658 | |
| *Eurycea quadridigitata* | bi | le | 17 | S36 | | | | KF562560 | JQ920863 | | JQ920750 | KF562658 | EF107397 |
| *Eurycea rathbuni** | pd | lo | 13 | S36 | 9.20 | | | KF562561 | | | | AY691708 | |
| *Eurycea sosorum* | pd | lo | 16 | S36 | 11.29 | | | KF562562 | JQ920815 | | | KF562664 | |
| *Eurycea spelaea* | bi | lo | 19 | S36 | 9.39 | | | AY528397 | | | | KF562667 | |
| *Eurycea subfluvicola* | pd | lo | 21 | S36 | | | | KJ372372 | | | | KJ372331 | |
| *Eurycea tonkawae* | pd | lo | 17 | S36 | | | | KF562564 | JQ920810 | | JQ920732 | AY691709 | |
| *Eurycea tridentifera* | pd | le | 14 | S36 | 8.40 | | | KF562565 | | | | KF562669 | |
| *Eurycea troglodytes* Metamorphic | f-bi | lo | | | | | | KF562567 | | | | KF562671 | |
| *Eurycea troglodytes* Paedomorphic | f-bi | lo | | | | | | KF562568 | JQ920813 | | JQ920734 | KF562672 | |
| *Eurycea tynerensis* Metamorphic* | f-bi | lo | 20 | S36 | | | | AY528367 | | | | KF562676 | |
| *Eurycea tynerensis* Paedomorphic* | pd | lo | 21 | S36 | 13.41 | | | AY528374 | | | | KF562675 | |
| *Eurycea wallacei* | pd | le | 14 | S23,S36 | 16.97 | | | KF562583 | | | | KF562693 | |
| *Eurycea waterlooensis* | pd | le | 13 | S36 | | | | KF562569 | | | | KF562679 | |
| *Eurycea wilderae* | bi | lo | 15 | S36 | 11.01 | | | KF562570 | DQ018650 | | JQ920727 | KF562680 | |
| *Gyrinophilus gulolineatus* | pd | lo | | | | | | KF562571 | | | | KF562681 | |
| *Gyrinophilus palleucus* | pd | lo | 19 | S50 | | | NC028297 | KF562574 | | | | KF562684 | |
| *Gyrinophilus porphyriticus** | bi | lo | 18 | S36 | 10.26 | | | KF562581 | | EU275899 | EU275853 | KF562691 | |
| *Gyrinophilus subterraneus* | f-bi | lo | | | | | | KF562582 | | | | KF562692 | |
| *Hemidactylium scutatum* | bi | le | 15 | S36 | 9.62 | | AY728231 | AY728231 | AY728231 | EU275898 | EU275852 | AY691711 | |
| *Hydromantes ambrosii* | dd | na | 13 | S51 | | | | FJ602258 | | FJ602195 | | FJ602321 | |
| *Hydromantes brunus* | dd | na | 14 | S36 | | | AY728234 | AY728234 | AY728234 | EU275871 | EU275825 | AY887134 | HM797690 |

