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Supplementary material

Exploring the microbial community and biotechnological potential of the sponge

***Xestospongia* sp. from an anchialine cave from the Yucatan peninsula**

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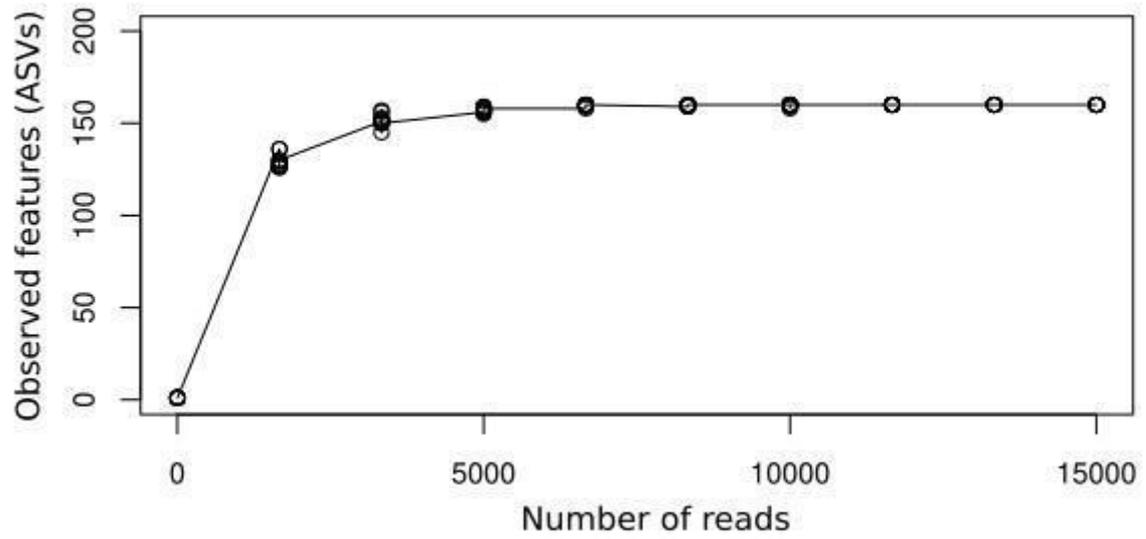
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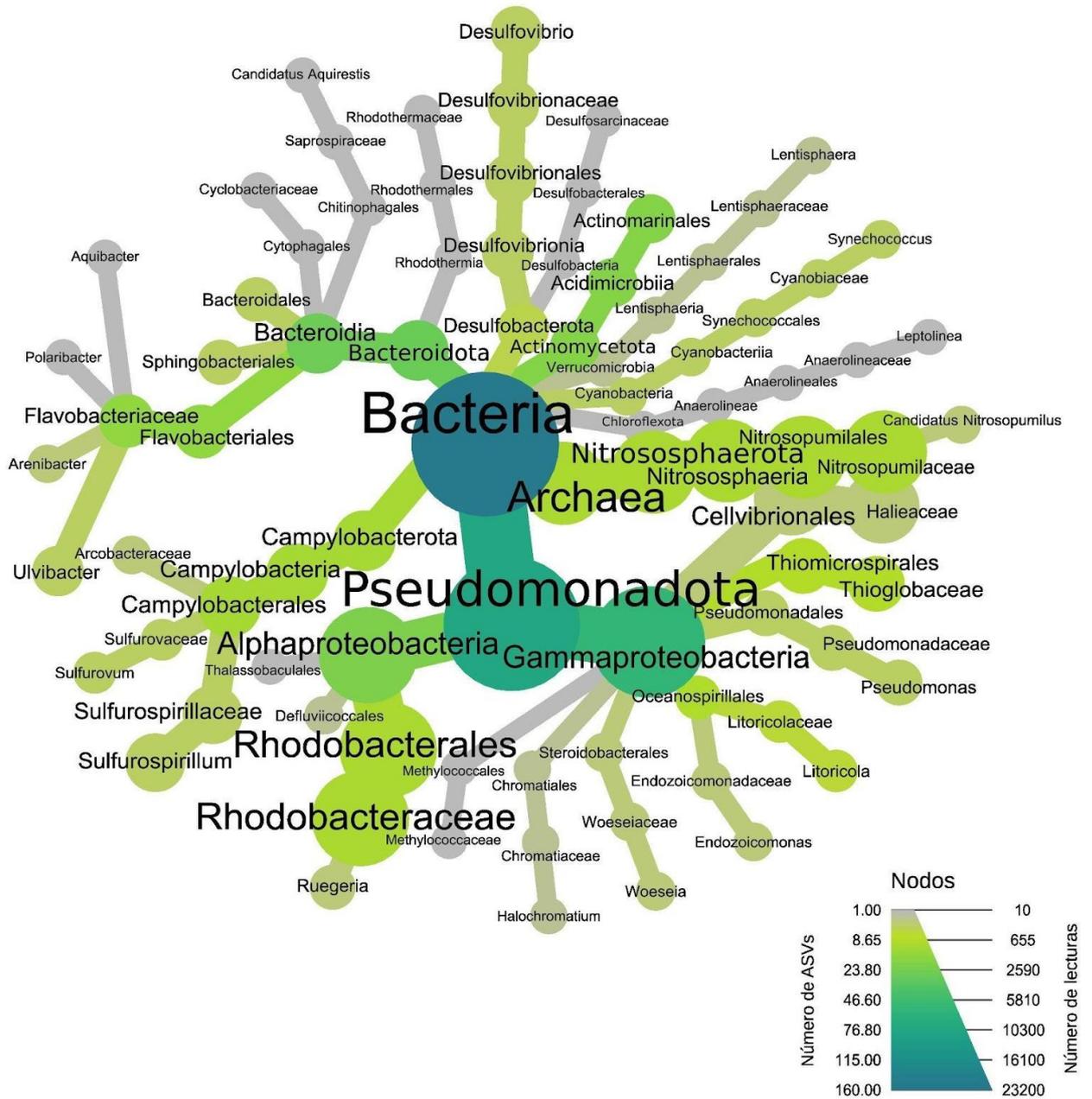
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Figure S1. Rarefaction curve of the ASVs observed in the *Xestospongia sp.*



