*Response to review from Dr. Peter Tango, “Quantifying seagrass light requirements using an algorithm to spatially resolve depth of colonization”, Beck et al. Aug. 2015.*

Reviewer comments:

First I want to say thank you for the opportunity to review your excellent paper. The paper is well organized, logically presented, easy to read, and technically well done. It was a pleasure to read.

That said, here are my struggles. I understand the substantive work for computing Z sub c, when I looked at the Big Bend map of figure 3, I saw all of these offshore grasses being excluded. So started wondering about the community make up of grasses. I did a little poking around the literature and read a bit about Tampa Bay, read a bit about Big Bend (Mattson et al. 2006, USGS SIR on Florida Big Bend), and it looks like for Big Bend there are deep water species like Paddlegrass. Along these likes, ecologically I am thinking some species are never abundant (Rabinowiz, 1981, 7 forms or rarity), and thinking that these offshore communities of deep water grasses could be highly important but by nature will be excluded from your binary continuous or absent analysis. It appears they may have always been rather patchy and patchiness may have been the dominant feature of extensive offshore grass beds going back in the 1980s any way.

The constraint of working with continuous grass bed distributions seems to focus on only species that would grow like this. For me then, two ways you could go with the paper. The first might be a minor revision to better express the communities represented are nearshore remnants of historical communities that covered vast acreages including deeper water, then include more detail about the species to bolster what you elude to about species differences across sites that explains the difference between inter-site results. The second that I favor would be to use your approach on a species specific basis. Do your maps give species level distribution information from the groundtruthing done to create the base layers? In this way, embracing the species level information and embracing the patchiness distributions which may be characteristic of populations of the species that never grow in continuous meadows but represent another niche, i.e., deep water, and provide Z sub c and light relationships that are species specific, that would be my preferred result of your revision work. You may have such work done already. That would be a major revision I believe. That is why I suggested "acceptable after major revision". However, I do offer you an alternative that might just be a minor revision for you and your coauthors to consider. I think there is some flexibility here in the final publication product and maybe an opportunity to turn it into two publications with the second being the more detailed species specific distribution analysis of what you elude to. I also appreciate you could add to that by including additional work that includes assessment of other factors you suggest could affect inter-site variability in your results. I'm not suggesting you do this in either of the revision scenarios that I recommend. That probably gets you to a third paper :).

I hope you find the review and recommendations helpful Marcus. Please give my best to Jim. I am sure we will see this in publication and again commend you on excellent work you have done here. Good luck and take good care.

Author response to comments:

We appreciate the comments and suggestions provided by Peter. He suggests two options for improving the manuscript. The first is a minor revision that suggests we provide additional commentary to describe the limitations of our approach, including information about the species present in our data. The second is a major revision that proposes we modify the analysis to include species-specific data and estimates of light attenuation to potentially explain inter-site variation in our results. After considering each option, we have not modified the text and provide justification below.

The suggested major revision would require additional data beyond which is currently available in the geospatial datasets used in our analysis. An advantage of our method is the potential for application to broad geographic areas. The availability of generic geospatial data for applying our method is an asset that we emphasize in the manuscript. Although information on species distributions can be obtained from alternative sources (e.g., references provided by the reviewer and works cited in our manuscript), the ability to combine these data with routine assessments of seagrass areal coverage remains a logistical challenge that prevents application of our algorithm to individual species. Moreover, the information on seagrass response to light attenuation provided by our method has considerable value in identifying potential factors that affect aquatic habitat. Although we agree that extending this analysis to individual species is worthwhile, the current manuscript provides sufficient information given our objectives.

As an alternative, the minor revision suggests we describe the limitations of the method within the constraints of the data. However, we feel that this limitation is readily apparent from the current text and we make no claims that the estimated depth of colonization or light requirements provided by our methods are applicable to all seagrasses. The true value of these estimates are as metrics that describe variation in seagrass communities, which we have shown as having value for describing variation within sites as well as between sites. Additional site-level research, including field studies, would be a logical extension that information from our analyses could motivate. As such, we feel that providing additional discussion on limitations of our method may potentially undermine our goal of demonstrating the improved spatial resolution of depth estimates and light requirements provided by our method.

We hope that our response has made our opinion clear on the matter. We are certainly interested in pursuing the reviewer’s suggestions but will not do so in the current manuscript.