# SUPPORTING INFORMATION: APPENDIX S1, SUPPLEMENTARY FIGURES AND TABLES

## Progenesis as an intrinsic factor of ecological opportunity in a polyphenic amphibian

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# APPENDIX S1: Additional details on stable isotope data processing, rescaling method and mixing model analysis.

## Additional details on stable isotope data processing

Samples collected for stable isotope analysis were oven-dried at 60°C for 72 h (Binder, Tubingen, Germany) and subsequently ground into a homogeneous powder. Stable isotope ratios of carbon and nitrogen were measured using an isotope ratio mass spectrometer (Isoprime 100; Isoprime, Cheadle Hulme, UK) coupled in continuous flow to an elemental analyser (Vario MICRO cube; Elementar, Langensbold, Germany) and conventionally expressed as δ values in ‰. Certified reference materials from the International Atomic Energy Agency (IAEA, Vienna, Austria) used were ammonium sulphate (IAEA-N2; $\delta^{15}N = 20.3 \pm 0.2$‰) and sucrose (IAEA C-6; $\delta^{13}C = -10.8 \pm 0.5$‰). Both these reference materials are calibrated against the international references Vienna Pee Dee Belemnite for carbon samples and atmospheric air for nitrogen. Internal standards (glycine) were inserted into all runs at regular intervals to assess potential drift over time. Repetitive measurements of glycine ($\delta^{15}N = 2.3 \pm 0.3$‰; $\delta^{13}C = -47.5 \pm 0.3$‰) were also used to calibrate isotopic data and as an elemental standard. One of the samples was randomly selected and analysed multiple times (once every 15 analyses). Analytical precision (SD) on replicated samples equalled 0.2‰ for $\delta^{13}C$ and 0.3‰ for $\delta^{15}N$.

## Detailed description of the rescaling method

Stable isotopes are particularly reliable ecological tools to complement stomach content data for assessing diet and trophic niche information, as they are time- and space-integrative tracers of the assimilated diet and have been widely used to address trophic differences at the community and population levels (Layman *et al.* 2007; Newsome *et al.* 2007; Jackson *et al.* 2011). They can be used to infer species interactions by comparing isotopic niches (i.e. proxy for trophic niches) of organisms in a Bayesian framework (Jackson *et al.* 2011). However, stable isotope values of consumers are not directly comparable across sites because apparent changes in their isotope composition can be confounded by variation in the isotopic diversity of their own resources (Newsome *et al.* 2007). Different methods have been proposed to standardise the isospace to make measured isotope data comparable across sites while attempting to control for baseline variation. Recently, Fry and Davis (2015) proposed a 'top-down' approach to standardise food webs by rescaling the isotope data of consumers into modified *Z*-scores. While the original method does not take into account baseline variation *per se*, it is possible to use it to inform about changes in the isotopic composition of a consumer species of interest while controlling for across sites variation in resources supporting it. To do so, we rescaled the isotope values of newts into modified *Z*-scores based on mean and standard deviation of their prey at each site. In this case, the isospace is centered according to local prey community, therefore taking into account potential community shifts due to baseline variation, and newt isotope variation is normalized according to local prey isotope variation. This allows to limit the potentially confounding impact of biogeochemical processes affecting basal resources in the systems being compared and to better reveal trophic information contained in isotope data for traditional niche analysis.

This adaptation involves modifications in steps 1, 6 and 7 of the original method described by Fry and Davis (2015), as presented below. In particular, rescaling of standard deviations involves multiplying by 3.55‰/prey community *SD* (for $\delta^{13}C$) or 1.51‰/prey community *SD* (for $\delta^{15}N$), instead of 1.0 and 1.5‰ respectively in the original method, where 3.55 and 1.51‰ are average *SD* values of the prey communities considered in this study. Accordingly, different X multipliers are calculated (step 4 of the original method), but without any change to the original equations (Table A).

## *Example of the modified rescaling steps for paedomorphs of pond A*

(see corresponding values in Table A, see supplementary material in Fry & Davis (2015) for the complete steps, here we only detail the steps that we modified)

For C isotopes:

**Step 1.** $SD_{\text{RESCALED OF PAEDOMORPHS OF POND A}} = 3.55 * SD_{\text{PAEDOMORPHS OF POND A}} / SD_{\text{PREY COMMUNITY A MEAN}}$.

**Step 6.** Mean for paedomorphs of pond $A_{\text{RESCALED FOR C}} = 3.55$*(Mean for paedomorphs of pond A – Mean across taxa in the prey community of pond A)/(*SD* across taxa in the prey community of pond A).

**Step 7.** $\text{Individual}_{\text{RESCALED FOR C ISOTOPES}} = \Delta * X_{\text{FOR C ISOTOPES}} + 3.55$*(Mean for paedomorphs of pond A – Mean across taxa in the prey community of pond A)/(*SD* across taxa in the prey community of pond A).

> Here, 'Δ' = individual value of a paedomorph of pond A – mean value of paedomorphs of pond A (see Step 2 of the original method).

For N isotopes:

**Step 1.** $SD_{\text{RESCALED OF PAEDOMORPHS OF POND A}} = 1.51 * SD_{\text{PAEDOMORPHS OF POND A}} / SD_{\text{PREY COMMUNITY A MEAN}}$.

**Step 6.** Mean for paedomorphs of pond $A_{\text{RESCALED FOR N}} = 1.51$*(Mean for paedomorphs of pond A – Mean across taxa in the prey community of pond A)/(*SD* across taxa in the prey community of pond A).

**Step 7.** $\text{Individual}_{\text{RESCALED FOR N ISOTOPES}} = \Delta * X_{\text{FOR N ISOTOPES}} + 1.51$*(Mean for paedomorphs of pond A – Mean across taxa in the prey community of pond A)/(*SD* across taxa in the prey community of pond A).

