

The importance of long-term genetic monitoring of reintroduced populations: inbreeding in the natterjack toad (*Epidalea calamita*)

Susanna Phillips¹, Matthew Geary¹, Matthew Allmark², Sarah Bennett², Kim Norman³, Rachel J. Ball¹, Catherine M. Peters¹, Anna P. Muir^{1*}

¹Conservation Biology Research Group, University of Chester, Chester, CH1 4BJ, UK.

²Cheshire Wildlife Trust, Bickley Hall Farm, Bickley, Malpas, Cheshire, SY14 8EF, UK.

³Eni Liverpool Bay Asset, Eni Field Study Centre, Station Road, Talacre, CH8 9RD, UK.

*Author for correspondence: a.muir@chester.ac.uk; ORCID: 0000-0002-6896-6915

Supplementary Material

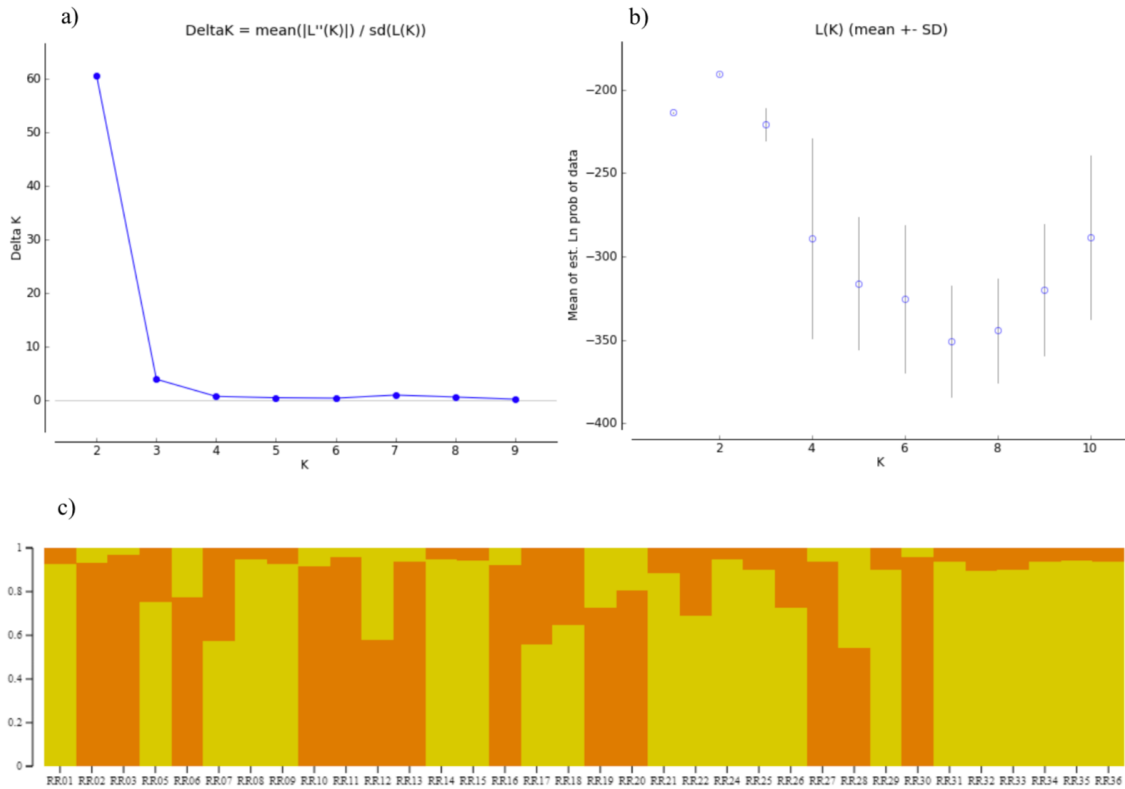


Fig. S1 Genetic structure within Red Rocks based on Bayesian clustering analysis (STRUCTURE) of seven microsatellite loci. (a) DK for each value of K (putative number of populations), averaged over ten replicates. The peak at K = 2 shows the most likely number of genetic clusters within the sample. (b) Likelihood probability profile estimated for K = 1–10 showing the mean and variance for each value of K. K = 2 showed the highest likelihood and had low variance, indicative of the best-fitting estimate. (c) STRUCTURE barplot for K = 2 within the sampled Red Rocks population. Columns are individuals, with the proportion of an individual's genotype assigned to each cluster (K) denoted by orange or yellow. Unique sample ID is shown below the plot.

