Trophic Ecology of Three Caribbean Sponges From Shallow to Mesophotic Depths

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Marine sponges represent a significant component of the total biodiversity on Caribbean coral reefs (1) and are crucial for benthic-pelagic coupling where they filter large quantities of dissolved organic matter (DOM) and particulate organic matter (POM) from the water column (2). Sponges in the mesophotic zone (30-150 m) exhibit increased growth rates, abundances and diversities compared to shallow reefs (2). Increased availability of POM with low C:N ratios in the mesophotic zone may provide more nitrogen for sponge growth compared to shallow coral reefs. Using compound specific isotope analysis of amino acids (CSIA-AA), we can assess the trophic mode and position of sponges with greater resolution (3). Here we present CSIA-AA data of $\delta^{15}N$ and $\delta^{13}C$ from three Caribbean sponges (*Xestospongia muta*, *Plakortis angulospiculatus* and *Agelas tubulata*) along a shallow to mesophotic depth gradient (10 – 91 m).

Methods

- *Xestospongia muta, P. angulospiculatus* and *A. tubulata* samples (n=3) were collected from 10-18, 30, 61 and 91 m at Little Cayman Island. CSIA of amino acids was quantified by gas chromatography/combustion-isotope ratio mass spectrometry (GC/C-IRMS) after amino acid derivatization.
- Divers surveyed percent cover of each sponge along the depth gradient using randomly placed 1 m^2 quadrats.
- The CSIA-AA fingerprinting method was applied with a PCA using the $\delta^{13}C$ of essential amino acids Phenylalanine, Lysine, Valine, Leucine, Threonine and Isoleucine (3).
- Trophic position and ΣV values (microbial resynthesis) were calculated (4,5) with the $\delta^{15}N$ values from the CSIA-AA data.