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Hydromantes flavus* | dd | na | 13 | S51 | | | | | | FJ602199 | | FJ602327 | |
| *Hydromantes genei* | dd | na | | | 12.39 | | | | | FJ602205 | EU275840 | FJ602333 | |
| *Hydromantes imperialis* | dd | na | 13 | S51 | | | | FJ602288 | KJ834057 | FJ602219 | | FJ602359 | |
| *Hydromantes italicus* | dd | na | 13 | S51 | 11.48 | 9.1 | AY728215 | AY728215 | AY728215 | EU275872 | EU275826 | EU275792 | EF107415 |
| *Hydromantes platycephalus* | dd | na | | | 9.48 | | KU985943 | | | EU275874 | EU275828 | HM797646 | HM797672 |
| *Hydromantes shastae* | dd | na | | | | | | HSU89610 | | EU275875 | EU275829 | HM797671 | HM797759 |
| *Hydromantes strinatii* | dd | na | 13 | S51 | | | | FJ602305 | KJ834039 | FJ602245 | | FJ602367 | |
| *Hydromantes supramontis* | dd | na | 13 | S51 | | | | | KJ834058 | FJ602248 | | FJ602370 | |
| *Isthmura bellii* | dd | na | 14 | S23 | 8.77 | 7.1 | | AY864681 | | | | | |
| *Ixalotriton parvus* | dd | na | | | | | | | | | KP900117 | | KP900205 |
| *Ixalotriton niger* | dd | na | | | | | | | | | KP900118 | | KP900206 |
| *Karsenia koreana* | dd | na | 16 | S52 | | | | JF449367 | JF449367 | EU275868 | EU275822 | AY887135 | |
| *Nototriton abscondens* | dd | na | | | | | AY728229 | AY728229 | | JF449371 | JF449373 | JF449379 | |
| *Nototriton barbouri* | dd | na | 14 | S48 | | | JN377401 | AF199138 | | | | | |
| *Nototriton brodei* | dd | na | | | | | KP886938 | KP735285 | | KP735276 | KP735305 | KP735322 | KP735325 |
| *Nototriton limnospectator* | dd | na | | | | | KP886937 | JQ899197 | | | KP735304 | KP735321 | KP735324 |
| *Nototriton picadoi* | dd | na | 14 | S48 | 6.89 | 5.5 | | AF199145 | | | | | |
| *Nototriton picucha* | dd | na | | | | | JN377404 | | | | | | |
| *Nototriton richardi* | dd | na | 14 | S48 | | | | AF199147 | | | | | |
| *Nototriton saslaya* | dd | na | | | | | JN377406 | | | | | | |
| *Nyctanolis pernix* | dd | na | | | 11.40 | | | | | KP735277 | JN560023 | AY691714 | JN560057 |
| *Oedipina carablanca* | dd | na | 18 | S53 | | | | FJ196869 | | | | | |
| *Oedipina complex* | dd | na | 18 | S53 | 15.70 | 13.1 | | AF199157 | | | | | |
| *Oedipina cyclocauda* | dd | na | | | 14.94 | | | AF199158 | | | | | |
| *Oedipina elongata* | dd | na | 18 | S53 | | | | AF199160 | | | | | |
| *Oedipina gephyra* | dd | na | | | | | | AF199161 | | | | | |
| *Oedipina gracilis* | dd | na | | | | | | AF199163 | | | | | |
| *Oedipina grandis* | dd | na | | | | | | AF199165 | | | | | |
| *Oedipina maritima* | dd | na | 18 | S24 | | | | AF199166 | | | | | |
| *Oedipina nica* | dd | na | | | | | KP886941 | JN560005 | | KP735261 | JN560022 | JN560039 | JN560056 |
| *Oedipina parvipes* | dd | na | 18 | S53 | 13.95 | 11.7 | FJ766760 | AF199155 | | | | | |
| *Oedipina poelzi* | dd | na | | | | | NC006326 | NC_006326 | NC006326 | | | | |
| *Oedipina pseudouniformis* | dd | na | | | | | | AF199178 | | | | | |
| *Oedipina savagei* | dd | na | 18 | S24 | | | | AF199153 | | | | | |
| *Oedipina taylori* | dd | na | 22.5 | S36,S53 | | | | KP900080 | | | KP900121 | KP900167 | KP900209 |
| *Oedipina tomasi* | dd | na | | | | | KP886942 | KP900079 | | | KP900120 | KP900166 | KP900208 |
| *Oedipina uniformis* | dd | na | 20.5 | S53 | 15.09 | 13 | | AF199188 | | | | | |
| *Parvimolge townsendi* | dd | na | 14 | S23 | 9.09 | 7.1 | KP886932 | KP900078 | AY916024 | | KP900119 | KP900164 | KP900207 |
| *Phaeognathus hubrichti* | dd | na | 22 | S23,S54 | 12.13 | 10.5 | | AY728233 | AY728233 | | EU275814 | AY691700 | |
| *Plethodon albagula* | dd | na | | | 9.15 | | KU986279 | JF504320 | AY874996 | | | DQ995008 | |
| *Plethodon amplus* | dd | na | | | | | | DQ994912 | AY874880 | | | DQ995010 | |
| *Plethodon angusticlavius* | dd | na | 19 | S55 | 11.72 | 9.8 | | DQ994913 | DQ018677 | | | DQ995011 | |
| *Plethodon asupak* | dd | na | | | | | | AY688299 | | | | KF911898 | |
| *Plethodon aureolus* | dd | na | | | | | | DQ994914 | AY874997 | | | DQ995012 | |
| *Plethodon caddoensis* | dd | na | 17 | S55 | 10.56 | 8.3 | KU985859 | FJ266743 | AY874875 | | | DQ995013 | |
| *Plethodon chattahoochee* | dd | na | | | | | | DQ994919 | AY874999 | | | DQ995014 | |
| *Plethodon cheoah* | dd | na | | | | | | | AY875045 | | | DQ995015 | |
| *Plethodon chlorobryonis* | dd | na | | | 8.30 | | | DQ994923 | AY875010 | | | | EF107404 |
| *Plethodon cinereus* | dd | na | 20 | S55 | 12.68 | 10.7 | AY728232 | AY728232 | AY728232 | JF449368 | FJ951365 | AY691703 | KM884463 |
| *Plethodon cylindraceus* | dd | na | | | 9.74 | | | DQ994928 | AY875011 | | | DQ995022 | |
| *Plethodon dorsalis* | dd | na | 19 | S55 | 12.34 | 10.3 | | GQ464404 | DQ018679 | | | DQ995023 | |
| *Plethodon dunni* | dd | na | 16 | S36 | 10.80 | 9.0 | | AY183763 | DQ018662 | | | KF911900 | |
| *Plethodon electromorphus* | dd | na | | | | | | AY378065 | DQ018665 | | | DQ995024 | |
| *Plethodon elongatus* | dd | na | 19 | S36,S55 | 11.52 | 9.4 | | AY728223 | AY728223 | EU275882 | EU275836 | AY650120 | |
| *Plethodon fourchensis* | dd | na | | | | | KU986243 | FJ611346 | AY874876 | EU275884 | EU275838 | DQ995026 | |
| *Plethodon glutinosus* | dd | na | 17 | S55 | 9.53 | 7.9 | KU986027 | DQ994937 | AY875024 | | | DQ995027 | |
| *Plethodon grobmani* | dd | na | | | 9.69 | | KU986107 | DQ994941 | AY875026 | | | DQ995028 | |
| *Plethodon hoffmani* | dd | na | | | 13.56 | | KU985922 | AY378048 | DQ018666 | EU275883 | EU275837 | DQ995029 | |
| *Plethodon hubrichti* | dd | na | 20 | S55 | 12.94 | 11.0 | JF731302 | AY378056 | DQ018668 | | | DQ995030 | |
| *Plethodon idahoensis* | dd | na | 15 | S55 | 9.93 | 7.9 | | AY572059 | | | | GQ247792 | |
| *Plethodon jordani* | dd | na | 17 | S55 | 9.74 | 8.1 | KU986146 | DQ994947 | AY874897 | EU275881 | EU275835 | DQ995032 | |
| *Plethodon kentucki* | dd | na | | | 10.64 | | | DQ994948 | AY875027 | | | DQ995033 | |
| *Plethodon kiamichi* | dd | na | | | | | | FJ266739 | DQ018697 | | | DQ995034 | |
| *Plethodon kisatchi* | dd | na | | | | | | DQ994951 | DQ018699 | | | DQ995035 | |
| *Plethodon larselli* | dd | na | 16 | S36,S55 | | | | | | EU275885 | EU275839 | DQ995036 | |
| *Plethodon longicrus* | dd | na | | | | | | DQ994952 | | | | DQ995037 | |
| *Plethodon meridianus* | dd | na | | | | | | DQ994954 | AY874901 | | | DQ995038 | |
| *Plethodon metcalfi* | dd | na | | | | | | DQ994956 | AY874995 | | | DQ995040 | |
| *Plethodon mississippi* | dd | na | | | 10.11 | | | DQ994958 | DQ018701 | | | | |
| *Plethodon montanus* | dd | na | | | | | KU985917 | DQ994962 | AY874994 | | | DQ995041 | |
| *Plethodon neomexicanus* | dd | na | 20 | S36,S55 | 12.95 | 10.9 | | | | | | DQ995044 | |
| *Plethodon nettingi* | dd | na | 19 | S36,S55 | 13.17 | 11.0 | | AY378059 | DQ018669 | | | DQ995045 | |
| *Plethodon ocmulgee* | dd | na | | | | | | DQ994967 | AY875028 | | | DQ995048 | |
| *Plethodon oconaluftee* | dd | na | | | | | | DQ994966 | | | | DQ995047 | |
| *Plethodon ouachitae* | dd | na | 17 | S55 | 10.51 | 8.4 | KU986090 | FJ266744 | AY874877 | EU275877 | EU275831 | AY691704 | |
| *Plethodon petraeus* | dd | na | | | | | AY728222 | AY728222 | AY728222 | | | DQ995049 | |
| *Plethodon punctatus* | dd | na | | | 10.70 | | | AY378078 | DQ018685 | | | DQ995050 | |
| *Plethodon richmondi* | dd | na | 22 | S55 | 14.10 | 12.2 | | AY378071 | DQ018670 | | | DQ995054 | |
| *Plethodon savannah* | dd | na | | | | | | DQ994978 | AY875042 | | | DQ995055 | |
| *Plethodon sequoyah* | dd | na | | | | | | DQ994979 | DQ018705 | | | DQ995056 | |
| *Plethodon serratus* | dd | na | | | 12.13 | | | AY691748 | DQ018673 | EU275876 | EU275830 | AY691705 | |
| *Plethodon shenandoah* | dd | na | | | 11.96 | | | AY378043 | DQ018674 | | | DQ995062 | |
| *Plethodon shermani* | dd | na | | | | | | DQ994987 | AY875050 | | | DQ995063 | |
| *Plethodon stormi* | dd | na | 18 | S36 | | | | AY183825 | | | | | |
| *Plethodon teyahalee* | dd | na | | | 11.44 | | KU985764 | DQ994990 | AY875030 | EU275880 | EU275834 | DQ995068 | |
| *Plethodon vandykei* | dd | na | 15 | S36,S55 | 10.67 | 8.9 | | AY691759 | | EU275879 | EU275833 | AY691715 | |
| *Plethodon variolatus* | dd | na | | | | | | AY691759 | AY875043 | | | DQ995069 | |
| *Plethodon vehiculum* | dd | na | 17 | S36,S55 | 11.56 | 9.8 | | AY691760 | DQ018661 | | | AY691716 | |
| *Plethodon ventralis* | dd | na | | | 12.84 | | | DQ994994 | DQ018681 | | | DQ995071 | |
| *Plethodon virginia* | dd | na | | | | | | AY378049 | DQ018675 | | | DQ995072 | |
| *Plethodon websteri* | dd | na | | | | | | AY378076 | DQ018682 | | | DQ995073 | |
| *Plethodon wehrlei* | dd | na | 18 | S55 | 11.54 | 9.6 | | AY378079 | DQ018687 | | | DQ995075 | |
| *Plethodon welleri* | dd | na | 17 | S55 | 11.30 | 9.3 | | AY691761 | DQ018684 | | | AY691717 | |
| *Plethodon yonahlossee* | dd | na | 17 | S55 | 9.63 | 7.9 | KU985784 | AY691762 | AY874879 | EU275878 | EU275832 | AY691718 | |
| *Pseudoeurycea altamontana* | dd | na | | | | | KP886917 | KP900064 | | | KP900106 | KP900150 | KP900196 |
| *Pseudoeurycea aurantia* | dd | na | | | | | KP886901 | KP900048 | | | KP900090 | KP900134 | |
| *Pseudoeurycea cochranae* | dd | na | | | | | KP886920 | KP900067 | | | KP900109 | KP900153 | KP900199 |
| *Pseudoeurycea firscheini* | dd | na | | | | | KP886921 | KP900068 | | | KP900110 | KP900154 | |
| *Pseudoeurycea gadovii* | dd | na | 14 | S23 | 9.00 | 7.1 | KP886903 | KP900050 | | | KP900092 | KP900136 | KP900183 |
| *Pseudoeurycea juarezi* | dd | na | | | | | KP886905 | KP900052 | | | KP900094 | KP900138 | KP900185 |
| *Pseudoeurycea leprosa* | dd | na | 14 | S23 | 10.76 | 9.2 | KP886922 | KP900069 | | | | KP900155 | |
| *Pseudoeurycea lineola* | dd | na | 14 | S24 | | | KP886923 | KP900070 | | | KP900111 | KP900156 | KP900200 |

