

I commend the authors on their efforts. The manuscript is greatly improved. With minor revisions, I think it can be a valuable contribution.

The authors have done a good job 1) better aligning their conclusions with the data and 2) adding caveats and highlighting the limitations of the data. I would suggest a couple additions to shore up these efforts:

1. In the discussion, the authors discuss two scenarios: "out-of-guam" and "local outbreaks". Out-of-Guam is pretty clear, but local outbreaks is not explained very well. I think I know what the authors mean, because later in the discussion they propose that the sponge might arrive at a reef and exist at a low level undetected for a long time, then an outbreak is triggered by some action. Perhaps the authors could move this explanation up to where it is first discussed?

2. Also, I think the authors need to change "out of guam" to "recent expansion, perhaps from Guam". They do a good job of presenting evidence that the sponge has only recently arrived at some reefs. They can also say that Guam is a good candidate source, because of the historical knowledge about the outbreak. On the other hand, diversity at some other sites is as high or higher than Guam, so perhaps it was a recent expansion from a different source?

3. There are a few places where the authors could make a simple change in language that I think would be better. For example:

"demographic analyses indicated that most *T. hoshinota* populations were in mutation-drift equilibrium, except for the Sulawesi Sea and Maldives, which had bottlenecks following recent expansions."

I think it would be better to say that the analyses were consistent with mutation-drift equilibrium; this clearly states what the data show, while acknowledging the possibility that an expansion is not detected due to lack of statistical power. There are other places where it is stated that one population has recently expanded, but again those conclusions are supported by modest evidence, as TajD might be significant but other indices were not.

4. The figure captions need more information. They should explain everything on the figures. For example, figure one has labels like "H22/H23"...what are these? Figure three has a cluster diagram or phylogeny...what is that?

5. You have an asterisk to designate significant values in your table, but I don't see where you say what value was used as a threshold for those values. Is it 0.001 as in your other data? If it is only 0.05, you can't say those values are significant because you have a multiple testing problem.

Other points:

discussion:

line 390: "is represented by its two most "invasive" ITS2 haplotypes, H3 and H2": I don't think you can say these haplotypes are more invasive, they are just more common. You expect some common genotypes and a bunch of rare ones in a neutral model.

Line 407: "The "out-of-Guam" hypothesis is further supported by the analyses of pairwise F_{ST} and isolation-by-distance (IBD). Only 32.73% of pairwise F_{ST} values were significant, suggesting that moderate gene flow existed among marine ecoregions in the West Pacific, Coral Triangle, and eastern Indian Ocean, but not the central Indian Ocean."

I don't think those values support either model, and certainly not Guam as a source specifically. Non-significant F_{ST} could mean that there is some natural population connectivity or that the populations have recently expanded.

Table 1: N vs. phased seqs number: I don't understand this phased seq number, shouldn't it be $N*2$? Why is it small?

References: some works cited not in refs, like Sperling 2012 (which should maybe be 2011?), maybe others?

I don't see any figure caption for the suppl. figure.