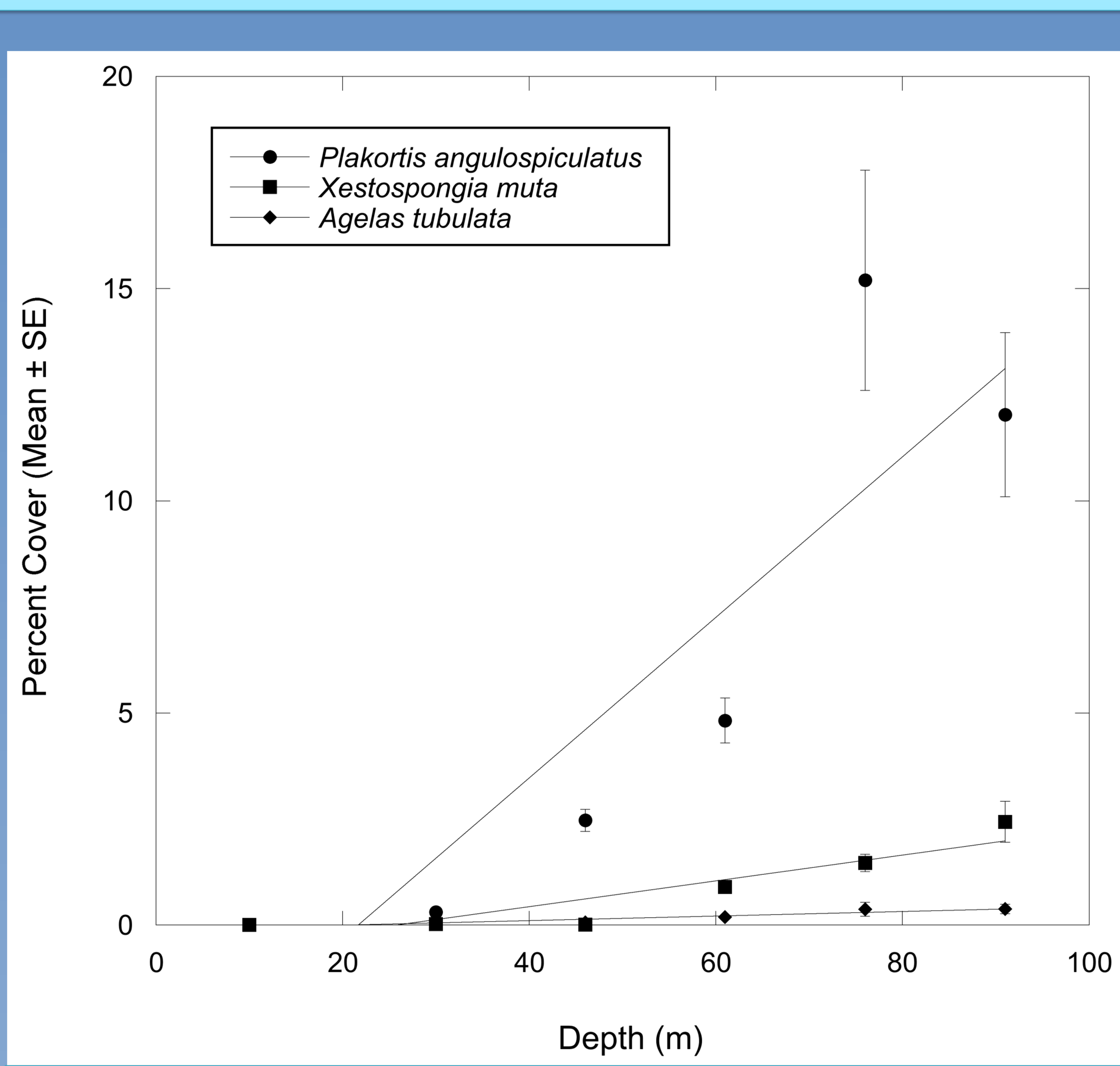


Figure 1. Mean percent cover of *A. tubulata, P. angulospiculatus* and *X. muta* from shallow to mesophotic depths.