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Pseudoeurycea longicauda* | dd | na | | | | | KP886906 | KP900053 | | | KP900095 | KP900139 | KP900186 |
| *Pseudoeurycea melanomolga* | dd | na | | | | | KP886924 | KP900071 | | | KP900112 | KP900157 | KP900201 |
| *Pseudoeurycea mixcoatl* | dd | na | | | | | KP886925 | KP900072 | | | KP900113 | KP900158 | KP900202 |
| *Pseudoeurycea obesa* | dd | na | | | | | KP886926 | KP900073 | | | KP900114 | KP900159 | KP900203 |
| *Pseudoeurycea orchileucos* | dd | na | | | | | | | | | KP900104 | KP900148 | KP900195 |
| *Pseudoeurycea orchimelas* | dd | na | 14 | S24 | 13.68 | 11.4 | KP886916 | KP900063 | | | KP900105 | KP900149 | |
| *Pseudoeurycea papenfussi* | dd | na | | | | | KP886907 | KP900054 | | | KP900096 | KP900140 | KP900187 |
| *Pseudoeurycea rex* | dd | na | 14 | S23 | 10.58 | 8.2 | KP886908 | KP900056 | AY916025 | | KP900098 | AY650125 | KP900189 |
| *Pseudoeurycea robertsi* | dd | na | 14 | S23,S36 | 9.00 | 7.2 | KP886909 | KP900057 | | | KP900099 | KP900143 | KP900190 |
| *Pseudoeurycea ruficauda* | dd | na | | | | | KP886927 | KP900074 | | | KP900115 | KP900160 | KP900204 |
| *Pseudoeurycea saltator* | dd | na | | | | | KP886910 | KP900058 | | | KP900100 | KP900144 | KP900191 |
| *Pseudoeurycea smithi* | dd | na | 14 | S23 | | | KP886911 | KP900059 | | | KP900101 | KP900145 | KP900192 |
| *Pseudoeurycea tenchalli* | dd | na | | | | | KP886912 | KP900060 | | | KP900102 | KP900146 | KP900193 |
| *Pseudoeurycea unguidentis* | dd | na | | | | | | AF380774 | | | | | |
| *Pseudoeurycea werleri* | dd | na | 14 | S23 | 8.01 | 6.1 | KP886928 | KP900075 | | | KP900116 | KP900161 | |
| *Pseudotriton montanus* | bi | lo | 17 | S36 | 9.56 | | | KF562585 | AY916021 | | | KF562695 | EF107443 |
| *Pseudotriton ruber** | bi | lo | 17 | S36 | 9.31 | | AY728220 | AY728220 | AY728220 | EU275900 | EU275854 | KF562697 | |
| *Stereochilus marginatus* | bi | le | 19 | S36 | 14.79 | | AY728212 | AY728212 | AY728212 | EU275859 | EU275813 | AY691713 | |
| *Thorius arboreus* | dd | na | | | | | | KC884119 | | | | KC884221 | |
| *Thorius aureus* | dd | na | 15 | S56 | | | | KC884065 | | | | KC884197 | |
| *Thorius boreas* | dd | na | | | | | | KC884067 | | | | KC884198 | |
| *Thorius dubitus* | dd | na | 14 | S57 | | | | DQ640019 | | | | KC884200 | |
| *Thorius grandis* | dd | na | 14 | S58 | | | | KC884115 | | | | KC884181 | |
| *Thorius lunaris* | dd | na | 14 | S57 | | | | KC884069 | | | | KC884201 | |
| *Thorius macdougalli* | dd | na | 14 | S23 | 10.24 | 8.2 | | KC884072 | | | | KC884202 | |
| *Thorius magnipes* | dd | na | 14 | S57 | | | | KC884122 | | | | KC884191 | |
| *Thorius maxillabrochus* | dd | na | | | | | | KC884103 | | | | KC884182 | |
| *Thorius minutissimus* | dd | na | | | | | | DQ640021 | | | | KC884194 | |
| *Thorius minydemus* | dd | na | 14 | S57 | | | | KC884100 | | | | | |
| *Thorius munificus* | dd | na | 14 | S57 | | | KP886944 | KP900081 | | | KP900122 | KP900168 | KP900210 |
| *Thorius narisovalis* | dd | na | | | | | | KC884077 | | | | KC884206 | |
| *Thorius omiltemi* | dd | na | 14 | S58 | | | | KC884079 | | | | KC884208 | |
| *Thorius papaloae* | dd | na | 14 | S59 | | | | KC884081 | | | | KC884214 | |
| *Thorius pennatulus* | dd | na | 14 | S23,S57 | 10.83 | 8.6 | | KC884082 | | | | KC884210 | |
| *Thorius pulmonaris* | dd | na | 14 | S23 | 11.63 | 9.5 | | KC884101 | | | | | |
| *Thorius schmidti* | dd | na | 14 | S57 | | | | KC884084 | | | | KC884195 | |
| *Thorius spilogaster* | dd | na | 14 | S57 | | | | KC884087 | | | | KC884218 | |
| *Thorius troglodytes* | dd | na | 14 | S57 | | | KP886945 | KC884087 | | | KP900123 | KF911904 | KP900211 |
| *Urspelerpes brucei* | bi | lo | 15.5 | S60 | | | | FJ917634 | JQ920802 | | JQ920724 | FJ917630 | |
| **Proteidae** | | | | | | | | | | | | | |
| *Necturus alabamensis* | pd | lo | | | 9.79 | | KU985890 | AY691725 | DQ517763 | | JX144997 | JX145009 | JX145025 |
| *Necturus beyeri** | pd | lo | 18 | S37 | 9.40 | | GQ368658 | GQ368658 | GQ368658 | | JX144998 | JX145010 | JX145026 |
| *Necturus lewisi* | pd | lo | | | | | | | AY916042 | | JX144999 | JX145011 | JX145027 |
| *Necturus maculosus* | pd | lo | 18 | S37 | 8.28 | | KU985645 | AY691724 | | | JX145001 | JX145013 | JX145029 |
| *Necturus punctatus* | pd | lo | 18 | S37 | 8.58 | | KU985769 | | | | JX145002 | JX145014 | JX145030 |
| *Proteus anguinus* | pd | lo | 29 | S61 | 22.94 | | GQ368659 | GQ368659 | GQ368659 | | KC295576 | AY650138 | |
| **Rhyacotritonidae** | | | | | | | | | | | | | |
| *Rhyacotriton cascadae* | bi | lo | 16 | S62 | 9.76 | | | AY691727 | | | | AY691694 | |
| *Rhyacotriton kezeri* | bi | lo | 15 | S62 | 9.27 | | | AY691728 | | | | AY650129 | |
| *Rhyacotriton olympicus** | bi | lo | 16 | S62 | 9.49 | | KU985758 | EF036689 | | | | | |
| *Rhyacotriton variegatus** | bi | lo | 15 | S62 | 8.36 | | AY728219 | AY728219 | AY728219 | EU275869 | EU275823 | AY691693 | |
| **Salamandridae** | | | | | | | | | | | | | |
| *Calotriton arnoldi* | bi | lo | 14 | S61,S63 | | | EU880307 | EU880307 | EU880307 | | | KC665966 | |
| *Calotriton asper* | f-bi | lo | 14 | S61,S64 | 7.55 | | | KC665957 | DQ517766 | | | AY583348 | EF107346 |
| *Chioglossa lusitanica* | bi | lo | 13 | S61,S64 | 9.17 | | EU880308 | EU880308 | EU880308 | | | AY583347 | |
| *Cynops cyanurus** | bi | le | 13 | S65,S66 | | | EU880309 | EU880309 | EU880309 | | | | |
| *Cynops ensicauda* | bi | le | 13 | S66 | 6.74 | | EU880310 | EU880310 | EU880310 | | | AB754756 | |
| *Cynops orientalis* | bi | le | 13 | S65,S66 | | | EU880311 | EU880311 | EU880311 | | | KC165590 | |
| *Cynops orphicus* | bi | le | 13 | S66 | | | EU880312 | EU880312 | EU880312 | | | | |
| *Cynops pyrrhogaster* | bi | le | 13 | S66 | 6.58 | | EU880313 | EU880313 | EU880313 | | AB572298 | AB754794 | |
| *Echinotriton andersoni* | bi | le | 12 | S67 | 4.77 | | NC017870 | NC017870 | NC017870 | | HM462065 | AB856892 | |
| *Echinotriton chinhaiensis* | bi | le | 13 | S68 | | | EU880315 | EU880315 | EU880315 | | | | |
| *Euproctus montanus* | bi | lo | 13 | S61,S64 | | | EU880316 | EU880316 | EU880316 | | | | |
| *Euproctus platycephalus* | f-bi | lo | 14 | S61,S64 | | | EU880317 | EU880317 | EU880317 | | | | |
| *Lissotriton boscai* | f-bi | le | 12 | S69 | 9.10 | | JN379840 | DQ821219 | DQ517831 | | | | |
| *Lissotriton helveticus* | f-bi | le | 12 | S69 | 6.39 | | JF812747 | DQ821239 | AY951504 | | | | |
| *Lissotriton italicus* | f-bi | le | 12 | S69 | | | | DQ821243 | JN788173 | | | | |
| *Lissotriton montandoni* | bi | le | 12 | S69 | 8.28 | | EF526010 | DQ821259 | DQ517841 | | | | |
| *Lissotriton vulgaris* | f-bi | le | 13 | S69 | 7.54 | | EU880339 | EU880339 | EU880339 | | | | |
| *Lyciasalamandra antalyana* | vi | na | | | | | | | DQ517778 | | | | |
| *Lyciasalamandra atifi* | vi | na | 16 | S61,S64 | | | AF154053 | AF154053 | AF154053 | KF645905 | KF645786 | KF645737 | KF645521 |
| *Lyciasalamandra billae* | vi | na | 16 | S61,S64 | | | | | DQ517781 | | | | |
| *Lyciasalamandra fazilae* | vi | na | 16 | S61,S64 | | | | | DQ517782 | KF645908 | KF645788 | KF645740 | KF645524 |
| *Lyciasalamandra flavimembris* | vi | na | 16 | S61,S64 | | | EU880318 | EU880318 | EU880318 | | | | |
| *Lyciasalamandra helverseni* | vi | na | 16 | S61,S64 | | | | DQ473603 | DQ517785 | | | | |
| *Lyciasalamandra luschani* | vi | na | 16 | S61,S64 | | | KF645998 | KF645935 | DQ517783 | KF645907 | KF645787 | AY323753 | KF645523 |
| *Mertensiella caucasica* | bi | lo | 15 | S61,S64 | 7.25 | | EU880319 | EU880319 | EU880319 | | | | |
| *Mesotriton alpestris* | f-bi | le | 12 | S61,S64 | 6.15 | | EU880335 | EU880335 | EU880335 | | | | |
| *Neurergus crocatus* | bi | lo | 13 | S61,S64 | 7.23 | | | AY336661 | DQ517788 | | | | |
| *Neurergus kaiseri* | bi | lo | | | | | EU880320 | EU880320 | EU880320 | | | | |
| *Neurergus micropilotus* | bi | lo | | | | | | | DQ517790 | | | | |
| *Neurergus strauchii* | bi | lo | 13 | S61,S64 | 5.94 | | EU880321 | EU880321 | EU880321 | | | | |
| *Notophthalmus meridionalis* | f-bi | le | 13 | S61 | 7.20 | | EU880322 | EU880322 | EU880322 | | | | |
| *Notophthalmus perstriatus* | f-bi | le | | | 8.74 | | NC028278 | NC028278 | NC028278 | | | | |
| *Notophthalmus viridescens** | f-bi | le | 13 | S61 | 6.46 | | EU880323 | EU880323 | EU880323 | | | AY650134 | |
| *Ommatotriton ophryticus* | f-bi | le | | | | | EF526046 | DQ821267 | DQ517844 | | | | |
| *Ommatotriton vittatus* | f-bi | le | 12 | S70 | 9.80 | | EU880338 | EU880338 | EU880338 | | | | |
| *Pachytriton archospotus* | bi | lo | | | | | JN700858 | KU374978 | JX907837 | | KU375036 | GQ303708 | |
| *Pachytriton brevipes* | bi | lo | 12 | S65,S66 | 7.53 | | EU880324 | EU880324 | EU880324 | | KU375039 | GQ303700 | |
| *Pachytriton feii* | bi | lo | 12 | S61 | | | NC029345 | NC029345 | NC029345 | | KU375037 | JX907980 | |
| *Pachytriton granulosus* | bi | lo | 12 | S61 | | | | KU374999 | JX907843 | | KU375042 | JX907975 | |
| *Pachytriton inexpectatus* | bi | lo | | | | | | KU375002 | JX907834 | | KU375044 | JX907960 | |
| *Pachytriton labiatus* | bi | lo | | | | | EU880325 | EU880325 | EU880325 | | | AY583351 | |
| *Pachytriton moi* | bi | lo | 12 | S61 | | | | KU375004 | JX237746 | | KU375046 | | |
| *Pachytriton wuguanfui* | bi | lo | | | | | | KU374985 | | | KU375040 | | |
| *Pachytriton xanthospilos* | bi | lo | | | | | | JX237762 | JX237730 | | KU375047 | JX907997 | |
| *Paramesotriton caudopunctatus* | bi | lo | 12 | S61,S64 | 7.22 | | EU880326 | EU880326 | EU880326 | | | | |
| *Paramesotriton chinensis* | bi | lo | 12 | S61,S64 | 7.26 | | | AB638712 | DQ517800 | | | | |
| *Paramesotriton deloustali* | bi | lo | 12 | S61,S64 | | | EU880327 | EU880327 | EU880327 | | | GQ303710 | |

