TITLE: INTER-KINGDOM AND FUNCTIONAL TRAITS ASSOCIATED WITH PULSE THERMAL RESISTANCE IN CORALS

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ABSTRACT:

Thermal resistant corals have been reported in Brazilian cost over the last few years. We have been observed that the microbial community, especially the Beneficial Microorganisms for Corals (BMCs) play a role on conferring thermal resistance to their host. In this regard, fragments of the coral Mussismilia hispida were tagged and sampled from Maraú, Brazil after recovering from a massive coral bleaching event in 2016. Both affected (sensitive) and unaffected (resistant) colonies of the same coral species were collected and used in high temperature microcosm experiments, in order to measure the thermal thresholds of each phenotype and observe the microbiome dynamic during a heat pulse stress. To do so, two experiment were run, the first with resistant corals and the second one with sensitive corals, which started at 26°C, moving on to high temperatures (32°C/30,5°C, respectively) and going back to 26°C. Coral nubbins from each phenotype were sampled before the stress (T0), the last day of the peak of temperature (T1) and after the recovery period (T2). Maximum quantum yield of the zooxanthellae-associated Photosystem II (Fv/Fm) and morphologic changes were measured, as well as the DNA extracted and sequencing to disentangling microbiome roles in thermal resistance. Among all physicochemical factors measured, thermal stress was the main factor in Non-Metric Multi-Dimensional Scaling analysis promoting significant changes in the bacterial structure of both resistant and sensitive communities. No significant difference on the

(Fv/Fm) values and no visible signs of tissue damage were observed for resistant corals after the recovery period, while all sensitive corals bleached at 30,5 °C. Even though both resistant and sensitive coral types are classified as being from the same species, the microbial community was distinct since the beginning of experiment and some bacterial taxa were identified as putative bioindicators of resistance, based on amplicon sequencing analysis of the 16S rRNA gene. Alphaproteobacteria was the most abundant class among resistant indicators, sheltering Amplicon Sequencing Variant (ASVs) from Rhizobiales, Parvularculales and Rhodospirillales orders. The higher detection of photosystems genes in T2 thermal resistant samples from the metagenomic data may indicate the ability to uptake photosynthetic microbes and cope with the oxidative stress through chaperones activity, also having high detection in T2 resistant samples.