

Supporting Information

Genetic structure of lake and stream populations in a Pyrenean amphibian (*Calotriton asper*) reveals evolutionary significant units associated with paedomorphosis

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TABLE S1 Pairwise distance between sampled populations of *Calotriton asper*.

| | BGA | LIN | VAL | BPE | SOZ | BAC | ANS | IAC ¹ | BAR | BSA | IPE ¹ | BBA | BPI |
|------------------|--------|--------|-------|-------|-------|-------|-------|------------------|--------|-------|------------------|--------|-------|
| LIN | 0.002 | | | | | | | | | | | | |
| VAL | 0.005 | | | | | | | | | | | | |
| BPE | -0.001 | -0.003 | | | | | | | | | | | |
| SOZ | 0.054 | 0.044 | 0.050 | 0.031 | | | | | | | | | |
| BAC | 0.034 | 0.028 | 0.031 | 0.021 | 0.018 | | | | | | | | |
| ANS | 0.107 | 0.105 | 0.102 | 0.113 | 0.074 | 0.084 | | | | | | | |
| IAC ¹ | 0.091 | 0.087 | 0.096 | 0.072 | 0.087 | 0.084 | 0.188 | | | | | | |
| BAR | 0.169 | 0.176 | 0.18 | 0.163 | 0.164 | 0.182 | 0.247 | 0.249 | | | | | |
| BSA | 0.178 | 0.183 | 0.189 | 0.174 | 0.178 | 0.188 | 0.259 | 0.256 | -0.005 | | | | |
| IPE ¹ | 0.279 | 0.284 | 0.285 | 0.291 | 0.301 | 0.332 | 0.362 | 0.342 | 0.170 | 0.135 | | | |
| BBA | 0.167 | 0.17 | 0.172 | 0.162 | 0.167 | 0.185 | 0.248 | 0.252 | 0.033 | 0.031 | 0.179 | | |
| BPI | 0.176 | 0.177 | 0.182 | 0.168 | 0.178 | 0.196 | 0.262 | 0.243 | 0.034 | 0.024 | 0.141 | -0.010 | |
| IAL | 0.241 | 0.243 | 0.245 | 0.243 | 0.255 | 0.275 | 0.328 | 0.304 | 0.117 | 0.093 | 0.137 | 0.062 | 0.070 |

¹ Populations with paedomorphosis. See Table 1 for details on populations.

TABLE S2 Landscape genetic causal modelling approach. Partial Mantel tests evaluate the effects of four different elevation-based resistance surfaces (Alt, Alt1,000, Alt1,500 and Alt2,000, with the linear relationship between elevation and resistance starting at 0, 1,000, 1,500 and 2,000 m a.s.l., respectively), a slope effect (Slope) and Euclidean distances (Eucl) on observed genetic distances (Gen).

