In the Results section, “Page 6: Results: Sponge DNA barcoding: Lines 4 The 28S rRNA sequences from the three specimens showed similarities with other Spongillidae species when analyzed using BLAST. The sequences were matched to Spongillidae GenBank sequences that already existed. The following are the findings of the BLAST analysis for the three sponge samples' 28S rRNA sequence alignment with GenBank. Sponge 1 was determined to be Stelletta fibrosa, which is a member of the genus Stelletta, class Demospongiae, order Tetractinellida, and family Ancorinidae. The Sponge 2 was found to be Dactylospongia elegans, which is also a member of the class Demospongiae but belongs to the family Thorectidae, order Dictyoceratida, and genus Dactylospongia. Sponge 3 was found to be Haliclona manglaris, which is a member of the family Chalinidae, genus Haliclona, and order Haplosclerida under the class Demospongiae. The phylogenetic tree constructed using the Neighbor-joining method with 1000 bootstrap support indicates high 28s rRNA sequence similarities with previously mentioned species (Figure 2). The 28S rRNA (D3–D5) sequences from the three sponge specimens showed the highest BLAST matches to sequences of marine demosponges available in GenBank. Such matches indicate sequence similarity to the closest available records but do not alone confirm species-level identity. The BLAST results for the three specimens are as follows:

Sponge 1 (GenBank accession PX115704) matched a Stelletta species (family Ancorinidae, order Tetractinellida, class Demospongiae) with 90.64% identity and 96% query cover to Stelletta fibrosa (KC869612.1), and is designated here as Stelletta sp. Sponge 2 (GenBank accession PX115703) matched Dactylospongia elegans (family Thorectidae, order Dictyoceratida, class Demospongiae) with 97.8% identity and 100% query cover (KY970158.1), and is designated as Dactylospongia cf. elegans. Sponge 3 (GenBank accession PX115705) matched Haliclona manglaris (family Chalinidae, order Haplosclerida, class Demospongiae) with 84.73% identity and 100% query cover (KC869599.1), and is designated as Haliclona sp.

The phylogenetic tree, constructed using the Neighbor-Joining method with 1000 bootstrap replicates, shows each specimen clustering with its respective closest-matching reference sequence in GenBank. Given the relatively low identity values for some matches and the limitations of single-marker identification, these taxonomic assignments should be considered provisional pending morphological and multi-locus confirmation (Figure 2).”

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