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Paramesotriton ermizhaoi* | bi | lo | | | | | | GQ303671 | FJ744601 | | | GQ303711 | |
| *Paramesotriton fuzhongensis* | bi | lo | 12 | S61,S64 | | | JN700852 | JX480893 | DQ517803 | | | | |
| *Paramesotriton guanxiensis* | bi | lo | 12 | S61,S64 | | | JN700851 | KU375006 | DQ517804 | | | | |
| *Paramesotriton hongkongensis* | bi | lo | 12 | S71 | 6.11 | | AY458597 | AY458597 | AY458597 | | | | |
| *Paramesotriton laoensis* | bi | lo | 12 | S61,S64 | | | EU880328 | EU880328 | EU880328 | | | | |
| *Paramesotriton longliensis* | bi | le | | | | | | JX480885 | FJ169608 | | | | |
| *Paramesotriton wulingensis* | bi | lo | | | | | | | KJ650056 | | | | |
| *Paramesotriton yunwuensis* | bi | lo | | | | | | | GU980577 | | | | |
| *Paramesotriton zhijinensis* | f-bi | le | | | | | | | FJ169609 | | | | |
| *Pleurodeles poireti* | bi | le | 13 | S72 | | | EU880329 | EU880329 | EU880329 | EF453368 | EU275820 | EU275787 | |
| *Pleurodeles waltl* | f-bi | le | 14 | S72 | 4.66 | | EU880330 | EU880330 | EU880330 | | | AY523736 | AY948856 |
| *Salamandra algira* | ovi | lo | | | | | KF645992 | KF645930 | KF645992 | KF645900 | KF645790 | KF645961 | KF645520 |
| *Salamandra atra* | vi | na | 14 | S61,S64 | 8.79 | | KP697931 | AY042786 | DQ517816 | KF645878 | KF645798 | KF645939 | KF645496 |
| *Salamandra corsica* | ovi | le/lo | 14 | S61,S64 | | | KT365336 | KT365391 | KF645971 | KF645882 | KF645817 | KF645943 | KF645499 |
| *Salamandra infraimmaculata* | ovi | le | 15 | S61,S64 | | | KF645976 | KF645919 | DQ517819 | KF645887 | KF645819 | KF645949 | KF645503 |
| *Salamandra lanzai* | vi | na | 14 | S61,S64 | | | KF645974 | AF356699 | DQ517820 | KF645884 | KF645822 | KF645946 | KF645500 |
| *Salamandra salamandra* | ovi | lo | 14 | S61,S64 | 5.56 | | EU880331 | EU880331 | EU880331 | EF453369 | KF645824 | AY650135 | EF107368 |
| *Salamandrina perspicillata* | bi | lo | 13 | S61,S64 | | | | HQ915638 | | | HQ915029 | HQ915231 | |
| *Salamandrina terdigitata* | bi | lo | 13 | S61,S64 | 9.71 | | | KF431264 | DQ517823 | | HQ915067 | HQ915372 | |
| *Taricha granulosa* | f-bi | le | 12 | S61 | 7.19 | | EU880333 | EU880333 | EU880333 | | HM462064 | | |
| *Taricha rivularis* | bi | lo | 12 | S61 | 6.77 | | EU880334 | EU880334 | EU880334 | | KF550381 | AY650133 | |
| *Taricha sierrae* | bi | lo | 12 | S61 | | | | DQ196282 | | | | | |
| *Taricha torosa* | bi | le | 12 | S61 | 6.60 | | KU986086 | DQ196271 | DQ517826 | | | EF107340 | EF107444 |
| *Triturus carnifex* | f-bi | le | 14 | S61,S64 | | | NC015788 | NC015788 | NC015788 | | | | |
| *Triturus cristatus* | f-bi | le | 15 | S61,S64 | 9.68 | | HQ697273 | HQ697273 | HQ697273 | | | | |
| *Triturus dobrogicus* | f-bi | le | 16 | S61,S64 | | | HQ697274 | HQ697274 | HQ697274 | | | | |
| *Triturus karelinii* | bi | le | 13 | S61,S64 | | | HQ697277 | HQ697277 | HQ697277 | | | | |
| *Triturus macedonicus* | f-bi | le | 14 | S61,S64 | | | HQ697278 | HQ697278 | HQ697278 | | | | |
| *Triturus marmoratus* | f-bi | le | 12 | S61,S64 | | | HQ697279 | HQ697279 | HQ697279 | | | AY583354 | EF107350 |
| *Triturus pygmaeus* | f-bi | le | 12 | S61,S64 | 6.56 | | HQ697280 | HQ697280 | HQ697280 | | | | |
| *Tylototriton anguliceps* | bi | lo | | | | | | | LC017832 | | | | |
| *Tylototriton asperrimus* | bi | le | 13 | S73 | | | EU880340 | EU880340 | EU880340 | | HM462069 | KC165601 | |
| *Tylototriton hainanensis* | bi | le | | | | | | | DQ517850 | | HM462070 | | |
| *Tylototriton himalayanus* | bi | le | | | | | | | KT765173 | | | | |
| *Tylototriton kweichowensis* | bi | le | 15 | S73 | 5.52 | | NC029231 | NC029231 | NC029231 | | KC733384 | | |
| *Tylototriton lizhenchangi* | bi | le | | | | | | | AB769532 | | AB856873 | AB856886 | |
| *Tylototriton liuyangensis* | bi | le | | | | | | | KJ205598 | | | | |
| *Tylototriton notialis* | bi | lo | | | | | | | AB769535 | | | | |
| *Tylototriton panhai* | bi | le | 13 | S74 | | | | AB856889 | KT304305 | | AB856876 | AB856889 | |
| *Tylototriton shanjing* | bi | le | | | | | KR154461 | KR154461 | KR154461 | | HM462066 | AB856888 | |
| *Tylototriton shanorum* | bi | le | | | | | | | AB922822 | | | | |
| *Tylototriton taliangensis* | bi | le | 15 | S73 | | | KP979646 | KP979646 | KP979646 | AF497712 | AB856878 | AB856891 | EF107437 |
| *Tylototriton uyenoi* | bi | le | 13 | S74 | | | | AB856882 | AB830729 | | AB856868 | AB856882 | |
| *Tylototriton verrucosus* | bi | le | 13 | S73 | 5.94 | | NC017871 | NC017871 | NC017871 | | HM462067 | AB856884 | |
| *Tylototriton vietnamensis* | bi | le | 13 | S75,S76 | | | JQ046329 | AB856883 | HM770088 | | HM770091 | AB856883 | |
| *Tylototriton wenxiaensis* | bi | le | | | | | NC027507 | NC027507 | NC027507 | EU275867 | HM462071 | EU275788 | |
| *Tylototriton yangi* | bi | le | | | | | | | AB830739 | | AB856872 | AB856885 | |
| *Tylototriton ziegleri* | bi | le | | | | | | | AB769539 | | AB856874 | AB856887 | |