Supplementary Material

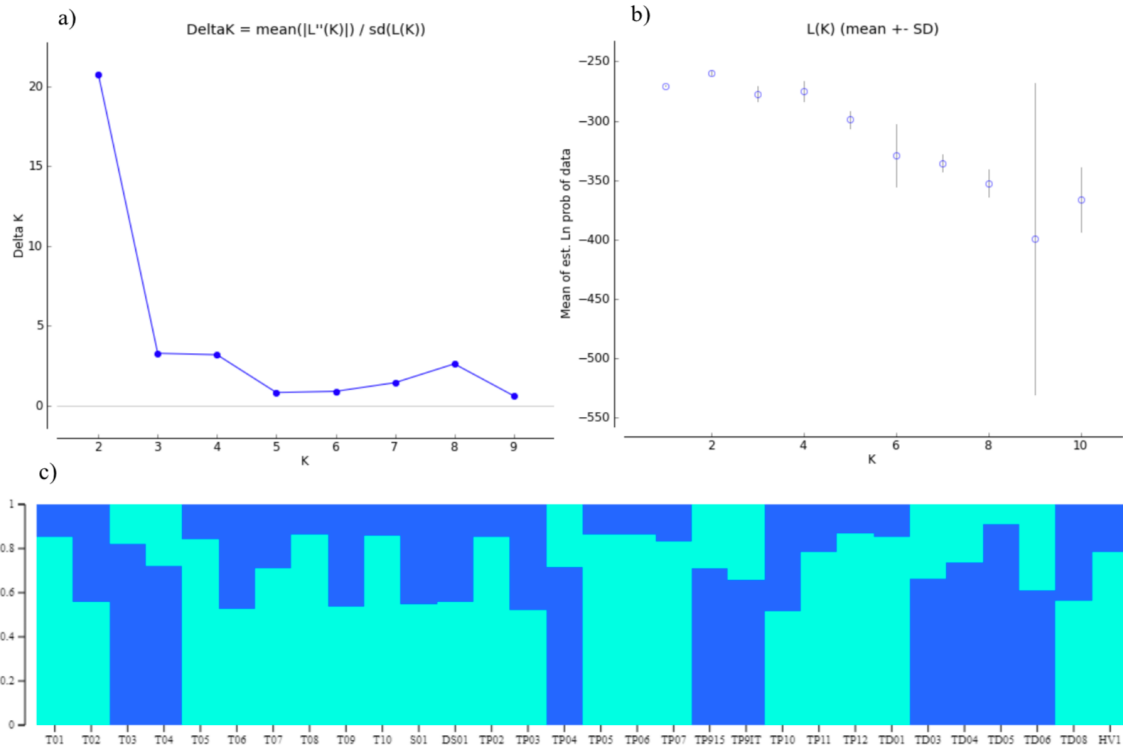


Fig. S2 Genetic structure within Talacre based on Bayesian clustering analysis (STRUCTURE) of seven microsatellite loci. (a) ΔK for each value of K (putative number of populations), averaged over ten replicates. The peak at K = 2 shows the most likely number of genetic clusters within the sample. (b) Likelihood probability profile estimated for K = 1–10 showing the mean and variance for each value of K. K = 2 showed the highest likelihood and had low variance, indicative of the best-fitting estimate. (c) STRUCTURE barplot for K = 2 within the sampled Red Rocks population. Columns are individuals, with the proportion of an individual's genotype assigned to each cluster (K) denoted by orange or yellow. Unique sample ID is shown below the plot.