Microsatellites Reveal Genetic Homogeneity among Outbreak Populations of Crown-of-Thorns Starfish (*Acanthaster cf. solaris*) on Australia’s Great Barrier Reef

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**Figure S1.** Mean likelihood probability of describing the population structure of CoTS in the Great Barrier Reef into K clusters with standard deviation around the mean. Three runs were performed for each value of K and compiled in Structure Harvester (Earl et al. [1]).
Figure S2. Change in the mean likelihood probability of K clusters describing the population structure of CoTS in the Great Barrier Reef. Three runs were performed for each value of K and compiled in Structure Harvester (Earl et al. [1]).
Figure S3. Parameter posterior density estimates from Scenario 4. \( N_{\text{anc}} \): the effective population size of an ancestral population. NP and NS correspond to \( N_{\text{prim}} \) and \( S_{\text{amp}} \) in table 5, the the effective population size of the primary and secondary outbreaks, respectively. \( t_1 \): the divergence time of outbreaks. \( db \): the foundation time of primary outbreaks. All time priors are represented in number of generations. \( \mu_{\text{mic}} \): the mean mutation rate. \( \text{pmic} \) the mean distribution of the number of repeats of microsatellite markers. \( \text{snmic} \): mean rate of single nucleotide insertions and deletions.
Figure S4. Comparing the posterior probabilities of modelled scenarios using direct estimates – the number of times a given scenario is chosen to best represents the observed data.

References