## Sirenidae

| Species | Life Cycle | Larval Eco | Trunk Vert | Vert Refs | Adult Body Form | Adult Trunk Form | *Co1* Accession | *Cytb* Accession | *ND2* Accession | *BDNF* Accession | *Pomc* Accession | *RAG1* Accession | *Slc8a3* Accession |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *Pseudobranchus axanthus** | pd | le | 35 | S36,S37 | 23.97 | | | AY713226 | | | JX145003 | JX145015 | JX145031 |
| *Pseudobranchus striatus* | pd | le | 36 | S36,S37 | | | | AY713120 | | | JX145004 | JX145016 | JX145032 |
| *Siren intermedia intermedia* | pd | le | 31 | S36,S37 | 15.90 | | | | | | JX145005 | | JX145033 |
| *Siren intermedia nettingi* | pd | le | | | | | | | | | JX145006 | JX145017 | JX145034 |
| *Siren lacertina** | pd | le | 31 | S36,S37 | 14.07 | | | JX145019 | | | JX145008 | JX145019 | JX145036 |

**Supplemental Table S10.** Partitions and models of sequence evolution were estimated with Partitionfinder [S77], based on the greedy algorithm and AIC model selection. Partitions were reduced from 21 (3 codon position of 7 genes) to 13. p# = codon position number (i.e., p1, p2, and p3 for each gene). The total number of nucleotide positions in each partition is also noted.

| Partitions | Models | # pos in partition |
|---|---|---|
| *BDNF* p1, *Slc8a3* p1, *Rag1* p1, *POMC* p1, *POMC* p2 | GTR+I+G | 1452 |
| *BDNF* p2, *Rag1* p2, *Slc8a3* p2 | HKY+I+G | 1086 |
| *BDNF* p3 | K80+G | 235 |
| *Co1* p1 | GTR+I+G | 511 |
| *Co1* p2 | TRN+I+G | 511 |
| *Co1* p3 | GTR+I+G | 511 |
| *ND2* p1 | GTR+I+G | 337 |
| *ND2* p2 | GTR+I+G | 337 |
| *ND2* p3 | GTR+G | 337 |
| *POMC* p3, *Slc8a3* p3, *Rag1* p3 | SYM+I+G | 1034 |
| *Cytb* p1 | GTR+I+G | 350 |
| *Cytb* p2 | HKY+I+G | 350 |
| *Cytb* p3 | GTR+I+G | 350 |

**Supplemental Table S11.** Calibration priors used for Bayesian phylogenetic analysis in BEAST [S78]. Calibration priors were set as normal distributions and mostly based on Shen et al. [S22]. Their study was based on 50 nuclear loci and currently provides the most robust estimates of divergence times for salamanders. Hynobiid calibrations were based on Chen et al. [S79], which used 29 nuclear genes. Node numbers are plotted on the phylogeny (Figure S2).

| Node Number | Inclusive Taxa | Mean (mya) | Sigma (mya) |
|---|---|---|---|
| 1 | Cryptobranchoidea | 159 | 4 |
| 2 | Salamandroidea | 160 | 10 |
| 3 | Ambystomatidae + Dicamptodontidae + Salamandridae | 137 | 10.5 |
| 4 | Hynobiidae | 126 | 8 |
| 5 | Amphiumidae + Plethodontidae | 110 | 8 |
| 6 | Plethodontidae | 66 | 5 |
| 7 | Hemidactyliinae | 58 | 4 |
| 8 | Bolitoglossini + Batrachosepini + Hemidactyliini | 54 | 4 |
| 9 | Bolitoglossini + Batrachosepini | 51 | 4 |
| 10 | Plethodontinae | 43 | 3.5 |
| 11 | Hynobiidae except *Onychodactylus* | 41 | 3 |
| 12 | Spelerpini | 37 | 4 |

**Comments on divergence time estimates:** Even though we based our tree calibrations on previous molecular estimates [S22, S79], the date ranges of Late Jurassic and Early Cretaceous fossils assigned to the Salamandroidia or Cryptobranchoidia [S3-S14] either fall within these calibration ranges or are younger. Late Jurassic crown group salamander fossils indicate that the divergence between the two main clades (salamandroids and cryptobranchoids) was at least 160 to 185 mya [S4, S5, S80]. Our estimated deepest divergence among extant salamanders is at the upper end of this range (average 160 mya; range 152 to 175 mya), and still accommodates the Late Jurassic fossil salamanders assigned to crown groups. It is important to note that the most recent molecular estimates found this date to be somewhat older (average 180 to 225, depending on the method [S22]). In our analysis, the relatively large number of shallow node calibrations may have drawn the distribution of divergence time estimates for the deepest nodes toward younger dates. Nevertheless, the trait evolution analyses presented here are based on relative (not absolute) divergence.


**Supplemental Figure S2.** Bayesian chronogram of 516 salamander taxa. Topology and divergence time estimates from BEAST were based on three mitochondrial (Co1, Cytb, ND2) and four nuclear (BDNF, Pomc, RAG1, Slc8a3) protein-coding genes (totaling 7401 character states; S1 Appendix, Table S9 ). Asterisks indicate Baysian posterior probability ≥0.90, and bars on major nodes (for clarity) represent 95% highest posterior density intervals on divergence dates. The 12 large numbers placed at major nodes indicate calibration priors based on Shen et al. [S22] or Chen et al. [S79] and are listed in Tables S11.


**Supplemental Figure S3. Landmarks and methods for larval body shape analyses.** Seven homologous landmarks were placed on images of 27 taxa (n = 3 to 5 individuals per taxon; Table S9 see species with asterisk). Specimens were anesthetized by submerging with MS-222 and laid in a set of parallel tracks to ensure body straightness. We used anesthetized live larvae in order avoid preservation variation. No larvae had yolk and all had developed hind limbs (except Sirenidae, which never develop hind limbs). Larvae did not show signs of metamorphosis such as head shape changes or external gill reabsorption (except Amphiumidae, which rapidly resorb external gills after hatching, but otherwise maintain a larval morphology).