> Here, 'Δ' = individual value of a paedomorph of pond A – mean value of paedomorphs of pond A (see Step 2 of the original method).

**Table A: Calculated statistics used in steps 1, 4, 6 and 7 described in the original rescaling method by Fry and Davis (2015).**

| Calculated statistics | Pond | $\delta^{13}C$ | $\delta^{15}N$ |
|---|---|---|---|
| Mean across taxa in the prey community (‰) | A | −20.64 | 1.06 |
| | B | −19.64 | 1.91 |
| | C | −21.89 | 2.08 |
| | D | −18.47 | 2.63 |
| *SD* across taxa in the prey community (‰) | A | 2.95 | 1.38 |
| | B | 3.72 | 1.67 |
| | C | 2.65 | 1.41 |
| | D | 4.88 | 1.60 |
| Mean *SD* of prey communities (‰) | ABCD | 3.55 | 1.51 |
| X multiplier | A | 1.20 | 1.10 |
| | B | 0.95 | 0.91 |
| | C | 1.34 | 1.08 |
| | D | 0.73 | 0.95 |

## Additional details on mixing models parameterization

Without prior knowledge of the trophic ecology of the studied species, important but inconspicuous food sources are frequently missed in field sampling. However, having too many sources of food and too few tracers reduce the discriminatory ability of mixing models as multiple food source combinations are possible for the same set of isotope data (Mantel, Salas & Dudgeon 2004). To overcome these problems, sources implemented into the models were selected on the basis of stomach content data, as reflecting different microhabitats or feeding strategies of newts. Multiple models were ran, gradually pooling sources into ecologically relevant categories and according to their isotopic similarity. To further improve discriminatory ability of the models, prior information from stomach content data was incorporated into Mixsiar by setting informative dirichlet hyperparameters. Indeed, while using informative or uninformative priors had no consequences on the critical interpretation of the final results (see Table B for a comparison of the final results of mixing models using informative or uninformative priors), the use of informative priors from local stomach content data specifically helped decipher between contributions of potential food sources that would show some level of correlation in the uninformed models. For each source implemented in the model, α priors were calculated as the sum of the square root transformed abundance of the corresponding prey in the stomach content of newts, for each group in each population. This data transformation allows to down-weight the impact of small over abundant prey in numerical abundance data (typically zooplankton compared to larger prey). Finally, to avoid constraining the models too much, α priors were rescaled to have a weight equal to that of the 'uninformative prior', following Stock and Semmens (Stock & Semmens 2016). By default, sources that were absent from stomach content data were set to $\alpha = 0.01$. Mixing models were set to account for process and residual errors and minimum MCMC parameters were: 3 chains, length = 100,000, burn-in = 50,000 and thin = 50. Markov Chain convergence was assessed by visual analysis of trace plots, complemented with Gelman-Rubin, Geweke, and Heidelberger and Welch diagnostics. We used Deviance Information Criterion (DIC) to compare model performances and select those that were most supported by the data (Spiegelhalter *et al.* 2002). All models gave similar results and different ways of pooling sources had no consequences on their critical interpretation. However, only the most performant model for each pond was presented. Final selected sources for each population and corresponding α priors implemented in the models are presented in Table C.

**Table B: A posteriori grouped solutions of mixing models using informative *vs.* uninformative priors.**

| | | Informative priors | | Uninformative priors | |
|---|---|---|---|---|---|
| Pond | Group | B-V | T-OW-A | B-V | T-OW-A |
| A | P♀ | Models with informative priors in pond A were dropped due to low convergence | | 83 (63−97) | 17 (3−37) |
| | P♂ | | | 75 (53−98) | 25 (2−47) |
| | M♀ | | | 42 (21−68) | 58 (32−79) |
| | M♂ | | | 44 (29−74) | 56 (26−71) |
| B | P♀ | 86 (78−94) | 14 (6−22) | 88 (80−94) | 12 (6−20) |
| | P♂ | 75 (58−88) | 25 (12−42) | 85 (70−94) | 15 (6−30) |
| | M♀ | 32 (11−44) | 68 (56−89) | 25 (6−42) | 75 (58−94) |
| | M♂ | 49 (21−60) | 51 (40−79) | 37 (15−56) | 63 (44−85) |
| C | P♀ | 34 (12−62) | 66 (38−88) | 39 (15−63) | 61 (37−85) |
| | P♂ | 41 (14−71) | 59 (29−86) | 41 (14−71) | 59 (29−86) |
| | M♀ | 23 (6−47) | 77 (53−94) | 27 (7−49) | 73 (51−93) |
| | M♂ | 33 (14−54) | 67 (46−86) | 39 (18−59) | 61 (41−82) |
| D | P♀ | 79 (55−98) | 21 (2−45) | 80 (60−96) | 20 (4−40) |
| | P♂ | 74 (42−96) | 26 (4−58) | 79 (53−96) | 9 (1−20) |
| | M♀ | 53 (39−72) | 47 (28−61) | 66 (49−83) | 34 (17−51) |
| | M♂ | 39 (15−71) | 61 (29−85) | 60 (30−84) | 40 (16−70) |

Note: Results are given as mode ($CI_{95}$) of the percent contribution of each food source category to the diet of newts. Informative priors = Bayesian models including prior information from stomach content data of each population. Uninformative priors = Bayesian models uninformed by prior data. P♀ = Paedomorphic females, P♂ = Paedomorphic males, M♀ = Metamorphic females, M♂ = Metamorphic males. 'B-V' = benthic and vegetation associated invertebrates, and 'T-OW-A' = terrestrial, open water and amphibian prey.

