

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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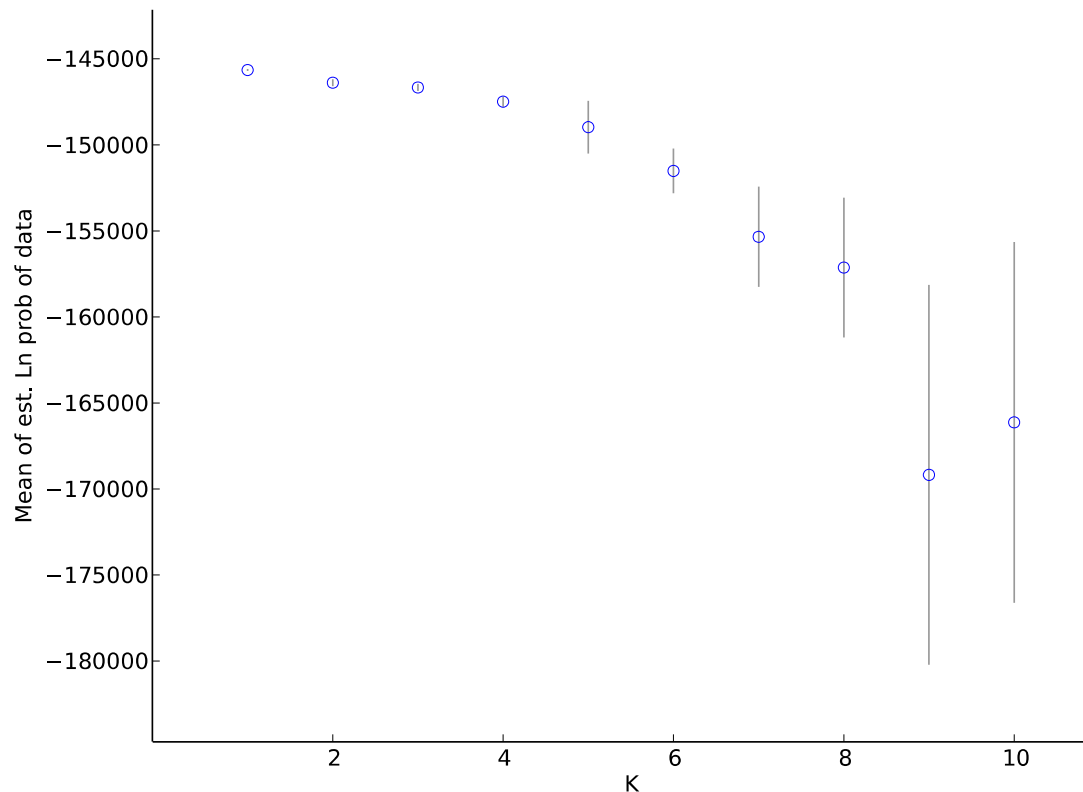


Figure S1. Mean likelihood probability of describing the population structure of CoTS in the Great Barrier Reef into K clusters with standard deviation around the mean. Three runs were performed for each value of K and compiled in Structure Harvester (Earl et al. [1]).