Dorsal body images were taken with a Canon G9 12 Mega pixel camera from a fixed stand. The landmarks were placed on images as follows: 1) at the most medial position on the snout, 2) anterior to the 1st gill ramus on left side of the head, 3) anterior of the forelimb on left side of the body, 4) on the left side of the body parallel to the posterior margin of the cloaca, 5) on the right side of the body parallel to the posterior margin of the cloaca, 6) anterior of the forelimb on right side of the body, 7) anterior of the 1st gill ramus on right side of the head. We placed the posterior margin of the cloaca over the grid line to mark its position. We did not use hind limb landmarks because one family (Sirenidae) lacks hind limbs. Landmarks 8 and 9 were placed on the scale bar for initial landmarking in tpsDig [S81], but these landmarks were discarded prior to analyses in geomorph [S16]. For this study we were interested in capturing overall body shape. Analyses based on more detailed landmarks on larval salamander heads will be presented elsewhere.

## Supplemental References and Voucher Specimen Numbers


S1. Pagel M, Meade A (2013) BayesTraits v. 2.0. (University of Reading, Reading, UK) (http://www.evolution.rdg.ac.uk)

S2. Elliot MG, Mooers AØ (2014) Inferring ancestral states without assuming neutrality or gradualism using a stable model of continuous character evolution. *BMC Evol Biol* 14:226.

S3. Wang Y (2004) A new Mesozoic caudate (*Liaoxitriton daohugouensis* sp. nov.) from Inner Mongolia, China. *Chinese Science Bulletin* 49(8):858—860.

S4. Gao K-Q, Shubin NH (2012) Late Jurassic salamandroid from western Liaoning, China. *Proc Natl Acad Sci USA* 109(15):5767–5772.

S5. Ascarrunz E, Rage J-C, Legreneur P, Laurin M (2016) *Triadobatrachus massinoti*, the earliest known lissamphibian (Vertebrata: Tetrapoda) re-examined by µCT scan, and the evolution of trunk length in batrachians. *Contrib Zool* 85(2):201–234.

S6. Gao K, Cheng Z, and Xu X (1998) First report of a Mesozoic urodele from China. *Chinese Geology* 250:40–41.

S7. Wang Y, Evans SE (2006) A new short-bodied salamander from the Upper Jurassic/Lower Cretaceous of China. *Acta Palaeontologica Polonica*, 51(1):127–130.

S8. Evans SE, Lally C, Chure DC, Elder A, Maisano JA (2005) A Late Jurassic salamander (Amphibia: Caudata) from the Morrison Formation of North America. *Zool J Linnean Soc* 143(4):599–616.

S9. Jia J, Gao K (2016) A new hynobiid-like salamander (Amphibia, Urodela) from Inner Mongolia, China, provides a rare case study of developmental features in an Early Cretaceous fossil urodele. *PeerJ* 4:e2499.

S10. Evans S, Milner A (1996) A metamorphosed salamander from the Early Cretaceous of Las Hoyas, Spain. *Philos Trans R Soc Lond, Biol Sci* 351(1340): 627–646.

S11. Jia J, Gao K-Q (2016) A new basal salamandroid (Amphibia, Urodela) from the Late Jurassic of Qinglong, Hebei Province, China. *PLoS ONE* 11(5):e0153834.

S12. Gao K-Q, Shubin NH (2001) Late Jurassic salamanders from northern China. *Nature* 410:574–577.

S13. Gao K-Q, Shubin NH (2003) Earliest known crown-group salamanders. *Nature* 422:424–428.

S14. Wang Y, Rose C (2005) *Jeholotriton paradoxus* (Amphibia: Caudata) from the Lower Cretaceous of southeastern Inner Mongolia, China. *J Vertebr Paleontol* 25(3): 523–532.

S15. Skutschas P, Martin T (2011) Cranial anatomy of the stem salamander *Kokartus honorarius* (Amphibia: Caudata) from the Middle Jurassic of Kyrgyzstan. *Zool J Linnean Soc* 161(4):816–838.

S16. Adams DC, Otarola-Castillo E (2013) Geomorph: an R package for the collection and analysis of geometric morphometric shape data. *Methods Ecol Evol* 4(4):393–399.

S17. Adams DC (2014) Quantifying and comparing phylogenetic evolutionary rates for shape and other high-dimensional phenotypic data. *Syst Biol* 63(2):166–177.

S18. Beaulieu JM, Jhwueng DC, Boettiger C, O'Meara BC (2012) Modeling stabilizing selection: expanding the Ornstein-Uhlenbeck model of adaptive evolution. *Evolution* 66(8):2369–2383.

S19. Soul LC, Benson RBJ (2017) Developmental mechanisms of macroevolutionary change in the tetrapod axis: A case study of Sauropterygia. *Evolution* 71(5):1164–1177.

S20. Mueller RL (2006) Evolutionary rates, divergence dates, and the performance of mitochondrial genes in Bayesian phylogenetic analysis. *Syst Biol* 55(2):289–300

S21. Vieites DR, Min M-S, Wake DB (2007) Rapid diversification and dispersal during periods of global warming by plethodontid salamanders. *Proc Natl Acad Sci USA* 104(50):19903–19907.

S22. Shen XX et al. (2016) Enlarged multilocus data set provides surprisingly younger time of origin for the Plethodontidae, the largest family of salamanders. *Syst Biol* 65(1):66–81.

S23. Wake DB (1966) Comparative osteology and evolution of the lungless salamanders, Family Plethodontidae. *Mem So Cal Acad* 4:1–111.

S24. Parra-Olea G, Wake DB (2001) Extreme morphological and ecological homoplasy in tropical salamanders *Proc Natl Acad Sci USA* 98(14):7888–7891.
S25. Mueller RL, Macey JR, Jaekel M, Wake DB, Boore JL (2004) Morphological homoplasy, life history evolution, and historical biogeography of plethodontid salamanders inferred from complete mitochondrial genomes. *Proc Natl Acad Sci USA* 101(38):13820–13825.
S26. Chippindale PT, Bonett RM, Baldwin AS, Wiens JJ (2004) Phylogenetic evidence for a major reversal of life-history evolution in plethodontid salamanders. *Evolution* 58(12):2809–2822.
S27. Bonett RM, Steffen MA, Robison GA (2014) Heterochrony repolarized: a phylogenetic analysis of developmental timing in plethodontid salamanders. *EvoDevo* 5(1):27.
S28. AmphibiaWeb (2017) Information on amphibian biology and conservation. http://amphibiaweb.org/). Berkeley, California.
S29. Buckley D (2012) Evolution of viviparity in salamanders (Amphibia, Caudata). *eLS* 2012:1–13. 9780470015902.a0022851
S30. Sparreboom M (2014) Salamanders of the Old World. KNNV Publishing, Zeist, Netherlands.
S31. Nishikawa K, Jiang J-P, Matsui M, Chen C-S (2009) Morphological variation in *Pachytriton labiatus* and a re-assessment of the taxonomic status of *P. granulosus* (Amphibia: Urodela: Salamandridae). *Curr Herpetol* 28(2):49–64.
S32. Nishikawa K, Jiang J-P, Matsui M (2011) Two new species of *Pachytriton* from Anhui and Guangxi, China (Amphibia: Urodela: Salamandridae). *Curr Herpetol* 30(1):15–30.
S33. Wu Y, Wang Y, Hanken J (2012) Comparative osteology of the genus *Pachytriton* (Caudata: Salamandridae) from southeastern China. *Asian Herpetol Res* 3(2):83–102.
S34. Wiens JJ, Hoverman JT (2008) Digit reduction, body size, and paedomorphosis in salamanders. *Evol Dev* 10(4):449–463.
S35. Krebs SL, Brandon R (1984) A new species of salamander (Family Ambystomatidae) from Michoacan, Mexico. *Herpetologica* 40(3):238–245.
S36. *Vertebral data were based on specimens from the University of Tulsa field collections RMB (Ronald M. Bonett), MAS (Michael A. Steffen), and specimens housed at the following museums: Biodiversity Research and Teaching Collection at Texas A&M University (BRTC), Florida Museum of Natural History (FLMNH), Museum of Natural Science at Louisiana State University (LSUMNS), Museum of Vertebrate Zoology at the University of California Berkeley (MVZ), Texas Natural History Collection (Texas Memorial Museum) at the University of Texas, Austin (TNHC), Tulane Museum of Natural History, New Orleans LA (TU), and University of Michigan Museum of Zoology (UMMZ).
S37. Hilton WA (1948) The vertebrae of salamanders. *J Entom Zool* 40(3):47–65.
S38. Worthington RD, Wake D (1972) Patterns of regional variation in the vertebral column of terrestrial salamanders. *J Morphol* 137(3):257–277.
S39. Stokely PS, Holle P (1953) Variation in the vertebral axis of the Ambystomidae. *Herpetologica* 9(3):133–138.
S40. Litvinchuk SN, Borkin L (2003) Variation in number of trunk vertebrae and in count of costal grooves in salamanders of the family Hynobiidae. *Contrib Zool* 72(4):195–209.
S41. Zhang F (1985) On anatomy of the skeletal system of *Liua shihi* (Liu) (Amphibia, Hynobiidae). *Acta Herpet Sinica* 4(1):17–24.
S42. Fei L, Ye C (2000) A new hynobiid subfamily with a new genus and new species of Hynobiidae (Amphibia: Caudata) from West China. *Cultum Herpetol Sinica* 8:64–70.
S43. Jockusch EL, Martínez-Solano I, Hansen R, Wake D (2012) Molecular and morphological diversification of slender salamanders (Caudata: Plethodontidae: *Batrachoseps*) in the southern Sierra Nevada with descriptions of two new species. *Zootaxa* 3190:1-30.
S44. Jockusch EL (1997) Geographic variation and phenotypic plasticity of number of trunk vertebrae in slender salamanders, *Batrachoseps* (Caudata: Plethodontidae). *Evolution* 51(6):1966–1982.