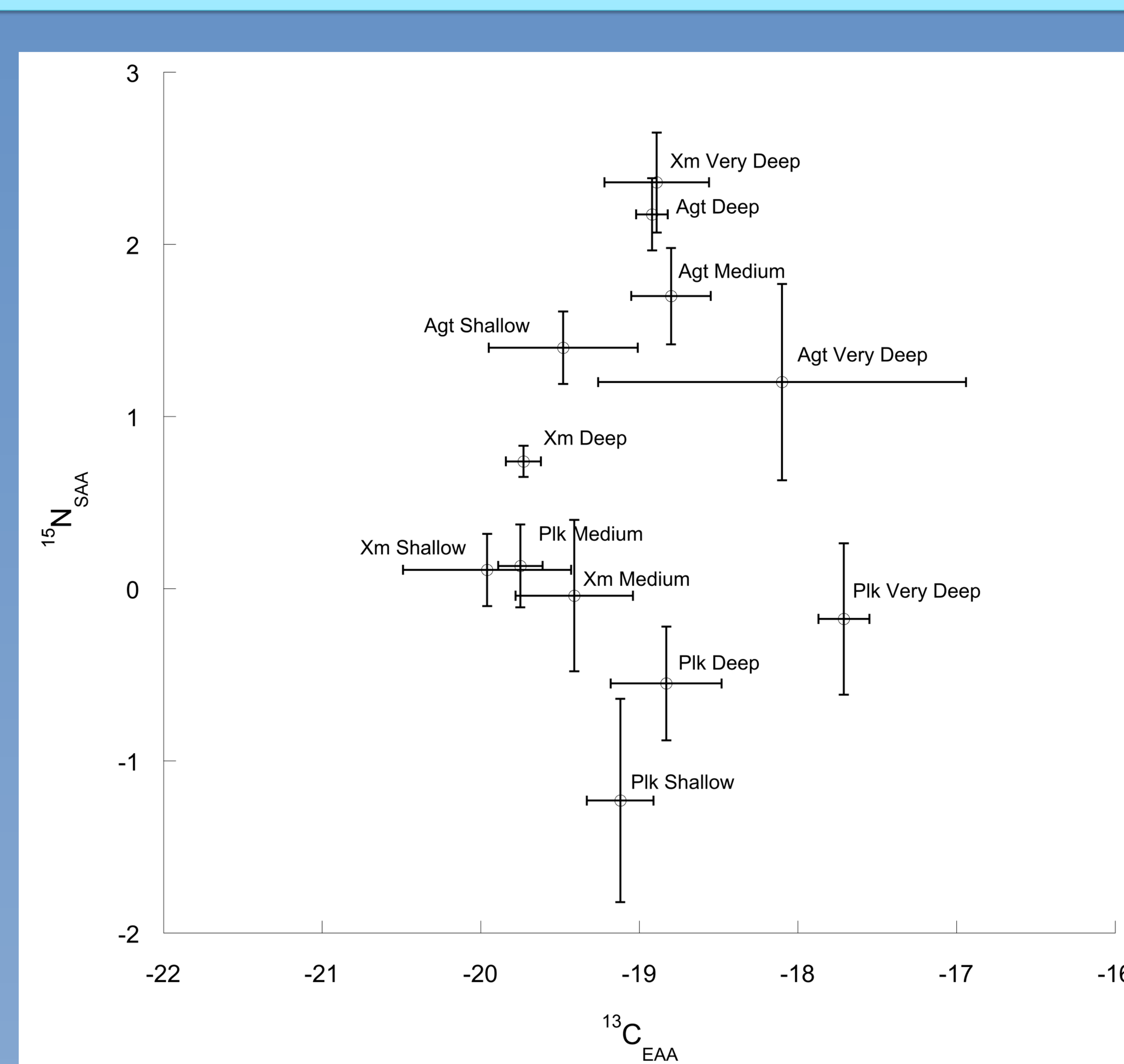


Figure 2. Bivrariate plot of mean $\delta^{15}N_{SAA}$ and $\delta^{13}C_{EAA}$ of *A. tubulata* (Agt), *P. angulospiculatus* (Plk) and *X. muta* (Xm).