| Western cluster | | | | | |
|------------------------|--------------|--------------|----------------------|---------------|--------------|
| Model | R | P | Model | R | P |
| Gen~Eucl | 0.110 | 0.565 | Gen~Eucl Alt | -0.329 | 0.068 |
| Gen~Alt | 0.219 | 0.250 | Gen~Alt Eucl | 0.375 | 0.034 |
| | | | Gen~Alt Slope | -0.135 | 0.507 |
| | | | Gen~Eucl Alt1,000 | -0.343 | 0.057 |
| Gen~Alt1,000 | 0.247 | 0.201 | Gen~Alt1,000 Eucl | 0.401 | 0.027 |
| | | | Gen~Alt1,000 Slope | 0.020 | 0.938 |
| | | | Gen~Eucl Alt1,500 | -0.461 | 0.007 |
| Gen~Alt1,500 | 0.396 | 0.038 | Gen~Alt1,500 Eucl | 0.573 | 0.002 |
| | | | Gen~Alt1,500 Slope | 0.458 | 0.008 |
| | | | Gen~Eucl Alt2000 | -0.267 | 0.162 |
| Gen~Alt2,000 | 0.190 | 0.335 | Gen~Alt2,000 Eucl | 0.307 | 0.104 |
| | | | Gen~Alt2,000 Slope | -0.227 | 0.248 |
| | | | Gen~Eucl Slope | -0.548 | 0.002 |
| Gen~Slope | 0.249 | 0.189 | Gen~Slope Eucl | 0.579 | 0.001 |
| | | | Gen~Slope Alt | 0.181 | 0.364 |
| | | | Gen~Slope Alt1,000 | 0.038 | 0.816 |
| | | | Gen~Slope Alt1,500 | -0.348 | 0.046 |
| | | | Gen~Slope Alt2,000 | 0.278 | 0.159 |
| Central cluster | | | | | |
| Model | R | P | Model | R | P |
| Gen~Eucl | 0.052 | 0.855 | Gen~Eucl Alt | -0.200 | 0.483 |
| Gen~Alt | 0.169 | 0.541 | Gen~Alt Eucl | 0.255 | 0.356 |
| | | | Gen~Alt Slope | 0.183 | 0.537 |
| | | | Gen~Eucl Alt1,000 | -0.102 | 0.724 |
| Gen~Alt1,000 | 0.104 | 0.702 | Gen~Alt1,000 Eucl | 0.136 | 0.617 |
| | | | Gen~Alt1,000 Slope | -0.028 | 0.914 |
| | | | Gen~Eucl Alt1,500 | -0.344 | 0.201 |
| Gen~Alt1,500 | 0.275 | 0.336 | Gen~Alt1,500 Eucl | 0.427 | 0.115 |
| | | | Gen~Alt1,500 Slope | 0.450 | 0.094 |
| | | | Gen~Eucl Alt2,000 | -0.321 | 0.254 |
| Gen~Alt2,000 | 0.181 | 0.513 | Gen~Alt2,000 Eucl | 0.361 | 0.187 |
| | | | Gen~Alt2,000 Slope | 0.288 | 0.314 |
| | | | Gen~Eucl Slope | -0.177 | 0.547 |
| Gen~Slope | 0.116 | 0.694 | Gen~Slope Eucl | 0.204 | 0.481 |
| | | | Gen~Slope Alt | -0.137 | 0.619 |
| | | | Gen~Slope Alt1,000 | 0.058 | 0.839 |
| | | | Gen~Slope Alt1,500 | -0.386 | 0.163 |
| | | | Gen~Slope Alt2,000 | -0.254 | 0.376 |

Models are named after the dependent variable (Gen) ~ the tested effect | and the partialled out covariable. Significant results are marked in bold.

FIGURE S1 Discriminant Analysis of Principal Components: Identification of the number of clusters with Bayesian Information Criterion (BIC) for the global data set (A) and for the Western (B) and Central (C) Pyrenees.

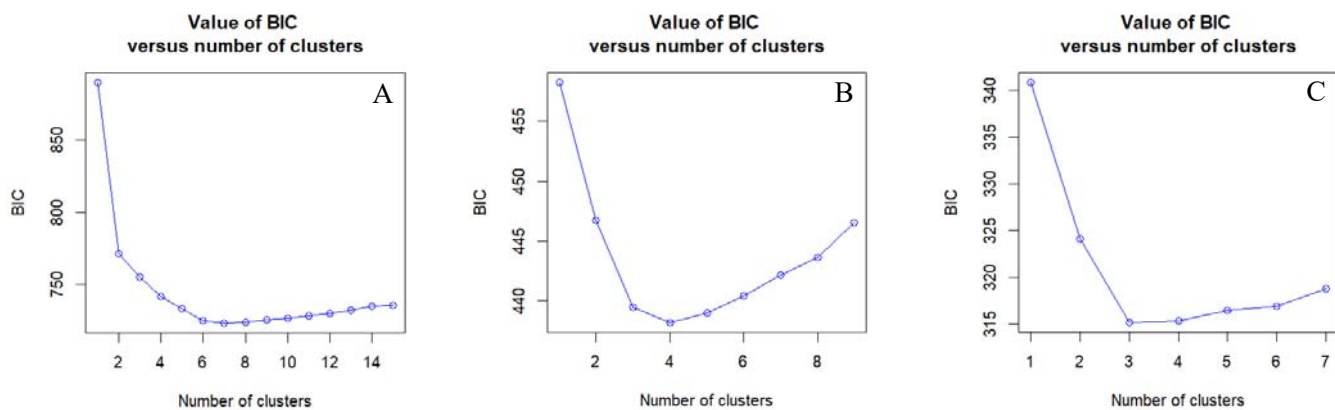


FIGURE S2 Discriminant Analysis of Principal Components (DAPCs) for the global data set (A) and for the Western (B) and Central (C) Pyrenees. Codification of clusters for the global data set: 5-IAC, 6-IPE, 1–3-the remaining Western populations, 4-the remaining Central populations; codification for the Western Pyrenees: 1-ANS+SOZ, 2–3-the remaining populations and 4-IAC); codification for the Central Pyrenees (1-IPE, 2-IAL and 3-the remaining populations). IAC and IPE are lakes with paedomorphosis. See Table 1 for details on populations.