**Table C: Summary of food sources isotope data and α priors implemented in Mixsiar mixing models.**

| Pond | Sources | $\delta^{13}C$ (‰) | $\delta^{15}N$ (‰) | Prior P♀ | Prior P♂ | Prior M♀ | Prior M♂ |
|---|---|---|---|---|---|---|---|
| A | Amphibian | −21.6 ± 0.4 | 3.6 ± 0.4 | 1 | 1 | 1 | 1 |
| | Benthic / Low TP invert. | −19.4 ± 2.4 | 1.1 ± 0.9 | 1 | 1 | 1 | 1 |
| | High TP invert. | −21.8 ± 0.8 | 3.7 ± 0.9 | 1 | 1 | 1 | 1 |
| | Terr. / Heteroptera | −26.1 ± 1.8 | −0.4 ± 0.7 | 1 | 1 | 1 | 1 |
| B | Amphibian | −24.1 ± 0.6 | 4.3 ± 1.2 | 0.34 | 0.57 | 1.80 | 1.1 |
| | Benthic / Low TP invert. | −16.8 ± 0.7 | 0.7 ± 0.8 | 2.37 | 2.14 | 1.53 | 1.72 |
| | High TP invert. | −17.1 ± 0.4 | 3.7 ± 0.8 | 0.48 | 0.01 | 0.84 | 1.41 |
| | Terr. / Heteroptera | −26.7 ± 0.6 | 0.1 ± 1.0 | 0.59 | 0.01 | 0.49 | 0.45 |
| | Zoo. | −21.1 ± 0.2 | 1.6 ± 0.4 | 1.21 | 2.29 | 0.35 | 0.32 |
| C | Amphibian | −24.0 ± 1.0 | 3.6 ± 0.3 | 0.33 | 1 | 0.69 | 0.61 |
| | Benthic / Low TP invert. | −19.0 ± 2.2 | 1.0 ± 0.8 | 1.06 | 1 | 0.6 | 0.52 |
| | High TP invert. | −21.1 ± 0.9 | 3.5 ± 0.4 | 1.33 | 1 | 1.48 | 1.32 |
| | Terr. / Heteroptera | −26.4 ± 1.1 | 0.1 ± 0.5 | 0.45 | 1 | 0.38 | 0.34 |
| | Zoo. | −22.1 ± 0.4 | 2.8 ± 0.1 | 1.83 | 1 | 1.85 | 2.2 |
| D | Benthic | −19.1 ± 0.5 | 1.9 ± 0.6 | 0.42 | 0.34 | 0.27 | 0.01 |
| | Low TP invert. | −15.0 ± 2.0 | 2.3 ± 0.6 | 1 | 0.48 | 0.79 | 0.01 |
| | High TP invert. | −15.5 ± 1.5 | 4.6 ± 0.6 | 2.34 | 2.76 | 1.8 | 2.78 |
| | Terr. / Heteroptera | −27.1 ± 0.1 | −0.7 ± 0.3 | 0.14 | 0.01 | 0.12 | 0.01 |
| | Zoo. | −18.7 ± 0.4 | 3.4 ± 0.5 | 1.1 | 1.43 | 2.02 | 2.22 |

Note: P♀ = Paedomorphic females, P♂ = Paedomorphic males, M♀ = Metamorphic females, M♂ = Metamorphic males. Amphibian = amphibian eggs and larvae, Benthic invert. = benthic invertebrates, Low TP and High TP invert. = low trophic position and high trophic position invertebrates associated to the aquatic vegetation, Terr. / Heteropt. = terrestrial insects and aquatic heteropterans, Zoo. = zooplankton. Food source categories were grouped in some ponds (e.g. 'Benthic invert.' and 'Low TP invert.') according to their isotopic similarity to improve discrimination ability and fit of the model. α priors are based on the proportion of each prey category in the stomach contents of the populations. Setting α = 1 for all prey items of a given consumer group is equivalent to an uninformative prior.

## References


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# SUPPLEMENTARY FIGURES AND TABLES

**Figure S1: Typical pond from Larzac Plateau (Occitanie, France), hosting paedomorphic and metamorphic palmate newts (*Lissotriton heveticus*).** Photo credits: B. Lejeune.