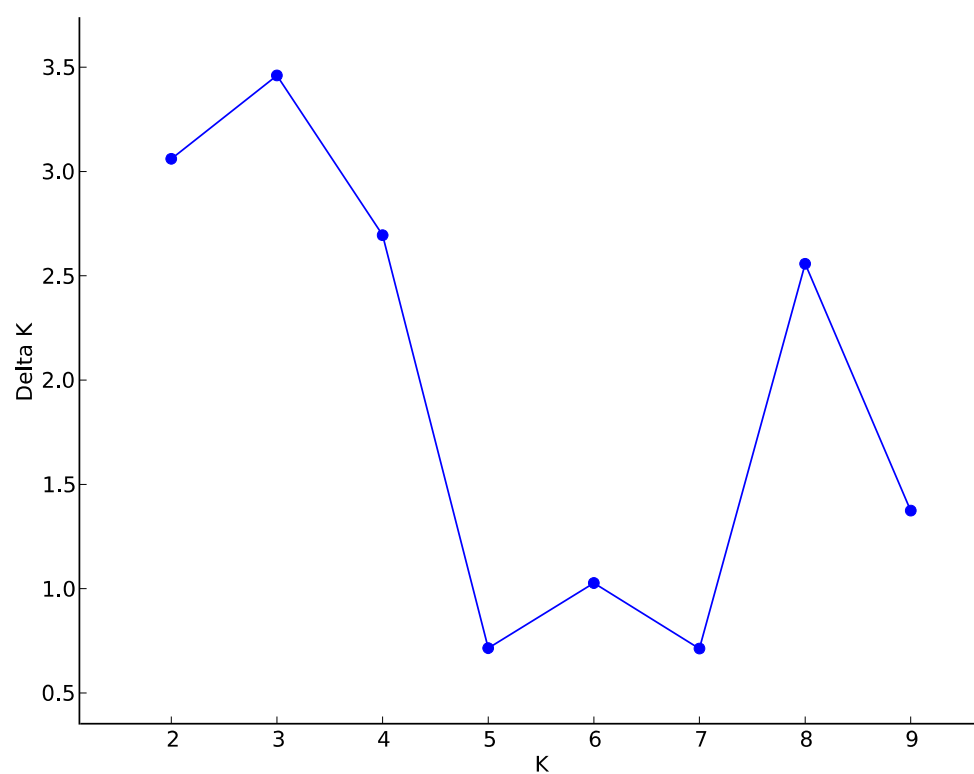


Figure S2. Change in the mean likelihood probability of K clusters describing the population structure of CoTS in the Great Barrier Reef. Three runs were performed for each value of K and compiled in Structure Harvester (Earl et al. [1]).

