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

This appendix details the DNA extraction, microsatellite genotyping, quality check and preliminary analyses (estimation of null alleles and linkage disequilibrium) conducted among the loci.

**DNA extraction and microsatellite genotyping:**

Total genomic DNA was extracted using a salting out procedure adjusted from Miller *et al.* (1988). All individuals were genotyped using thirteen microsatellite loci specifically developed for *A. calycularis* (Abdoullaye *et al.* 2010). Amplifications were done following Casado- Amezúa *et al*. (2012) for all loci. PCR products were analysed on an ABI 3730 Genetic Analyser with GeneScan 500 LIZ internal size standard (Applied Biosystems) at the Genoscreen company (France; http://www.genoscreen.fr/fr/). STRand 2.2.30 was used for scoring alleles (UC Davis Veterinary Genetics Laboratory). Ten percent of the samples were re-extracted and re-amplified to validate the genotyping procedure (not shown).

**Microsatellite characteristics, quality check and preliminary genetic diversity:**

Over the 13 microsatellites, one (*Ac31*) showed multiallelic pattern with more than two alleles. This marker was thus discarded from the final dataset. GIMLET 1.3.3 (Valiere 2002) was used for identification of identical genotypes resulting from mishandling during sampling processes or PCR. The number of multilocus repeated genotypes varied among populations from no multilocus repeated genotypes in AIK, CGD, LAM and ZEM to eight multilocus repeated genotypes in CAS. Considering the repeated genotypes as errors during sampling, we deleted the 53 repeated genotypes from the dataset. In addition, any individual with more than 2 un-amplified loci was also deleted, resulting in deletion of 9 individuals. From the 336 sampled colony fragments, the final dataset included 274 genotypes.

MICRO-CHECKER 2.2.3 (Van Oosterhout *et al.* 2004) was used to test scoring errors due to stutters and large allele dropout.

**Microsatellite characteristics:**

No evidence of scoring errors due to stuttering or large allele dropout was found in the whole data set with MICRO-CHECKER. In all populations, all loci were polymorphic (p-value < 0.01).

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