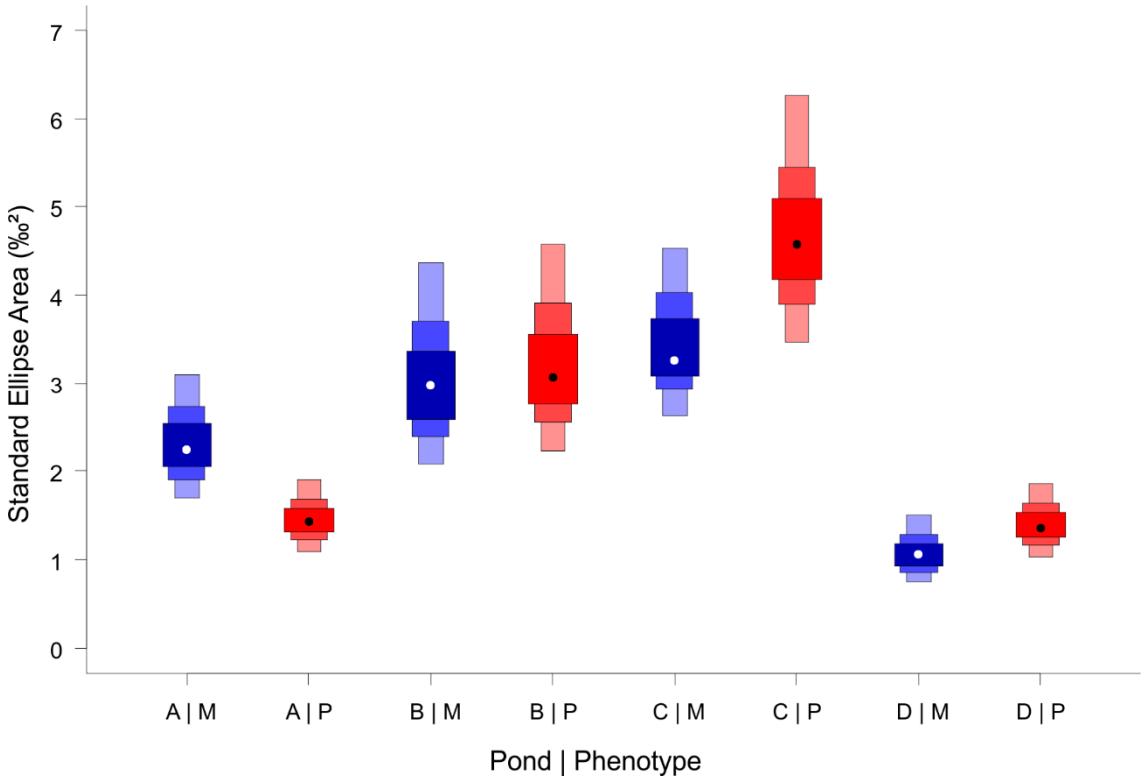


**Figure S2: Bayesian estimates of the Standard Ellipse Areas of paedomorphic and metamorphic palmate newts.**

A, B, C and D denote the four populations. Blue = Metamorph (M), Red = Paedomorph (P). Black and white dots indicate $SEA_B$ modes, rectangles encompass 50%, 75% and 95% credible intervals, from the darkest to the lightest, respectively.

**Table S1: Characteristics of the studied ponds inhabited by paedomorphic and metamorphic palmate newts.**

| Pond | A | B | C | D |
|---|---|---|---|---|
| Depth (m) | 0.8 | 1.5 | 2.4 | 3.6 |
| Area ($m^{-2}$) | 108 | 90 | 161 | 363 |
| Index of abundance ($n*m^{-2}*2h^{-1}$) | 4.3 | 2.5 | 1.4 | 0.3 |
| Paedomorphs (%) | 15 | 66 | 23 | 86 |
| Prey diversity (H') | 1.37 ± 0.12 | 1.37 ± 0.07 | 1.38 ± 0.48 | 2.04 ± 0.24 |

Note: Depth = maximum water depth, Area = pond area, Paedomorphs = percentage of paedomorphs in the adult population, H' = Shannon index (mean ± *SD*) per quadrat. Ponds were located in the municipalities of Saint-Maurice-Navacelles (Pond A and B), Saint-Etienne-de-Gourgas (Pond C) and La Vacquerie-et-Saint-Martin-de-Castries (Pond D). The coordinates are not given for conservation purposes as paedomorphs are endangered phenotypes.

**Table S2: Sample sizes of palmate newts for each type of analysis according to their phenotype, sex and population (i.e. pond).**

| Analysis | Phenotype | Pond | | | |
|---|---|---|---|---|---|
| | | A | B | C | D |
| Snout-vent length & Body Condition | P♀ | 31 | 30* | 33 | 30 |
| | P♂ | 21 | 26* | 17 | 24 |
| | M♀ | 22 | 16 | 30 | 35 |
| | M♂ | 21 | 15 | 30 | 8 |
| Stomach contents | P♀ | 25 | 22 | 33 | 29 |
| | P♂ | 21 | 6 | 15 | 20 |
| | M♀ | 20 | 10 | 30 | 30 |
| | M♂ | 17 | 11 | 28 | 7 |
| Stable isotopes | P♀ | 31 | 16 | 29 | 25 |
| | P♂ | 21 | 15 | 17 | 20 |
| | M♀ | 22 | 14 | 27 | 27 |
| | M♂ | 21 | 15 | 26 | 5 |

Note: P♀ = Paedomorphic females, P♂ = Paedomorphic males, M♀ = Metamorphic females, M♂ = Metamorphic males. * −1 individual for the calculation of Body Condition index.

**Table S3: Effect of snout-vent length (SVL), phenotype, sex and their interactions on the elemental C:N ratio in newts skin tissue (proxy for lipid content).**

| Effect | Estimate | *SE* | df | *t* | *p* |
|---|---|---|---|---|---|
| SVL | 0.003 | 0.010 | 315 | 0.345 | 0.730 |
| Phenotype (Paedo) | −0.023 | 0.505 | 315 | −0.047 | 0.963 |
| Sex (Male) | 0.246 | 0.701 | 315 | 0.350 | 0.726 |
| SVL × Phenotype (Paedo) | 0.000 | 0.012 | 315 | −0.010 | 0.992 |
| SVL × Sex (Male) | −0.004 | 0.017 | 315 | −0.225 | 0.822 |
| Phenotype (Paedo) × Sex (Male) | 0.112 | 0.816 | 315 | 0.138 | 0.891 |
| SVL × Phenotype (Paedo) × Sex (Male) | −0.005 | 0.021 | 315 | −0.237 | 0.813 |

Note: Statistical test: Linear mixed model. Paedo = paedomorph, Meta = metamorph, df = degrees of freedom. t = t-statistics. Boldface indicates statistical significance ($p < 0.05$).

**Table S4: Effect of phenotype, sex, pond and their interactions on snout-vent length and body condition.**

| Variable | Factor | df | SS | MS | Pseudo-*F* | *p* |
|---|---|---|---|---|---|---|
| Snout-vent length | Phenotype | 1 | 2.171 | 2.171 | 772.56 | **< 0.001** |
| | Sex | 1 | 0.541 | 0.541 | 192.35 | **< 0.001** |
| | Pond | 3 | 0.615 | 0.205 | 72.943 | **< 0.001** |
| | Phenotype × Sex | 1 | 0.007 | 0.007 | 2.418 | 0.118 |
| | Phenotype × Pond | 3 | 0.49 | 0.163 | 58.16 | **< 0.001** |
| | Sex × Pond | 3 | 0.013 | 0.004 | 1.556 | 0.2008 |
| | Phenotype × Sex × Pond | 3 | 0.01 | 0.003 | 1.211 | 0.3019 |
| | Residuals | 373 | 1.048 | 0.003 | | |
| Body condition | Phenotype | 1 | 0.295 | 0.295 | 19.628 | **< 0.001** |
| | Sex | 1 | 0.064 | 0.064 | 4.237 | **0.044** |
| | Pond | 3 | 1.833 | 0.611 | 40.606 | **< 0.001** |
| | Phenotype × Sex | 1 | 0.003 | 0.003 | 0.166 | 0.680 |
| | Phenotype × Pond | 3 | 0.348 | 0.116 | 7.702 | **< 0.001** |
| | Sex × Pond | 3 | 0.054 | 0.018 | 1.203 | 0.308 |
| | Phenotype × Sex × Pond | 3 | 0.094 | 0.031 | 2.083 | 0.099 |
| | Residuals | 371 | 5.582 | 0.015 | | |

