

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

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Supplementary Material

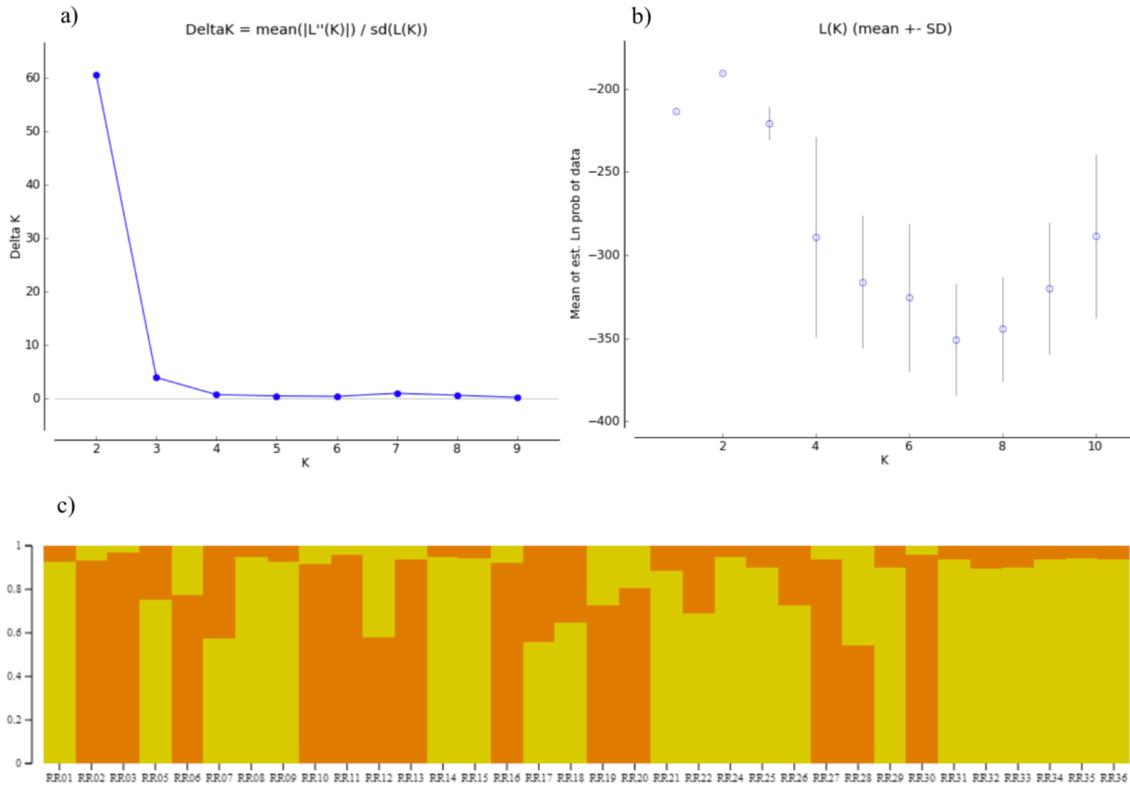


Fig. S1 Genetic structure within Red Rocks based on Bayesian clustering analysis (STRUCTURE) of seven microsatellite loci. (a) DK for each value of K (putative number of populations), averaged over ten replicates. The peak at K = 2 shows the most likely number of genetic clusters within the sample. (b) 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

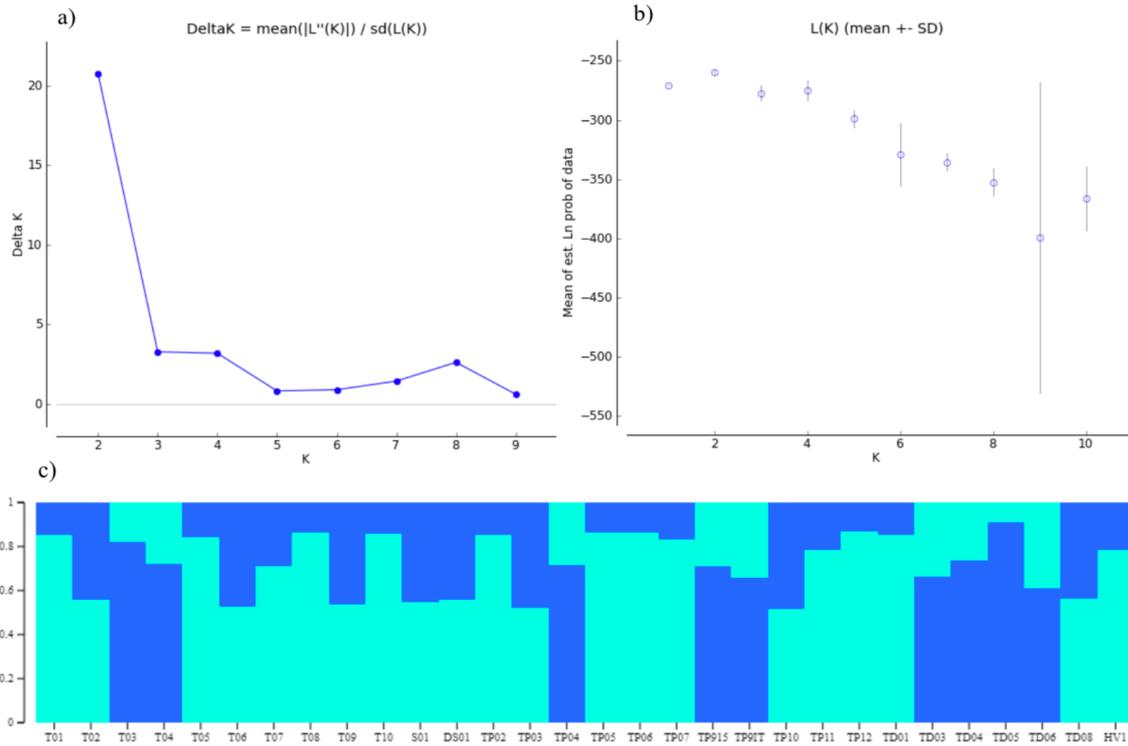


Fig. S2 Genetic structure within Talacre based on Bayesian clustering analysis (STRUCTURE) of seven microsatellite loci. (a) DK for each value of K (putative number of populations), averaged over ten replicates. The peak at K = 2 shows the most likely number of genetic clusters within the sample. (b) 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.