

REFERENCE GENOME INFORMATION

Sample collection and DNA extraction

We generated a de novo genome of *Montipora sp.1 aff. capitata* using a nubbing (piece of coral branch) from a single individual freshly collected in Falalop, Ulithi Atoll in September of 2014. Total DNA was extracted with Qiagen Blood and Cell Mini Kit following the manufacturer's protocol.

Sequencing and assembly

Sequencing and assembly was carried out using a combination of Oxford Nanopore Technology (ONT) and Illumina sequencing. Briefly, ONT libraries followed the manufacturers protocols. Four independent ONT runs were performed (all four used 9.4.1 flow cells and SQK-LSK109 chemistry). Bases were called with ONT's guppy basecaller and assembled with redbean. Later, genomic DNA was sheared and used to make an Illumina sequencing library (Meyer and Kircher, 2010). First, the DNA was sonicated to approximately 300 bp and end repaired. Next, sequencing adapters were ligated to both ends of the DNA. The adapters were filled-in, and the DNA was amplified in an indexing PCR. After library preparation, the library size distribution was confirmed by agarose gel electrophoresis, and the library was size-selected with a Sage Science BluePippin with a 2% agarose gel cassette. Illumina reads were run at the QB3 sequencing facility of UC Berkeley on a High seq4000. Assembly of the genome was done using packages run on the UCSC mainframe (hummingbird).

The genome accession number is: PRJNA812941. Raw data can also be accessed: Nanopore Accession: SRX14754050; Illumina Accession: SRX14754049.

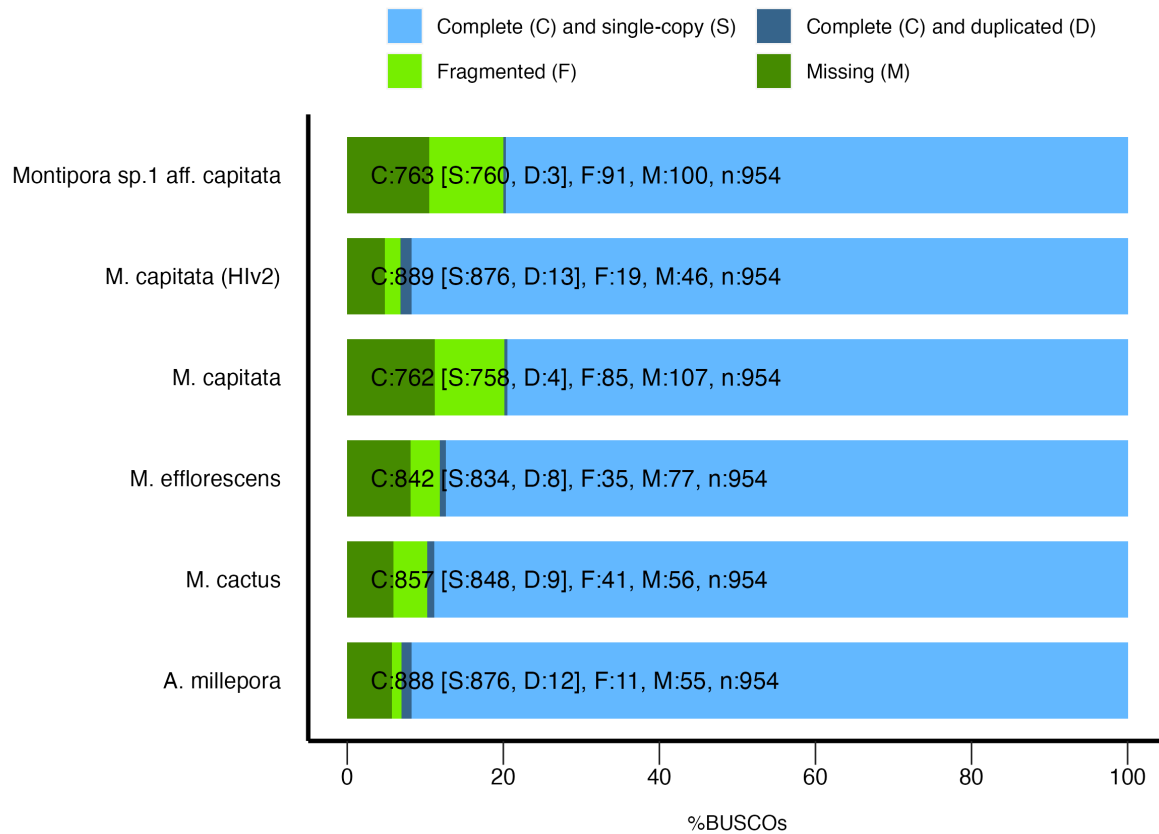
Characteristics of the genome are described below