Note: Statistical test: three-way PERMANOVA (Euclidean distance, 9,999 permutations), phenotype: paedomorph vs metamorph, df = degrees of freedom, SS = sum of squares, MS = mean sum of squares, Pseudo-*F* = *F* value by permutation. Boldface indicates statistical significance ($p < 0.05$).

**Table S5: Post hoc pairwise tests of snout-vent length and body condition differences across phenotypes and ponds.**

| | | Snout vent length | | | Body condition | | |
|---|---|---|---|---|---|---|---|
| Level | Pairs | df | *t* | *p* adjusted | df | *t* | *p* adjusted |
| Pond A | Paedo *vs.* Meta | 91 | 9.636 | **< 0.001** | 91 | 5.847 | **< 0.001** |
| Pond B | Paedo *vs.* Meta | 83 | 21.843 | **< 0.001** | 81 | 0.816 | 1.000 |
| Pond C | Paedo *vs.* Meta | 106 | 13.672 | **< 0.001** | 106 | 1.847 | 0.275 |
| Pond D | Paedo *vs.* Meta | 93 | 9.157 | **< 0.001** | 93 | 2.513 | 0.052 |
| Paedo | A *vs.* B | 104 | 14.514 | **< 0.001** | 102 | 6.022 | **< 0.001** |
| Paedo | A *vs.* C | 98 | 0.141 | 1.000 | 98 | 2.287 | 0.146 |
| Paedo | A *vs.* D | 102 | 6.934 | **< 0.001** | 102 | 1.799 | 0.453 |
| Paedo | B *vs.* C | 102 | 14.402 | **< 0.001** | 100 | 8.977 | **< 0.001** |
| Paedo | B *vs.* D | 106 | 24.865 | **< 0.001** | 104 | 5.528 | **< 0.001** |
| Paedo | C *vs.* D | 100 | 7.217 | **< 0.001** | 100 | 4.978 | **< 0.001** |
| Meta | A *vs.* B | 70 | 1.855 | 0.435 | 70 | 0.341 | 1.000 |
| Meta | A *vs.* C | 99 | 3.316 | **0.01** | 99 | 7.477 | **< 0.001** |
| Meta | A *vs.* D | 82 | 4.251 | **0.002** | 82 | 1.831 | 0.407 |
| Meta | B *vs.* C | 87 | 0.672 | 1.000 | 87 | 5.661 | **< 0.001** |
| Meta | B *vs.* D | 70 | 1.661 | 0.589 | 70 | 1.179 | 1.000 |
| Meta | C *vs.* D | 99 | 1.375 | 1.000 | 99 | 4.285 | **< 0.001** |

Note: PERMANOVA pairwise tests are computed for pairs of levels of the factor 'Pond' within each level of the factor 'Phenotype' and pairs of levels of the factor 'Phenotype' within each level of the factor 'Pond'. $t = t$ statistics calculated by permutation. *p* adjusted are *p*-value adjusted for multiple testing according to Bonferroni correction. Boldface indicates statistical significance ($p < 0.05$).

**Table S6: Post hoc pairwise tests of Shannon diversity (*H'*) for pairs of level of the factor 'Pond' using Monte-Carlo approximation of the *p*-value.**

| Pairs | *t* | *p* adjusted |
|---|---|---|
| A *vs.* B | 0.047 | 1 |
| A *vs.* C | 0.065 | 1 |
| A *vs.* D | 5.607 | **0.008** |
| B *vs.* C | 0.053 | 1 |
| B *vs.* D | 5.991 | **0.007** |
| C *vs.* D | 2.725 | 0.199 |

Note: *t* = *t* statistics calculated by permutation. *p* adjusted are *p*-values adjusted for multiple testing according to Bonferroni correction. Boldface indicates statistical significance ($p < 0.05$).

**Table S7: Rescaled isotope values and niche metrics of paedomorphic and metamorphic palmate newts.**

| Pond | Phenotype | $\Delta^{13}C$ (‰) | $\Delta^{15}N$ (‰) | $SEA_B$ ($‰^2$) | $CD_B$ (‰) | $SNS_B$ (%) | $PC_B$ (%) |
|---|---|---|---|---|---|---|---|
| A | P | 1.1 ± 0.7 | 3.5 ± 0.7 | 1.4 (1.1–1.9) | 2.4 | 0 | 38 |
| | M | −1.1 ± 0.6 | 2.6 ± 1.2 | 2.3 (1.7–3.1) | (2.0–2.8) | (0–0) | (29–48) |
| B | P | 2.0 ± 0.8 | 2.8 ± 0.3 | 3.1 (2.2–4.6) | 4.2 | 0 | 51 |
| | M | −2.0 ± 1.2 | 1.6 ± 1.9 | 2.9 (2.1–4.4) | (3.6–4.7) | (0–0) | (38–64) |
| C | P | −0.3 ± 1.3 | 2.9 ± 1.3 | 4.6 (3.4–6.2) | 1.1 | 35 | 43 |
| | M | −1.2 ± 1.1 | 2.3 ± 1.0 | 3.5 (2.6–4.5) | (0.6–1.5) | (22–48) | (28–58) |
| D | P | 0.6 ± 0.5 | 1.6 ± 0.9 | 1.4 (1.0–1.9) | 1.6 | 0 | 57 |
| | M | −0.8 ± 0.5 | 1.0 ± 1.7 | 1.0 (0.7–1.5) | (1.1–2.1) | (0–0) | (46–67) |

