The partial CO1 genes were sequenced using a pyrosequencing platform (Johnson et al., 2012). PCR was used to isolate and amplify a portion of the mitochondrial CO1 gene from all DNA present. Each specimen was tissue sampled and DNA was extracted from each subsample. For individuals larger than two mm, DNA sequences could not be successfully matched to a reference sequence in NCBI BLAST or BOLD Systems (>98% similarity). An additional 58.49% were identified using a phylogenetic approach, but 38.38% of sequences could not be confidently assigned to a higher taxonomic level.

As more ARMS were collected, the overall number of OTUs collected increased for both types of samples (Figure 3). However, as the number of ARMS surveyed increased in the bulk samples (500 μm - 2 mm) increased more drastically than the number of OTUs in the individual samples (>2 mm). Thus by increasing the sample size, the overall number of OTUs collected increased for both types of samples (Figure 3). As seen in Figure 2A and 2B, the number of OTUs found in ARMS from the Gulf of Aqaba is greater than the number of OTUs found in ARMS from Florida and Virginia (TMIN ongoing research). Since the biodiversity of the bulk samples was so much greater than the individual samples in the Gulf of Aqaba, a similar pattern would be expected in other regions.

Discussion

ARMS provide a standardized method of examining coral reef communities, and thus can be used to compare reefs around the world, as well as different locations within one reef, in a variety of ways. Still, there are limited data available to compare these Gulf of Aqaba findings with different locations. Since samples of 500 μm – 2 mm are not usually collected and studied, only the motile samples (>2mm) can be compared to those of different reefs. As seen in Figure 5, the number of OTUs found in ARMS from the Gulf of Aqaba is greater than the number of OTUs found in ARMS from Florida and Virginia (TMIN ongoing research). Since the biodiversity of the bulk samples was so much greater than the individual samples in the Gulf of Aqaba, a similar pattern would be expected in other regions.

Conclusions and Future Work

• Within the Gulf of Aqaba, the biodiversity of organisms 500 μm – 2 mm in size (bulk samples) is far greater than the biodiversity of organisms > 2 mm in size

• Metabarcoding is able to detect many OTUs that are overlooked in samples of large organisms identified by traditional barcoding, but many sequences obtained from bulk samples do not match sequences in existing databases.

• Since the number of OTUs found in the Gulf of Aqaba is greater than those found in Florida and Virginia for motile samples, it is likely the number of OTUs found in organisms 500 μm – 2 mm in size is also greater than what is present in Florida and Virginia

• Future data collection should include organisms 500 μm – 2 mm in size to provide a more in-depth look at the entire community

Big Picture

• Metabarcoding allows for the detection of organisms that have been previously overlooked due to their small size, which opens up possibilities for a variety of new biodiversity studies

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