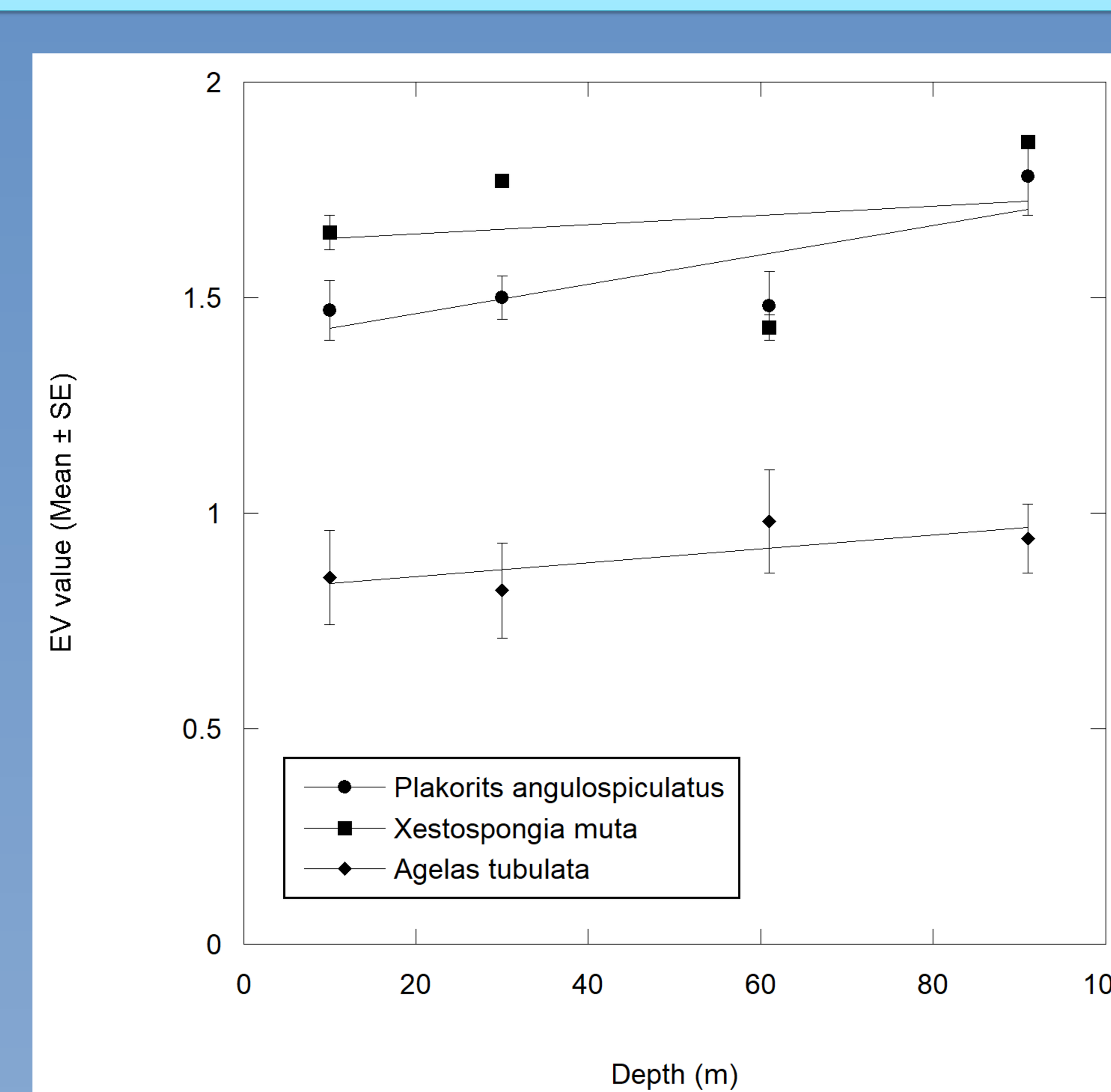


Figure 3. Mean ΣV value (microbial resynthesis of amino acids) from *A. tubulata, P. angulospiculatus* and *X. muta*.