Note: P = Paedomorphs, M = Metamorphs, $\Delta^{13}C$ and $\Delta^{15}N$ are the rescaled isotope values of newts, $SEA_B$ = Standard Ellipse Area, $CD_B$ = distance between the centroids of paedomorphs and metamorphs niche, $SNS_B$ = percentage of shared niche space and $PC_B$ = percentage of contribution of paedomorphosis to the total niche area of the population. Rescaled isotope values are given as mean ± *SD* and expressed as Δ (‰). $SEA_B$, $SNS_B$ and $PC_B$ are Bayesian estimates and are expressed as mode and 95% CI of the posterior distribution.

**Table S8: Pairwise comparisons of posterior distributions of centroid distance between paedomorphs and metamorphs, shared niche space and percent contribution of paedomorphosis to the total niche of the population.**

| Pairwise test | $CD_B$ | $SNS_B$ (%) | $PC_B$ (%) |
|---|---|---|---|
| A < B | 100% | 0% | 95% |
| A < C | 0% | 100% | 69% |
| A < D | 0% | 0% | 99% |
| B < C | 0% | 100% | 20% |
| B < D | 0% | 0% | 73% |
| C < D | 94% | 0% | 93% |

Note: Results are given for the 4 ponds (A, B, C and D). $CD_B$**:** centroid distance, $SNS_B$: shared niche space, PCB: percent contribution. Percentages indicate the posterior probability of group 1 metric being smaller than group 2 metric ($CD_B$, $SNS_B$ or $PC_B$) as specified in 'Pairwise test' column.

**Table S9: Effect of snout-vent length, phenotype, sex and their interactions on $\Delta^{13}C$ and $\Delta^{15}N$ of newts.**

| Variable | Effect | Estimate | *SE* | df | *t* | *p* |
|---|---|---|---|---|---|---|
| $\Delta^{13}C$ | SVL | 0.009 | 0.050 | 320 | 0.179 | 0.858 |
| | Phenotype (Paedo) | 8.987 | 2.025 | 320 | 4.438 | **< 0.001** |
| | Sex (Male) | −2.794 | 2.734 | 320 | −1.022 | 0.308 |
| | SVL × Phenotype (Paedo) | −0.184 | 0.049 | 320 | −3.780 | **< 0.001** |
| | SVL × Sex (Male) | 0.088 | 0.066 | 320 | 1.330 | 0.185 |
| | Phenotype (Paedo) × Sex (Male) | 1.230 | 3.188 | 320 | 0.386 | 0.700 |
| | SVL × Phenotype (Paedo) × Sex (Male) | −0.045 | 0.081 | 320 | −0.559 | 0.577 |
| $\Delta^{15}N$ | SVL | 0.058 | 0.043 | 320 | 1.357 | 0.176 |
| | Phenotype (Paedo) | 5.854 | 2.244 | 320 | 2.609 | **0.010** |
| | Sex (Male) | 2.028 | 3.071 | 320 | 0.660 | 0.510 |
| | SVL × Phenotype (Paedo) | −0.132 | 0.054 | 320 | −2.455 | **0.015** |
| | SVL × Sex (Male) | −0.055 | 0.075 | 320 | −0.739 | 0.460 |
| | Phenotype (Paedo) × Sex (Male) | −5.875 | 3.582 | 320 | −1.640 | 0.102 |
| | SVL × Phenotype (Paedo) × Sex (Male) | 0.165 | 0.090 | 320 | 1.830 | 0.068 |

Note: Results of linear mixed models. SVL: snout vent length, Paedo: paedomorph, Meta: metamorph, df = degrees of freedom. *t* = *t*-statistics. Boldface indicates statistical significance ($p < 0.05$).

**Table S10: Effect of body size reduction of paedomorphs compared to metamorphs due to progenesis, sex, pond depth and their interactions on the isotopic distance of paedomorphs to metamorphs.**

| Effect | Estimate | *SE* | *t* | *p* |
|---|---|---|---|---|
| BSr | 0.429 | 0.065 | 6.612 | **< 0.001** |
| Sex (Male) | 2.508 | 0.585 | 4.287 | **< 0.001** |
| Pond depth | 0.269 | 0.163 | 1.647 | 0.101 |
| BSr × Sex (Male) | −0.257 | 0.113 | −2.276 | **0.024** |
| BSr × Pond depth | −0.098 | 0.034 | −2.869 | **0.005** |
| Sex (Male) × Pond depth | −0.815 | 0.266 | −3.067 | **0.003** |
| BSr × Sex (Male) × Pond depth | 0.085 | 0.060 | 1.417 | 0.158 |

Note: Results of the linear model. *BSr*: body size reduction, *SE* = Standard Error. Boldface indicates statistical significance ($p < 0.05$).

**Table S11: Effects of phenotype, sex and their interaction on proportions of prey abundances in the stomach contents of palmate newts.**

| Pond A | df | SS | MS | Pseudo-*F* | *p* |
|---|---|---|---|---|---|
| Phenotype | 1 | 6514 | 6514 | 2.077 | **0.049** |
| Sex | 1 | 5477 | 5477 | 1.746 | 0.103 |
| Interaction | 1 | 5720 | 5720 | 1.824 | 0.089 |
| Residuals | 79 | 248000 | 3137 | | |
| Pond B | df | SS | MS | Pseudo-*F* | *p* |
| Phenotype | 1 | 15573 | 15573 | 4.732 | **< 0.001** |
| Sex | 1 | 3313 | 3313 | 1.007 | 0.433 |
| Interaction | 1 | 6952 | 6952 | 2.113 | **0.040** |
| Residuals | 45 | 148000 | 3291 | | |
| Pond C | df | SS | MS | Pseudo-*F* | *p* |
| Phenotype | 1 | 10112 | 10112 | 6.809 | **< 0.001** |
| Sex | 1 | 6373 | 6373 | 4.292 | **0.002** |
| Interaction | 1 | 2271 | 2271 | 1.529 | 0.1736 |
| Residuals | 102 | 151000 | 1485 | | |
| Pond D | df | SS | MS | Pseudo-*F* | *p* |
| Phenotype | 1 | 8497 | 8497 | 3.917 | **0.003** |
| Sex | 1 | 7791 | 7791 | 3.592 | **0.004** |
| Interaction | 1 | 2830 | 2830 | 1.305 | 0.255 |
| Residuals | 82 | 178000 | 2169 | | |

