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The genus Acropora constitutes the most species-rich clade of hermatypic corals, and its members are important reef builders throughout their broad tropical range. In the Caribbean, acroporid populations have declined over the last 2 decades due to disease, hurricanes, predation, and bleaching episodes, and some are now subjects of conservation efforts. Genetic estimates of population connectivity and clonal structure should be part of these efforts, but such studies have been hampered by low levels of mitochondrial DNA variation in corals, and an apparent dearth of variable single-copy nuclear markers. Developing microsatellite markers in Acropora has proven especially difficult. We used Southern blotting to reveal that, indeed, some microsatellite motifs (AAC, AAG) are rare in the genome of the Caribbean species Acropora palmata. However, repeats with the motif AAT are both abundant and variable. We developed 8 polymorphic microsatellite markers for A. palmata, and performed crosses to confirm codominant inheritance patterns. Five of the 8 markers tested show simple Mendelian inheritance (mean observed heterozygosity = 0.84, mean number of alleles per locus = 8.6). Along with outcrossed sexual larvae, individual egg donors also produced some triploid and selfed larvae that developed normally and survived for 80 h, when the experiment was terminated. The markers reveal variation among 3 Florida populations of A. palmata and among clones within 1 of these populations. Seven of the markers amplify DNA from A. cervicornis and 8 from the hybrid A. prolifera. These markers should prove to be valuable tools for developing conservation strategies for Caribbean acroporid species.