

Abstract

While there is a significant and growing body of knowledge describing the microbial communities of marine invertebrates such as sponges, there are very few such studies focused on octocorals. The octocoral *Eunicea fusca* is common on reefs in various regions of the Caribbean and has been the subject of natural product investigations. As part of an effort to describe the microbial community associated with octocorals, a culture-independent analysis of the bacterial community of *E. fusca* was conducted. Specifically, a 16S rDNA clone library analysis was performed to provide baseline data. A total of 40 bacteria members from 11 groups were found. In general, Proteobacteria were the dominant group with a total of 24 species and α -Proteobacteria represented the highest percentage of bacteria associated with *E. fusca* (27.5%). Other prominent groups observed were Acidobacteria, Actinobacteria, Cyanobacteria, Planctomycetes, δ -Proteobacteria, Lentisphaerae and Nitrospirae. This is the first analysis of bacterial populations associated with the gorgonian *E. fusca*.