**Gradients of genetic diversity and differentiation across the distribution range of a Mediterranean coral: patterns, processes and conservation implications.**

This appendix details the approximate Bayesian computation (ABC) analyses conducted to infer the evolutionary history of *A. calycularis* and reports different parameters used for the analyses such as summary statistics and length of simulations.

**Influence of historical processes:**

Briefly, ABCs allow for model-based inference in a Bayesian framework under complex evolutionary scenarios, for which the likelihood cannot be properly computed. ABCs use simulations and summary statistics (e.g. expected heterozygosity (*He*) or pairwise *FST*) to approximate the likelihood (see Cornuet et al. 2008; Bertorelle et al. 2010; Beaumont 2010). We considered five different scenarios to simulate the evolutionary history of the four sub-clusters identified with STRUCTURE. In Scenario I (null scenario), the four sub-clusters diverged simultaneously from an ancestral population at *to*. In Scenario 2, we simulated a secondary contact between the sub-clusters from the Eastern and Western Peripheries resulting in the Tunisian sub-cluster. The Eastern and Western Periphery sub-clusters diverged from an ancestral population at *to*. An admixture event among the two sub-clusters took place at *t1* with an admixture rate *ra* relative to the Western Periphery sub-cluster giving birth to the Tunisian sub-cluster. The Spanish and the Algerian sub-clusters diverged at *t3*. In Scenario 3, 4 and 5, we then stimulated different sequential recolonization scenarios with the oldest divergent event involving the Tunisian sub-cluster (Scenario 3), the sub-clusters from the Western Periphery (Scenario 4) or the South East Italian sub-cluster (Scenario 5). In Scenario 3, the Tunisian sub-cluster diverged from the ancestral population at *t0*, followed by the sub-clusters from the Western Periphery at *t1* and the South East Italian sub-cluster at *t2*. The Spanish and the Algerian sub-clusters diverged at *t3*. In Scenario 4, the sub-clusters from the Western Periphery diverged from the ancestral population at *t0*, followed by the Tunisian sub-cluster at *t1* and the South East Italian sub-cluster at *t2*. The Spanish and the Algerian sub-clusters diverged at *t3*. In Scenario 5, the South East Italian sub-cluster diverged from the ancestral population at *t0*, followed by the Tunisian sub-cluster at *t1* and the sub-clusters from the Western Periphery at *t2*. The Spanish and the Algerian sub-clusters diverged at *t3*. Effective population sizes remain constant in all the scenarios. Each sub-cluster was characterized by a proper effective population size (*N1* to *N4*). We considered one ancestral population (*NA*).

Five million datasets were simulated. We assessed the within sample genetic diversity (mean gene diversity across loci, Nei 1987) and the between sample population structure (mean size variance and pairwise *FST*) resulting in 16 summary statistics. Prior distributions for *to* (i.e. first divergence) was defined considering that the studied locations were colonized since the last glacial maximum (LGM, 24-18000 years ago) during which sea level was 120 m lower than it is today. Sexual maturity and generation time of *A. calycularis* are unknown. Based on sexual maturity in related species (i.e. *Leptopsammia pruvoti*; Goffredo et al. 2011), we considered a generation time of 3 to 5 years and set 50,000 generations as the upper bound of the prior distribution of *to*. The remaining historical, demographic and mutational parameters were drawn from prior distributions that were adjusted based on preliminary runs using principal component analysis, implemented in pre-evaluate scenario-prior combinations option (Table 2). We compared the competing scenarios using a logistic regression approach on 1% of the simulated scenario closest to the observed data, after transformation of the summary statistics with a linear discriminant analysis (Cornuet et al. 2008; Estoup et al. 2012). The confidence in scenario choice was assessed computing the posterior predictive error over 1000 datasets using the model-checking option. Following Bertorelle et al. (2010), the summary statistics used for model checking were different from the summary statistics used to compute the posterior distribution of parameters. We considered the mean number of allelesas one sample summary statistics and the mean number of alleles across loci and the shared allele distance and the *(dµ)2* distance as two sample summary statistics. Finally, parameters for the most likely scenario were estimated using the 1% simulated datasets closest to the observed dataset.

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