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Figure S2. Heat tree showing the taxonomic diversity of the microbial community associated with *Xestospongia* sp. The node width and color indicate the number of reads assigned to each taxon.



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Table S1. Coverage values and taxonomic annotation of the metagenomic contigs associated with mitochondrion complete genome.

| #Contig | Legth | Coverage | % | Genome | Kingdom | Phylum | Class | Order | Family | genus |
|------------|-------|----------|-------|------------|---------|------------|-----------------|-----------------|------------------|----------------------|
| NODE_167 | 19046 | 824,0 | 97,3 | Mitogenome | Metazoa | Porifera | Demospongiae | Haploclerida | Petrosiidae | <i>Xestospongia</i> |
| NODE_38384 | 1141 | 59,9 | 100,0 | Mitogenome | Metazoa | Arthropoda | Insecta | Neuroptera | Ithonidae | <i>Fontecilla</i> |
| NODE_10365 | 2843 | 54,0 | 90,0 | Mitogenome | No_rank | Chordata | Mammalia | Lagomorpha | Ochotonidae | <i>Ochotona</i> |
| NODE_20976 | 1766 | 53,3 | 87,3 | Mitogenome | No_rank | Evosea | Eumycetozoa | Dictyosteliales | Dictyosteliaceae | <i>Dictyostelium</i> |
| NODE_28422 | 1420 | 45,8 | 94,6 | Mitogenome | Metazoa | Arthropoda | Insecta | Coleoptera | Chrysomelidae | <i>Chrysomela</i> |
| NODE_19041 | 1891 | 44,5 | 95,0 | Mitogenome | Metazoa | Arthropoda | Insecta | Lepidoptera | Sphingidae | <i>Ambulyx</i> |
| NODE_27511 | 1456 | 29,1 | 100,0 | Mitogenome | Metazoa | Arthropoda | Insecta | Lepidoptera | Coleophoridae | <i>Coleophora</i> |
| NODE_16234 | 2117 | 28,1 | 100,0 | Mitogenome | Metazoa | Arthropoda | Insecta | Coleoptera | Lampyridae | <i>Lucidina</i> |
| NODE_5568 | 4097 | 22,3 | 97,1 | Mitogenome | Metazoa | Arthropoda | Insecta | Coleoptera | Ptinidae | <i>Anobiinae</i> |
| NODE_1972 | 7043 | 21,6 | 92,3 | Mitogenome | Fungi | Ascomycota | Sordariomycetes | Magnaporthales | Pyriculariaceae | <i>Pyricularia</i> |

Table S2. Values obtained for the antibiotic standard curve.

| Well | Staphylococcus aureus ATCC 43300 vancomycin hydrochloride | | | Staphylococcus aureus ATCC 25913 Ampicillin sodium | | |
|------|--|---------------------------------------|-------|---|---------------------------------------|-------|
| | C (µg /m L) Antibiotic | Absorbance (mean) 490nm 608nm | | C (µg /m L) Antibiotic | Absorbance (mean) 490nm 608nm | |
| 1 | 50,0 | 0,084 | 0,061 | 8000 | 0,145 | 0,130 |
| 2 | 25,0 | 0,086 | 0,060 | 4000* | 0,213 | 0,214 |
| 3 | 12.5* | 0,098 | 0,067 | 2000 | 0,592 | 0,760 |
| 4 | 6,25 | 0,572 | 0,689 | 1000 | 0,857 | 1,150 |
| 5 | 3,125 | 1,916 | 2,681 | 500 | 1,130 | 1,514 |
| 6 | 1,563 | 1,829 | 2,495 | 250 | 0,977 | 1,262 |
| 7 | 0,781 | 2,078 | 1,829 | 125 | 1,095 | 1,415 |
| 8 | 0,391 | 1,450 | 1,902 | 62,50 | 1,212 | 1,529 |
| 9 | 0,195 | 1,944 | 1,377 | 31,25 | 1,606 | 2,202 |
| 10 | Growth control | 1,948 | 1,539 | Growth control | 1,625 | 2,195 |
| 11 | Solvent control | 1,639 | 2,184 | Solvent control | 1,998 | 2,838 |
| 12 | CHM control | 0,115 | 0,070 | CHM control | 0,148 | 0,104 |

*Minimum inhibitory concentration for each treatment