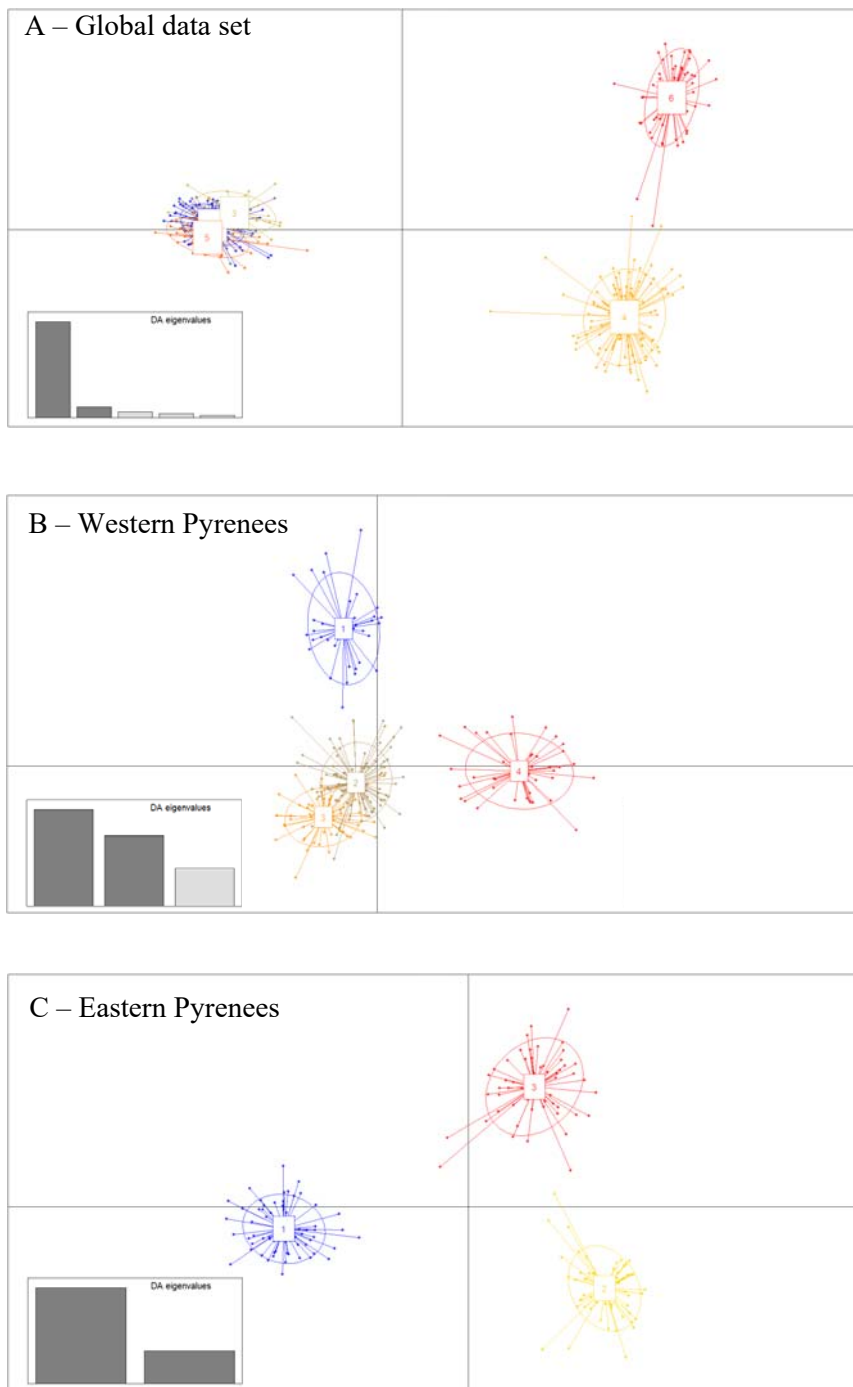


FIGURE S3 Spatial genetic structure of populations sampled in Western (A) and Central (B) Pyrenees with GENELAND for $K = 4$. The plots represent the assignment of pixels to each genetic cluster and the colours represent the probability of population membership (highest in white and yellow and lowest in red). IAC and IPE are lakes with paedomorphosis. See Table 1 for details on populations.