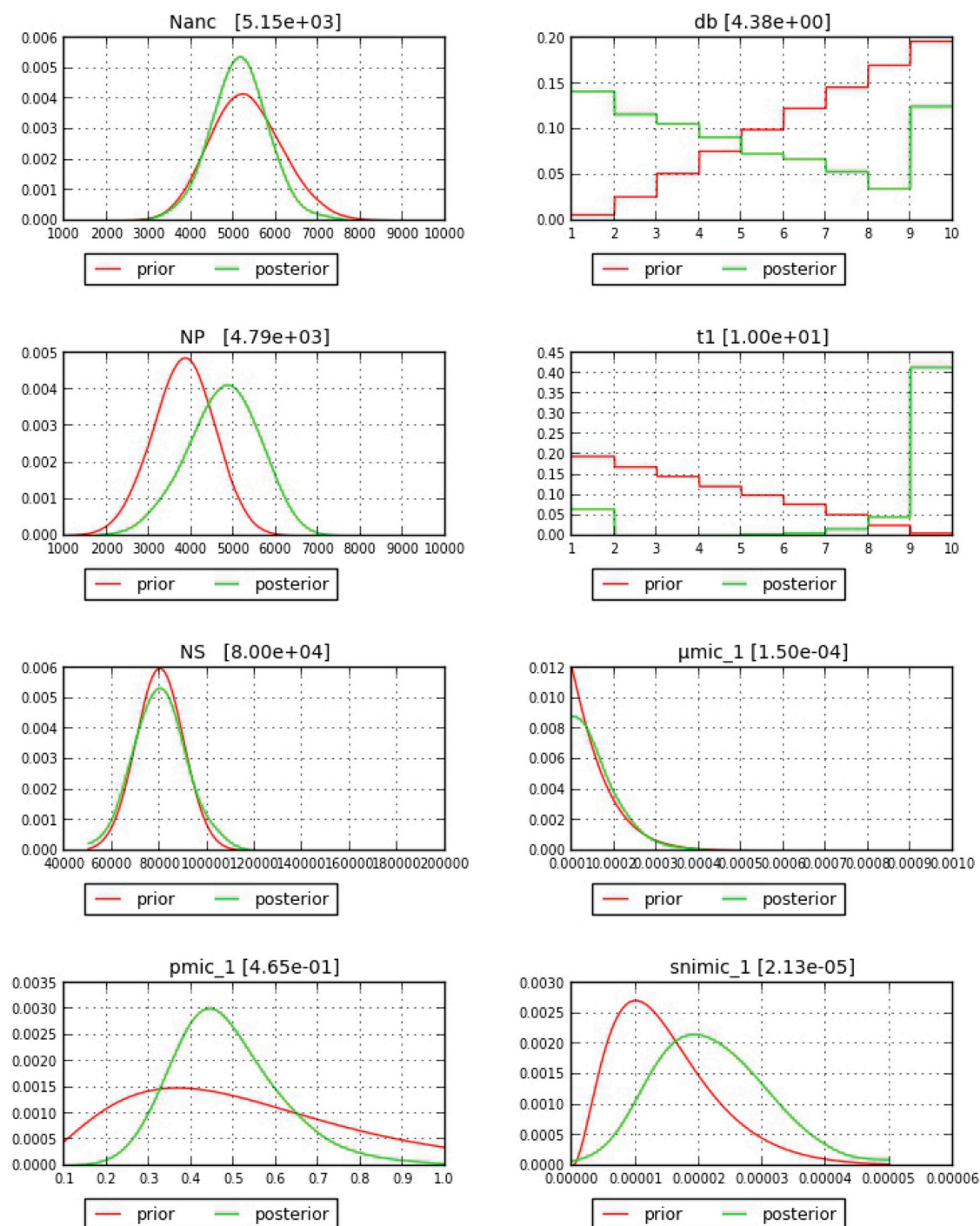


Figure S3. Parameter posterior density estimates from Scenario 4. Nanc: the effective population size of an ancestral population. NP and NS correspond to N_{prim} and S_{amp} in table 5, the the effective population size of the primary and secondary outbreaks, respectively. t1: the divergence time of outbreaks. db: the foundation time of primary outbreaks. All time priors are represented in number of generations. μ_{mic} : the mean mutation rate. pmic the mean distribution of the number of repeats of microsatellite markers. snimic: mean rate of single nucleotide insertions and deletions.

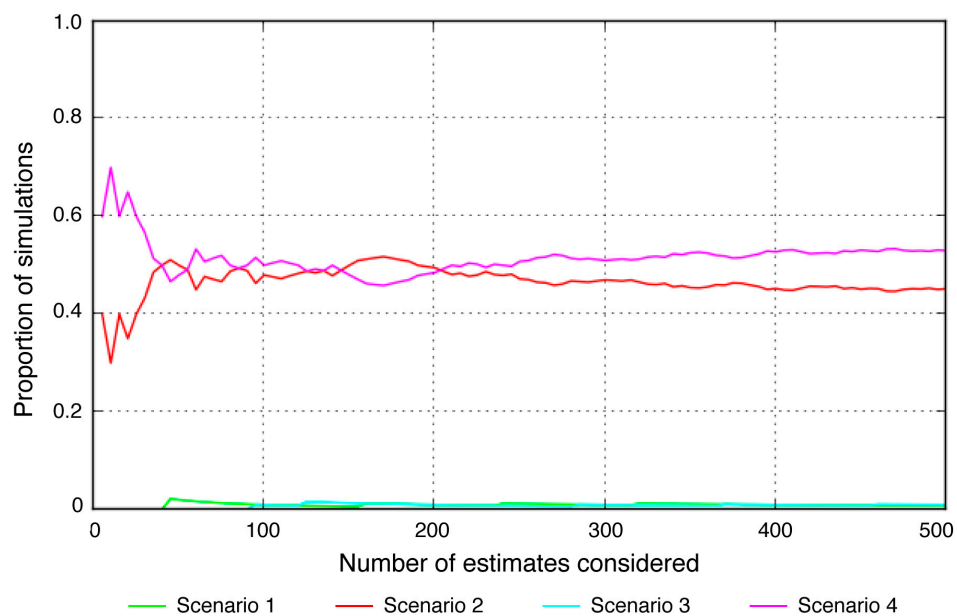


Figure S4. Comparing the posterior probabilities of modelled scenarios using direct estimates – the number of times a given scenario is chosen to best represents the observed data.

References

1. Earl, D.A.; vonHoldt, B.M. STRUCTURE HARVESTER: A website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conserv. Genet. Res.* **2012**, *4*, 359.