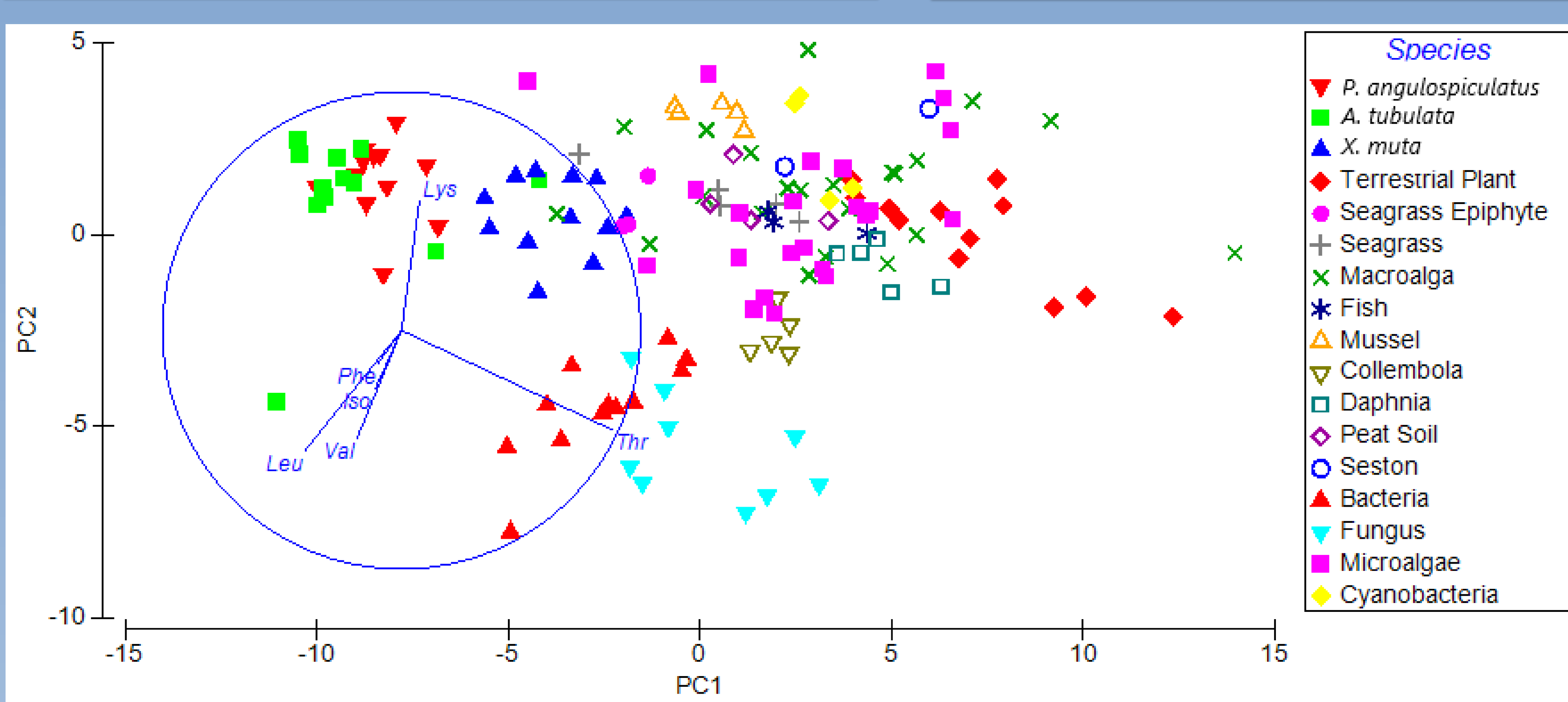


Figure 4. CSIA-AA fingerprinting approach using a PCA of *A. tubulata, P. angulospiculatus* and *X. muta* $\delta^{13}C_{EAA}$. Values and the Larsen et al. (2013) training data set.

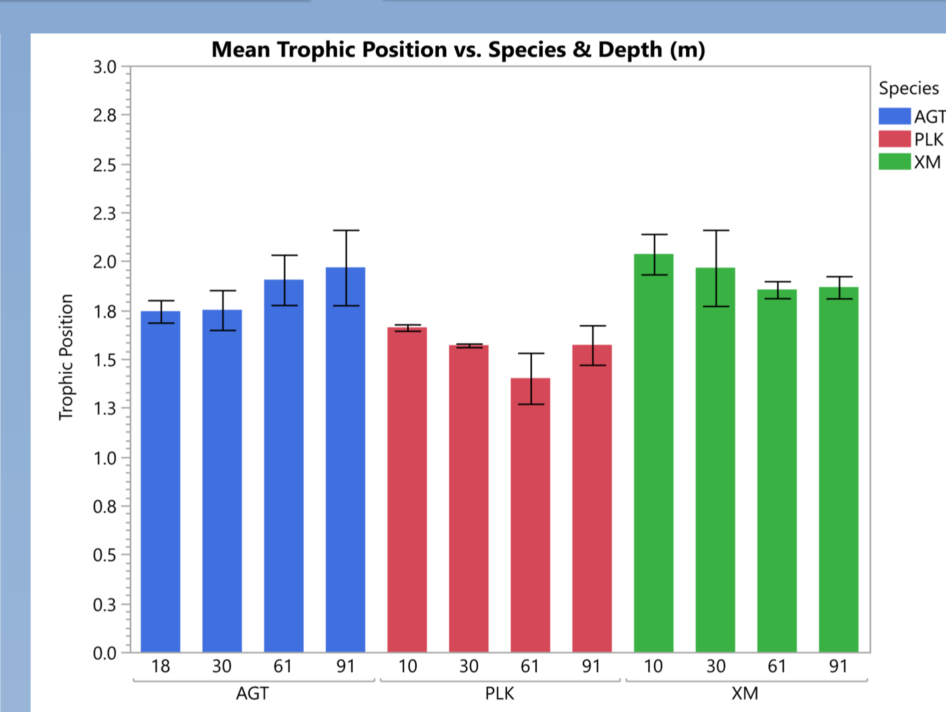
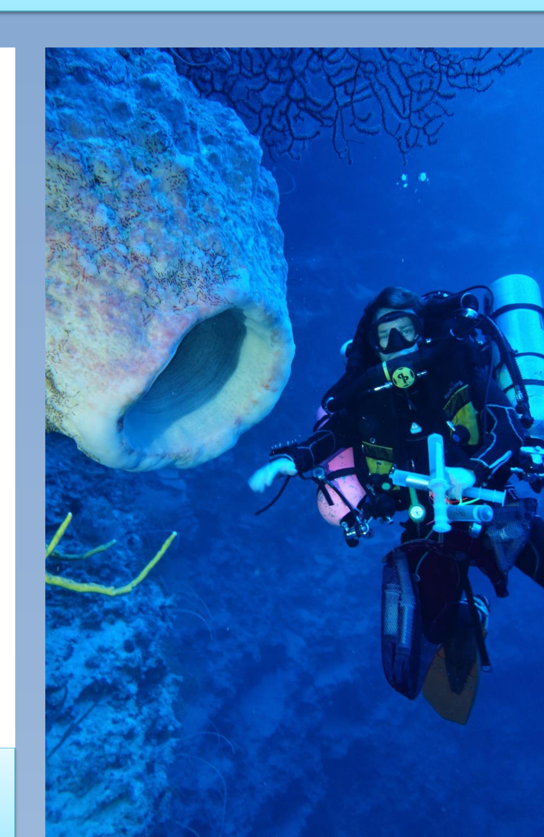