S45. Jockusch EL, Wake DB, Yanev KP (1998) New species of slender salamanders, *Batrachoseps* (Amphibia: Plethodontidae), from the Sierra Nevada of California. *Nat Hist Mus Los Angeles Co Contrib Sci* 472:1–17.
S46. Wake DB (1996) A new species of *Batrachoseps* (Amphibia: Plethodontidae) from the San Gabriel Mountains, southern California. *Nat Hist Mus Los Angeles Co Contrib Sci* 463:1–12.
S47. Jockusch EL, Yanev KP, Wake DB (2001) Molecular phylogenetic analysis of slender salamanders, genus *Batrachoseps* (Amphibia: Plethodontidae), from central coastal California with descriptions of four new species. *Herpetol Monogr* 15(1):54–99.
S48. Wake DB, Elias P (1983) New genera and a new species of Central American salamanders, with a review of the tropical genera (Amphibia, Caudata, Plethodontidae). *Nat Hist Mus Los Angeles Co Contrib Sci* 345:1–19.
S49. Wake DB, Lawson R (1973) Developmental and adult morphology of the vertebral column in the plethodontid salamander *Eurycea bislineata*, with comments on vertebral evolution in the Amphibia. *J Morphol* 139:251–300.
S50. Brandon RA (1966) Systematics of the salamander Genus *Gyrinophilus*. *Illinois Biological Monographs* 35:1-86.
S51. Lanza B, Caputo V, Nascetti G, Bullini L (1995) Morphologic and genetic studies of the European plethodontid salamanders: taxonomic inferences (Genus *Hydromantes*). *Monografie Museo Regionale di Scienze Naturali Torino* 16:1–366.
S52. Min MS, Yang SY, Bonett RM, Vieites DR, Brandon RA, Wake DB (2005) Discovery of the first Asian plethodontid salamander. *Nature* 435:87–90.
S53. Brame A (1968) Systematics and evolution of the Mesoamerican salamander genus *Oedipina*. *J Herpetol* 2(1/2):1–64.
S54. Brandon R (1965) Morphological variation and ecology of the salamander *Phaeognathus hubrichti*. *Copeia* 1965(1):67–71.
S55. Highton R (1962) Revision of North American salamanders of the genus *Plethodon*. *B Fla State Mus* 6:235–367.
S56. Hanken J, Wake D (1994) Five new species of minute salamanders, Genus *Thorius* (Caudata: Plethodontidae), from northern Oaxaca, Mexico. *Copeia* 1994(3):573–590.
S57. Hanken J, Wake D (1998) Biology of tiny animals: systematics of the minute salamanders (*Thorius*: Plethodontidae) from Veracruz and Puebla, Mexico, with descriptions of five new species. *Copeia* 1998(2):312–345.
S58. Hanken J, Wake D, Freeman H (1999) Three new species of minute salamanders (*Thorius*: Plethodontidae) from Guerrero, México, including the report of a novel dental polymorphism in Urodeles. *Copeia* 1999(4):917–931.
S59. Hanken, J, Wake D (2001) A seventh species of minute salamander (*Thorius*: Plethodontidae) from the sierra de Juarez, Oaxaca, Mexico. *Herpetologica* 57(4):515–523.
S60. Camp CD, Peterman W, Milanovich J, Lamb T, Maerz J, Wake D (2009) A new genus and species of lungless salamander (Family Plethodontidae) from the Appalachian highlands of the south-eastern United States. *J Zool* 279(1):86–94.
S61. Arntzen JW, Beukema W, Galis F, Ivanović A (2015) Vertebral number is highly evolvable in salamanders and newts (Family Salamandridae) and variably associated with climatic parameters. *Contrib Zool* 84(2):85–113.
S62. Good DA, Wake D (1992) Geographic variation and speciation in the torrent salamanders of the genus *Rhyacotriton* (Caudata: Rhyacotritonidae). *U Calif Publ Zool* 126:1–91.
S63. Carranza S, Amat F (2005) Taxonomy, biogeography and evolution of *Euproctus* (Amphibia: Salamandridae), with the resurrection of the genus *Calotriton* and the description of a new endemic species from the Iberian Peninsula. *Zool J Linn Soc Lond* 145(4):555–582.
S64. Lanza B, Arntzen JW, Gentile E (2010) Vertebral numbers in the Caudata of the western palaeartic (Amphibia). *Atti del Mus Civico di Storia Naturale di Trieste* 54:3–114.

S65. Zhao E, Hu Q, Jiang Y, Yang Y (1988) Studies on chinese salamanders. Society for the Study of Amphibians and Reptiles in cooperation with the Herpetological Society of Japan and Japan Wildlife Research Center, Oxford, Ohio, USA.
S66. Chan LM, Zamudio KR, Wake DB (2001) Relationships of the salamandrid genera *Paramesotriton*, *Pachytriton*, and *Cynops* based on mitochondrial DNA sequences. *Copeia* 2001(4):997–1009.
S67. Nussbaum RA, Brodie E (1982) Partitioning of the salamandrid genus *Tylototriton* Anderson (Amphibia: Caudata) with a description of a new genus. *Herpetologica* 38(2):320–332.
S68. Chang MLY (1932) Notes on two salamanders from Chekiang. *Contrib Biol Lab Sci Soc China Zool* 8:201–212.
S69. Skorinov DB, Litvinchuk S (2012) Axial skeleton variation in newts of the genus *Lissotriton*: comparative-evolutionary study. Pp. 285-288 in: The Problems of Herpetology. Proceedings of the 5th Congress of the Alexander M. Nikolsky Herpetological Society. Russian Academy of Sciences. Minsk, Russia.
S70. Litvinchuk SN, Zuiderwijk A, Borkin LJ, Rosanov M (2005) Taxonomic status of *Triturus vittatus* (Amphibia: Salamandridae) in western Turkey: trunk count, genome size and allozyme data. *Amphibia-Reptilia* 26(3):305–323.
S71. Stuart BL, Papenfuss T (2002) A new salamander of the genus *Paramesotriton* (Caudata: Salamandridae) from Laos. *J Herpetol* 36:145–148.
S72. Carranza S, Wade E (2004) Taxonomic revision of Algero-Tunisian *Pleurodeles* (Caudata: Salamandridae) using molecular and morphological data. Revalidation of the taxon *Pleurodeles nebulosus* (Guichenot, 1850). *Zootaxa* 488:1–24.
S73. Liu C-C (1950) Amphibians of western China. (Natural History Museum, Chicago).
S74. Nishikawa K, Khonsue W, Pomchote P, Matsui M (2013) Two new species of *Tylototriton* from Thailand (Amphibia: Urodela: Salamandridae). *Zootaxa* 3737:261–279.
S75. Stuart BL, Phimmachak S, Sivongxay N, Robichaud W (2010) A new species in the *Tylototriton asperrimus* group (Caudata: Salamandridae) from central Laos. *Zootaxa* 2650:19–32.
S76. Böhme W, Schöttler T, Nguyen Q, Köhler J (2005) A new species of salamander, Genus *Tylototriton* (Urodela: Salamandridae), from northern Vietnam. *Salamandra* 41(4):215–220.
S77. Lanfear R, Calcott B, Ho SY, Guidon S (2012) Partitionfinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Mol Biol Evol* 29(6):1695–1701.
S78. Bouckaert R et al. (2014). BEAST 2: A software platform for Bayesian evolutionary analysis. *PLoS Comput Biol* 10(4): e1003537.
S79. Chen MY, Mao RL, Liang D, Kuro-o M, Zeng XM, Zhang P (2015) A reinvestigation of phylogeny and divergence times of Hynobiidae (Amphibia, Caudata) based on 29 nuclear genes. *Mol Phylogenet Evol* 83:1–6.
S80. Anderson JS (2012) Fossils, molecules, divergence times, and the origin of Salamandroidea. *Proc Natl Acad Sci USA* 109(15):5557–5558.
S81. Rohlf FJ (2010) TpsDig, v. 2.16 Department of Ecology and Evolution, State University of New York at Stony Brook. (http://life.bio.sunysb.edu/morph/)

