

The manuscript by Kelly Brener-Raffalli and colleagues describes how laboratory experimental increase of temperature affect the transcription of genes and the diversity of the associated symbionts in colonies of *Pocillopora* corals. Metabarcoding and metatranscriptomics are effectively useful but demanding technologies to get insights into the effect of heat stress on a worldwide in-danger taxon, greatly considered here as an holobiont. This work is based on a big amount of data and certainly implied big efforts to extract from bioinformatics' outputs a significant and biologically-relevant wider picture of what is going on.

Unfortunately, there are reservations with the experimental design and how far data are analyzed that limited my enthusiasm as a reviewer. I need major justifications from authors to better appreciate the value of this study. Here are the points that need to be addressed:

1- Corals were collected at two different localities at two different time points; No initial information is given about the local water temperature and abiotic parameters (pH, photoperiod, ion concentration, *c.f.* 1.167 & 1.178 p.6 & 7) when collection was made. I have read table 1 but I have no idea how stressful was the transfer by aircraft and the delayed maintenance at 26 degrees in the cited lab conditions. How similar is the lab filtered seawater to the *in situ* water properties? Then, I guess that lab experiments were run separately for the Om (collected in June) and the NC colonies (collected in November) as acclimatation runs for 2 months. This point is not mentioned. Is this acclimatation period deals with potential parental effect? More importantly, if I understood well, acclimatation was made at 26 degrees but when the experiment of heat stress started, control temperatures were set at 27 or 31 degrees. If I am getting it right, this made already a change for the Om colonies of +5 degrees. Can the authors clarify this point and with respect to the biology of organisms?

2- It seems to me that both barcoding and transcriptomics analyses could be more deeply conducted. On the bacterial metabarcoding side, analysis of OTU richness is not sufficient to claim that community remains stable. By analogy with what is done in RNAseq analysis, authors could use normalization and DESeq2 or edgeR package tools (available in phyloseq) to identify differentially abundant OTUs. Change or no change in relative abundances of OTUs are valuable information, not only during the heat stress experiment in lab conditions but also when transferring field-collected corals to lab conditions. My feeling is that authors could observe changes in relative abundance between field and lab conditions, with a bias toward the already abundant OTUs in the field. Although authors may observe many more less abundant OTUs once in lab, abundance analysis of this "rare biosphere" may be informative after the transfer or during experiment as shown in other coral studies. On the other side, it is still widely accepted that transcriptome data need quantitative PCR experiments to confirm the accuracy of the results on a selected set of genes, in particular differentially expressed genes. About differentially expressed genes, is there any potential link between the greater variance in the Om and the above cited point 1 of control temperature?

3- There are confounding factors that may limit the interpretation of results. Here, the study deals with one genus made of 3 species (at least 2 genotypes with the NC and 1 more corresponding to the Om). By the way, the Species Hypothesis is not that obvious for a non-initiated person. Gelin *et al.* 2017a and this concept could be detailed. So, in this study, locality can merely be confounded with coral genotype. Genotypes of *Symbiodinium* are also well different between localities. By the way, heat tolerance of these two *Symbiodinium* genotypes are not presented although authors have arguments (*c.f.* Brener-Raffalli *et al.* 2018 *Microbiome*). This added to the above points make it hard to generalize on plasticity and frontloading. The authors talked about plasticity but never mentioned local adaptation. For the constitutive upregulation or frontloading, it is even harder to me. It also raises more general questions that are likely not the scope of the study. How does the frontloading gene expression response happen in normal populations (*e.g.* not under controlled lab conditions), and how is it turned on over time in response to environmental variation? Given that some of the identified genes are involved in multiple cellular pathways, how do gene expression changes ultimately (and simultaneously) affect both coral health and stress tolerance?

4- Another point is the format of the discussion and the long text on the functional aspect of the study. It is in between an analysis/result and a discussion. Do the authors plan to submit this paper to a specific journal afterwards and made a specific formatting for that reason? Although super interesting, I think it would more valuable to incorporate data from other studies made on corals. At the moment, many studies have investigated the effect of heat stress on different coral models. Moreover, Barshis *et al.* (2013) observed that heat-tolerant populations of *Acropora hyacinthus* displayed front-loading of 60 genes associated with stress and immune response following simulated bleaching. Haslun *et al.* 2018 (*Marine Biology*) also focused on a meaningful set of genes. Maybe for these genes in particular or others, it is worth bringing details, this would prevent from reading a too long catalogue of what is moving. In addition, and related to point 2 and line 586 p.22, can authors anyway get some information from some of the *Symbiodinium* genes?