Figure 5. Trophic position of *A. tubulata* (Agt), *P. angulospiculatus* (Plk) and *X. muta* (Xm).



Results

Sponge Percent Cover (Fig. 1)

- Sponge percent cover increased with increasing depth (P = <0.05).

Mean Sponge $\delta^{13}C_{EAA}$ and $\delta^{15}N_{SAA}$ (Fig. 2)

- The $\delta^{13}C_{EAA}$ of all sponges show a trend of enrichment with depth, indicating increased reliance on heterotrophic resources (i.e. POM)
- The $\delta^{15}N_{SAA}$ of all sponges indicate that sponges consume isotopically light picoplankton at all depths and trends of enrichment with depth could indicate increased heterotrophy at depth.

ΣV Values (Fig. 3)

- The ΣV Values of each sponge show species specific reliance on microbial resynthesis of consumed DOM but all species rely on a mixed diet of DOM and POM.

Sponge $\delta^{13}C$ Fingerprinting Analysis (Fig. 4)

- Using the Larsen (2013) training dataset sponges show a species specific and unique isotopic signal separate from free-living bacteria and cyanobacteria, which are primary food sources.

Trophic Position (Fig. 5)

- All sponges reflect primary consumers of a combined diet of POM and DOM at all depths.

Conclusions

- Sponges rely on a mixed diet of DOM and POM along the depth gradient into the mesophotic with increasing reliance on POM at depth. Sponge trophic mode is species specific and can be driven by changes to the microbiome.
- Increased contributions of POM could drive the pattern of enrichment seen in isotope space (Fig. 2) as depth increases. Increased consumption of POM in the mesophotic would support increased sponge growth rates and abundances.
- Further study in the form of *in-situ* feeding measurements, metabolic measurements and microbiome analyses is required to fully understand sponge distributions in the mesophotic.

References

(1) Van Soest *et al.*, (2012) *PLoS ONE* **7**: e35105. (2) Slattery *et al.*, (2013) *Mar Ecol Prog Ser* **476**:71-86. (3) Larsen *et al.*, (2013) PLoS ONE **8**: e73441. (4) Chikaraishi *et al.*, (2014) *Eco & Evo* **4:** 2423-2449. (5) McCarthy *et al.*, (2007)

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