## Voucher Numbers (See Table S9; Supplemental Reference S36)

**Specimens use in the vertebral analyses were from the following museums: Biodiversity Research and Teaching Collection at Texas A&M University (BRTC), Florida Museum of Natural History (FLMNH), Museum of Natural Science at Louisiana State University (LSUMNS), Museum of Vertebrate Zoology at the University of California Berkeley (MVZ), Texas Natural History Collection (Texas Memorial Museum) at the University of Texas, Austin (TNHC), Tulane Museum of Natural History, New Orleans LA (TU), and University of Michigan Museum of Zoology (UMMZ). Abbreviations from field series: RMB (Ronald M. Bonett) and MAS (Michael A. Steffen).**

Amphiumidae: *Amphiuma means*: FLMNH 18176; FLMNH Lot: 2707 (Specimen: 2-14); FLMNH 124145. *Amphiuma pholeter:* FLMNH 77797-77800. *Amphiuma tridactylum*: LSU 55707; RMB 5410-5411. Ambystomatidae: *Ambystoma annulatum*: RMB 5425-5429. Cryptobranchidae: *Cryptobranchus alleganiensis*: LSU 54897. Dicamptodontidae: *Dicamptodon copei*: UMMZ 171168; UMMZ 171171; UMMZ 171173-171174; UMMZ 171177-171178; UMMZ 171193; UMMZ 171196; UMMZ 171201-171202; UMMZ 171205. *Dicamptodon ensatus*: UMMZ 170933; UMMZ 170935; UMMZ 170949; UMMZ 171392-171395; UMMZ 171397; UMMZ 170928; UMMZ 171402. Plethodontidae: *Aneides ferreus*: UMMZ 170814-170822. *Aneides flavipunctatus*: UMMZ 151153. *Aneides hardii*: UMMZ-150094; UMMZ 151154. *Bolitoglossa morio*: UMMZ 151168. *Bolitoglossa rostrate*: UMMZ 151169-51170; UMMZ 151176-151177. *Bolitoglossa salvinii*: UMMZ 151166. *Bolitoglossa subpalmata*: UMMZ 183398. *Bolitoglossa adspersa*: UMMZ 128541. *Chiropterotriton multidentatus*: UMMZ 151194. *Chiropterotriton chiropterus*: UMMZ 151162; UMMZ 151196. *Desmognathus auriculatus*: UMMZ 183519; UMMZ 183520-183521. *Desmognathus marmoratus*: UMMZ 151385. *Desmognathus monticola*: UMMZ 151148; UMMZ 151158. *Desmognathus quadramaculatus*: UMMZ 154395. *Ensatina eschscholtzii*: UMMZ 170799-70800; UMMZ 170802-170808; UMMZ 170811-170812. *Eurycea chisholmensis*: TNHC 51141; TNHC 51142; TNHC 52770. *Eurycea cirrigera*: UMMZ 154705-154708; UMMZ 154711; UMMZ 154714-154728; UMMZ 54731-154732; UMMZ 154735-154736; UMMZ 154738; UMMZ 154740-154741; UMMZ 154743-154744; UMMZ 154746; UMMZ 154748; UMMZ 154750-154757; UMMZ 154761; UMMZ 154763; LSUMNS 54944-54948; MVZ 184745-184747; MVZ 184750-184751; MVZ 184753-184754; MVZ 184758; MVZ 184760-184766. *Eurycea guttolineata*: UMMZ 154631-154639; UMMZ 154648; UMMZ 154650-154651; UMMZ 154660-154662; LSUMNS 54951-54953; LSUMNS 54955-54963; MVZ184508. *Eurycea latitans*: BRTC 78086; TNHC 59933-59934; TNHC 54536. *Eurycea longicauda*: UMMZ 142533; UMMZ 151271-151276; MVZ 184509-184510. *Eurycea longicauda melanopleura*: LSUMNS 54970-54973. *Eurycea lucifuga*: UMMZ 154663-154675; LSUMNS 54975; MAS 0148; RMB 4156-4163. *Eurycea nana*: BRTC 78116-78120; BRTC 78128. *Eurycea naufragia*: TNHC 51008-51009; TNHC 51026; TNHC 57752. *Eurycea neotenes*: MVZ 120924-120925; MVZ 120927; MVZ 120929; MVZ 120931; MVZ 120933-120937; RMB 4091-4101; RMB 4129-4155. *Eurycea pterophila*: BRTC 78101-78105; TNHC 52764-52765; TNHC 52772-52773. *Eurycea quadridigitata*: UMMZ 135615; UMMZ 154764-154765; UMMZ 154767; UMMZ 183240-183241; UMMZ 183236; UMMZ 183509-183511; UMMZ 185926; LSUMNS 54978-54980; LSUMNS 54983; TU Lot: 11088 (Specimens: 5, 12, 15, 16, 19, 21, 23, 24, 27). *Eurycea rathbuni*: RMB 4300; RMB 4302-4306; RMB 4310-4312; RMB 4314; UMMZ 173560. *Eurycea sosorum*: TNHC 50915; TNHC 50921; TNHC 50923; TNHC 51178-51179. *Eurycea spelaea*: LSU 55084-55085; RMB 2245; RMB 2287; RMB 4217-4228; TU-Lot: 17999 (Specimens: 1-15). *Eurycea tonkawae*: BRTC 78106-78107. *Eurycea tridentifera*: BRTC 78132-78136; TNHC 31522; TNHC 31526; TNHC 53856. *Eurycea troglodytes*: BRTC 78091-78098; BRTC 78108-78115. *Eurycea tynerensis* Metamorphic*:* RMB 3801-3805; 3825-3829. *Eurycea tynerensis* Paedomorphic*:* RMB 3291-3318. *Eurycea wallacei*: TNHC 53821; TU 21063-21067. *Eurycea wilderae*: RMB 5412-5418; UMMZ 154710; UMMZ 154713; UMMZ 154724; UMMZ 154729; UMMZ 154745. *Gyrinophilus porphyriticus*: UMMZ 128706; UMMZ 128800; UMMZ 135751; UMMZ 151310; UMMZ 151313; UMMZ 151314; UMMZ 151330; UMMZ 151334; UMMZ 151338; UMMZ 151341; UMMZ 170276; UMMZ 181906; MVZ 184094; MVZ 184111; MVZ 184714-184717. *Hemidactylium scutatum*: UMMZ 141219; UMMZ 141230; UMMZ 141726; UMMZ 151380-151383; UMMZ 178702. *Hydromates brunus*: UMM 152690-152695. *Oedopina uniformis*: UMMZ 171461-171462. *Plethodon dunni*: UMMZ 171209-171223; UMMZ 171225-171229. *Plethodon elongatus*: UMMZ

170863-170883. *Plethodon larselli*: UMMZ 171265-171269. *Plethodon neomexicanus*: UMMZ 151458; UMMZ 171465. *Plethodon netting*: UMMZ 154380. *Plethodon stormi*: UMMZ 170849-170858. *Plethodon vandykei*: UMMZ 170839-170848. *Plethodon vehiculum*: UMMZ 171206-171208; UMMZ 171224; UMMZ 171232-171233; UMMZ 171254. *Pseudoeurycea robertsi*: UMMZ 151478; UMMZ 151479. *Pseudotriton montanus*: UMMZ 170954. *Pseudotriton ruber*: UMMZ 130416; UMMZ 151485; UMMZ 171466; UMMZ 181908; UMMZ 183396-183397; MVZ 218640; MVZ 218642-218643; MVZ 218652-218654; MVZ 218658-218661. *Stereochilus marginatus*: UMM 151487, UMMZ 154379, UMMZ 171463-171464. *Thorius tryglodytes*: UMMZ 151495. Proteidae: *Necturus beyeri*: LSUMNS 54898. Rhyacotritonidae: *Rhyacotriton cascadae*: MVZ 173325-173326; MVZ 173328; MVZ 173335, MVZ 173341. *Rhyacotriton olympicus*: MVZ 173353-173356; MVZ 173358. *Rhyacotriton variegatus*: MVZ 173304; MVZ 173306; MVZ 173308; MVZ 173310; MVZ 173312. Sirenidae: *Pseudobranchus axanthus*: RMB 5419. *Pseudobranchus striatus*: LSUMNS 54892-54896. *Siren intermedia*: RMB 5420. *Siren lacertina*: RMB 5421-5424.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