Estimating intraspecific variation in *Spongia officinalis* with microsatellite DNA markers

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The common Mediterranean bath sponge *Spongia officinalis* presents difficulties regarding its taxonomy and estimation of diversity with morphological approaches due to high levels of plasticity and lack of appropriate anatomical characters. Using a set of 8 microsatellite DNA markers, developed *de novo* for the species, we managed to estimate intra- and inter-population structure for a sample set of 530 individuals originating from different Mediterranean regions. In total, 8 populations from the Aegean Sea (Greece), 5 from the Marseille area (France) and 1 from Gibraltar were examined, with intermediate geographic distances ranging form 10 to 3,000 km. Results showed substantial levels of intra-population variation in most geographic locations (mean observed heterozygosity: 0.845 ± 0.048), along with considerable levels of interpopulation genetic structure (average genetic distance F_{ST} : 0.126 ± 0.016). Further analyses exhibited good assignment of populations to sampled locations, along with a clear distinction between clusters belonging to three major Mediterranean phylogeographic regions: Eastern Mediterranean, Western Mediterranean and the Alboran Sea.