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Genetic Connectivity in The Branching Vase Sponge (*callyspongia Vaginalis*) Across The Florida Reef Tract And Caribbean

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The Porifera constitute a substantial fraction of the biomass on coral reefs and frequently have higher species diversity than corals and algae, making this phylum an important model for the investigation of reef connectivity. We examined genetic connectivity in the common branching vase sponge, *Callyspongia vaginalis*, by analyzing DNA sequence variation in 511 bp of the mitochondrial cytochrome oxidase I (COI) gene in 401 individuals sampled from 16 locations throughout the Florida reef tract and Caribbean. Populations of *Callyspongia vaginalis* were highly genetically structured over the study area ($\Phi_{ST} = 0.48$, $P < 0.0001$), including over distances as short as tens of kilometers within the Florida reef tract, and had a significant overall pattern of isolation by distance ($P = 0.0002$). However, nonsignificant pairwise $\Phi_{ST}$ values were also found between a few Florida sampling sites suggesting that long distance dispersal, perhaps by means of fragmentation, may occur over continuous, shallow coastlines. Indeed, sufficient gene flow appears to occur along the Florida reef tract to obscure a signal of isolation by distance ($P = 0.164$), but not to homogenize haplotype frequencies over 465 km from Palm Beach to the Dry Tortugas. Statistical parsimony analysis revealed two highly divergent haplotypes from Honduras suggestive of cryptic speciation. Inferences from a nested clade analysis supported the pattern of restricted gene flow and isolation by distance in the Caribbean, and suggested a northward range extension of *C. vaginalis* from a hypothesized Central American ancestral population into the Gulf of Mexico and Florida. The extensive genetic structuring in this common reef sponge is consistent with expectations based on typically short sponge larval durations, suggesting that sponge recruitment to coral reefs may be largely local source driven.