Note: Statistical test: two-way PERMANOVAs (Bray-Curtis distance, 9,999 permutations), phenotype: paedomorph vs metamorph, df = degrees of freedom, SS = sum of squares, MS = mean sum of squares, Pseudo-*F* = *F* value by permutation. Boldface indicates statistical significance ($p < 0.05$).

**Table S12: Results of the similarity percentage (SIMPER) analysis of the diet composition of paedomorphic and metamorphic palmate newts in each pond.**

| Pond A | | | | Pond B | | | |
|---|---|---|---|---|---|---|---|
| Species | Paedo | Meta | Cum. % | Species | Paedo | Meta | Cum. % |
| Baetidae | 2.93 | 2.92 | 13.96 | Amphibian eggs | 0.57 | 4.42 | 23.38 |
| Chironomidae pupae | 2.16 | 2.88 | 26.46 | Chironomidae | 3.97 | 1.5 | 39.2 |
| Haliplidae larvae | 1.54 | 2.76 | 38.73 | Cyclopoida | 2.84 | 0.44 | 50.69 |
| Chironomidae | 1.68 | 1.36 | 47.67 | Baetidae | 1.03 | 1.72 | 58.74 |
| Corixidae | 1.84 | 1.02 | 55.81 | Terrestrial invertebrates | 1.13 | 0.83 | 65.01 |
| Hygrobiidae larvae | 1.4 | 0.76 | 62.68 | Chaoboridae pupae | 0.41 | 1.1 | 71.04 |
| Ostracoda | 1.69 | 0.4 | 69.18 | Corixidae | 0.71 | 0.88 | 75.66 |
| Amphibian eggs | 0.15 | 1.16 | 74.25 | Notonectidae | 0.98 | 0 | 79.75 |
| Newt larvae | 0.78 | 0.39 | 78.09 | Libellulidae | 0.16 | 1.12 | 83.79 |
| Terrestrial invertebrates | 0.34 | 0.67 | 81.73 | Coenagrionidae | 0.25 | 1.29 | 87.48 |
| Ceriagrionidae | 0.56 | 0.5 | 85.29 | Hygrobiidae | 0 | 0.55 | 90.76 |
| Cyclopoida | 0.74 | 0.39 | 88.68 | Chaoboridae | 0.66 | 0.17 | 93.45 |
| Ancylidae | 0.1 | 0.51 | 90.86 | Pleidae | 0.36 | 0 | 95.09 |
| Anuran tadpoles | 0 | 0.48 | 92.78 | Ostracoda | 0.37 | 0 | 96.53 |
| Sphaeriidae | 0.45 | 0 | 94.64 | Dysticidae larvae | 0.25 | 0 | 97.62 |
| Physidae | 0 | 0.29 | 95.73 | Chironomidae pupae | 0.25 | 0 | 98.61 |
| Daphniidae | 0.2 | 0.09 | 96.72 | Daphniidae | 0.21 | 0 | 99.42 |
| Hydracarina | 0.22 | 0 | 97.58 | Aeshnidae | 0 | 0.34 | 100 |
| Naucoridae | 0 | 0.22 | 98.38 | | | | |
| Lumbriculidae | 0.13 | 0 | 98.86 | | | | |
| Caenidae | 0.09 | 0 | 99.19 | | | | |
| Notonectidae | 0 | 0.1 | 99.5 | | | | |
| Aeshnidae | 0 | 0.09 | 99.78 | | | | |
| Trichoptera | 0.07 | 0 | 100 | | | | |

Note: Table S12 continues on next page.

| Pond C | | | | Pond D | | | |
|---|---|---|---|---|---|---|---|
| Species | Paedo | Meta | Cum. % | Species | Paedo | Meta | Cum. % |
| Lestidae | 0.74 | 0.37 | 10.84 | Daphniidae | 2.41 | 4.26 | 16.87 |
| Chironomidae | 0.8 | 0.05 | 20.59 | Ostracoda | 4.8 | 2.73 | 33.15 |
| Daphniidae | 2.48 | 2.86 | 30.23 | Baetidae | 4.02 | 2.76 | 45.94 |
| Ostracoda | 0.73 | 0.24 | 39.75 | Amphibians eggs | 0.18 | 2.38 | 56.15 |
| Eggs | 0.08 | 0.62 | 48.69 | Chaoboridae larvae | 0.73 | 1.06 | 63.43 |
| Ceriagrionidae | 0.3 | 0.55 | 57.19 | Dysticidae larvae | 0.93 | 0.99 | 69.86 |
| Cyclopoida | 0.55 | 0.36 | 65.31 | Chironomidae pupae | 0.87 | 1.12 | 76.2 |
| Terrestrial invertebrates | 0.21 | 0.17 | 69.6 | Libellulidae | 0.17 | 0.79 | 79.81 |
| Corixidae | 0.11 | 0.27 | 73.76 | Chironomidae | 0.65 | 0.33 | 83.27 |
| Chironomidae pupae | 0.24 | 0.12 | 77.81 | Coenagrionidae | 0.4 | 0.47 | 86.67 |
| Hydracaria | 0.17 | 0.12 | 81.56 | Acaria | 0.44 | 0.36 | 89.7 |
| Chaoboridae pupae | 0.08 | 0.22 | 84.72 | Chaoboridae pupae | 0.22 | 0.49 | 92.4 |
| Libellulidae | 0.11 | 0.15 | 87.69 | Terrestrial invertebrates | 0.2 | 0.1 | 94.3 |
| Bivalvia | 0.21 | 0 | 90.08 | Polycentropodidae | 0.63 | 0 | 95.77 |
| Anuran tadpoles | 0.07 | 0.09 | 92.32 | Caenidae | 0.17 | 0.06 | 96.89 |
| Hygrobiidae | 0.12 | 0.05 | 94.28 | Corixidae | 0.07 | 0.17 | 97.88 |
| Notonectidae | 0.02 | 0.06 | 95.62 | Anuran tadpoles | 0 | 0.18 | 98.58 |
| Naucoridae | 0 | 0.1 | 96.74 | Ancylidae | 0.1 | 0 | 99.2 |
| Phryganeidae | 0.03 | 0.05 | 97.68 | Cyclopoida | 0.07 | 0 | 99.55 |
| Chaoboridae | 0.03 | 0.03 | 98.61 | Hygrobiidae larvae | 0.05 | 0 | 99.8 |
| Dysticidae larvae | 0.07 | 0 | 99.38 | Naucoridae | 0 | 0.06 | 100 |
| Aeshnidae | 0.05 | 0 | 100 | | | | |