Assembly Statistics for Montipora_sp_1_aff_capitata.fasta

	bp	n
sum	514,240,284	18550
N50	47,391	3091
N60	36,496	4327
N70	27,122	5964
N80	19,082	8209
N90	11,742	11602
N100	587	18550
N_count	0	
Gaps	0	
ave	27721.85	
largest	366,074	
BUSCO completeness	C:80.0%[S:79.7%,D:0.3%],F:9.5%,M:10.5%,n:954	
complete matches	763	
single completeness	760	
duplicate completeness	3	
fragmented	91	
missing	100	
total BUSCO groups	954	
dataset	metazoa_odb10	

BUSCO assessments provide a view of the completeness of the genome as it relates to genes. As expected, the genome is not fully complete, 80% of full genes were recovered, another 10% are partially sequenced, which means that approximately 10% of the genes are missing. Yet, within the context of other coral genomes, the genome of *Montipora sp1.aff. capitata* that was sequenced here is similar to another *Montipora* genome found in the literature, and not significantly different from most other published coral genomes.

BUSCO Assessment Results



BlobToolKit Snail plot showing a graphical representation of the quality metrics of *Montipora sp1.aff. capitata*. The plot circle represents the full size of the assembly. From the inside-out, the central plot covers length-related metrics. Scaffolds are arranged in size-order moving clockwise around the plot and drawn in grey starting from the outside of the central plot. Dark and light orange arcs show the scaffold N50 and scaffold N90 values. The central light grey spiral shows the cumulative scaffold count with a white line at each order of magnitude. White regions in this area reflect the proportion of Ns in the assembly. The dark vs. light blue area around it shows mean, maximum and minimum GC vs. AT content at 0.1% intervals.

Blobtools2 results:

*These results show the final assembly before contamination removal.

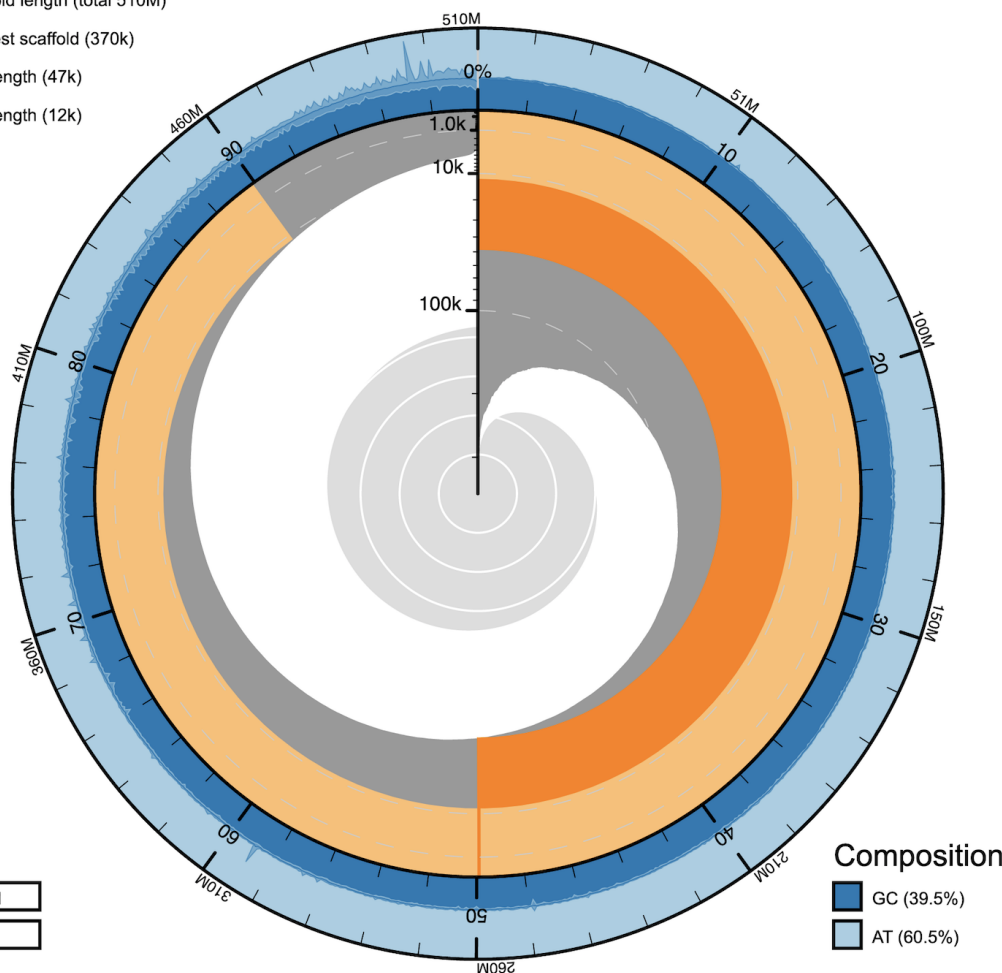
Scaffold statistics

-  Log10 scaffold count (total 19k)
-  Scaffold length (total 510M)
-  Longest scaffold (370k)
-  N50 length (47k)
-  N90 length (12k)

Scale

-  510M
-  370k

Dataset: MON_pilon_02_blob2



Composition

-  GC (39.5%)
-  AT (60.5%)