Note: ‘Paedo’ and ‘Meta’ = Average abundance of prey (after transformation as square root proportions) in the diet of paedomorphs and metamorphs, respectively. ‘Cum.%’ = Cumulative percentage of contribution to the Bray-Curtis dissimilarity between the diet of paedomorphs and metamorphs.

**Table S13: Contribution of different food sources implemented in stable isotope mixing models to the assimilated diet of newts before a posteriori grouping.**

| Pond A | Amphibian | Benthic / Low TP invert. | High TP invert. | Terr. / Heteropt. | |
|---|---|---|---|---|---|
| P♀ | 14.1 (0.9–33.5) | 68.4 (54.4–82.2) | 13 (0.6–32.3) | 2.6 (0.1–9.1) | |
| P♂ | 23.1 (1.2–44) | 58.4 (45.7–70.5) | 16.2 (0.7–41.7) | 1 (0–5) | |
| M♀ | 19.5 (1.1–45.8) | 36.7 (19.8–52.8) | 19.9 (1.1–46.5) | 22.1 (14.9–30.5) | |
| M♂ | 5.4 (0.3–21.6) | 50.2 (17.9–66.3) | 4.8 (0.2–19.5) | 36.9 (24.8–65.7) | |
| Pond B | Amphibian | Benthic / Low TP invert. | High TP invert. | Terr. / Heteropt. | Zoo. |
| P♀ | 1.2 (0–9.2) | 19.4 (6.2–36.5) | 66.8 (48–82.5) | 1.3 (0–6.8) | 9.1 (0.7–21) |
| P♂ | 2.7 (0–15.1) | 72.3 (39.5–86.9) | 0 (0–39.8) | 0 (0–0) | 21.3 (5.6–40.5) |
| M♀ | 22.4 (4.9–47.7) | 22.1 (4.1–37.5) | 6.8 (0.2–28.4) | 34 (11.8–51.2) | 7.4 (0–49.2) |
| M♂ | 10.7 (1.1–28.2) | 30.8 (10.4–48.7) | 15.1 (1.7–37.2) | 25.8 (5.1–38.9) | 9.7 (0–63) |
| Pond C | Amphibian | Benthic / Low TP invert. | High TP invert. | Terr. / Heteropt. | Zoo. |
| P♀ | 2.8 (0–28.5) | 15.4 (3.1–30.5) | 17.5 (1.6–45.3) | 18.1 (3.8–30.3) | 41.1 (8.3–73.6) |
| P♂ | 20.1 (1–51.2) | 13.5 (0.9–29.7) | 27.2 (2.3–61) | 6.7 (0.3–20.3) | 27.2 (1.7–66.6) |
| M♀ | 6.4 (0.1–30.4) | 5.3 (0.1–18.2) | 16.5 (1.7–42.1) | 29.5 (18.9–40.3) | 37.9 (8.9–64.8) |
| M♂ | 4 (0–23.7) | 18.5 (3.9–32.4) | 13.2 (1.5–35) | 24.8 (13.2–37) | 35.4 (10–61.7) |
| Pond D | Benthic invert. | Low TP invert. | High TP invert. | Terr. / Heteropt. | Zoo. |
| P♀ | 10.9 (0.7−38.9) | 28.5 (0−63.7) | 41.4 (21.2−68.2) | 6.4 (0.2−22.9) | 7 (0−21.7) |
| P♂ | 21.6 (2.8−56) | 32.2 (0.1−60.5) | 35.4 (19.5−61) | 2.3 (0−22.4) | 0.7 (0−18.3) |
| M♀ | 13.2 (2.5−30.2) | 2.7 (0.0−47.6) | 42 (17.5−54.2) | 3.2 (0.1−14.3) | 33.1 (19.2−40) |
| M♂ | 37.6 (11.7−70.6) | 0.0 (0.0−37.7) | 33.7 (10.9−59.6) | 0.0 (0.0−11.6) | 23 (0.0−37.1) |

Note: Results are given as mode ($CI_{95}$). P♀ = Paedomorphic females, P♂ = Paedomorphic males, M♀ = Metamorphic females, M♂ = Metamorphic males. Amphibian = amphibian eggs and larvae, Benthic invert. = benthic invertebrates, Low TP and High TP invert. = low trophic position and high trophic position invertebrates associated to the aquatic vegetation, Terr. / Heteropt. = terrestrial insects and aquatic heteropterans, Zoo. = zooplankton.