Learning from the 4th global coral bleaching event in the Maldives: unravelling microbial and symbiont shifts in *Acropora muricata* and *Porites lutea*

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Background

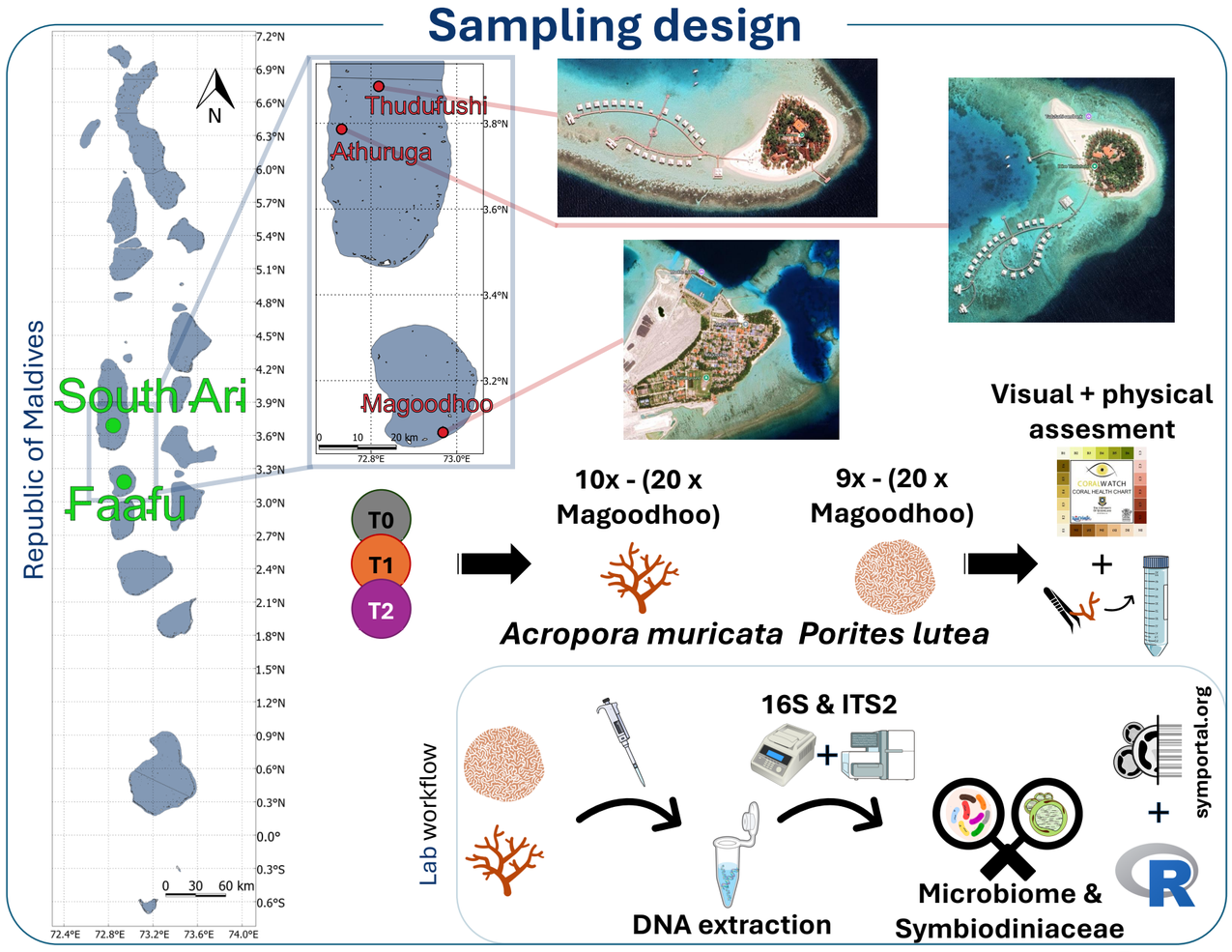
Maldivian reefs have experienced repeated **thermal coral bleaching** events from 1998 to 2024 [1,2,3], causing mass mortality, yet some reefs showed remarkable resilience [2]. The 2024 global coral bleaching event was characterised by degree heating weeks (DHW) exceeding **9 °C-weeks**, resulting in mass bleaching events [4].

Thermally resilient symbionts and microbiome **composition** have been linked to coral resilience [5,6,7,8], though whether resilience derives from the **stability** of the microbiome [9, 10] or compositional **shifts** [11] remains debated. Since bleaching responses have been highly site-specific [12,13], **microbial** and **symbiont dynamics** may help explain why some reefs recover while others experience severe mortality.

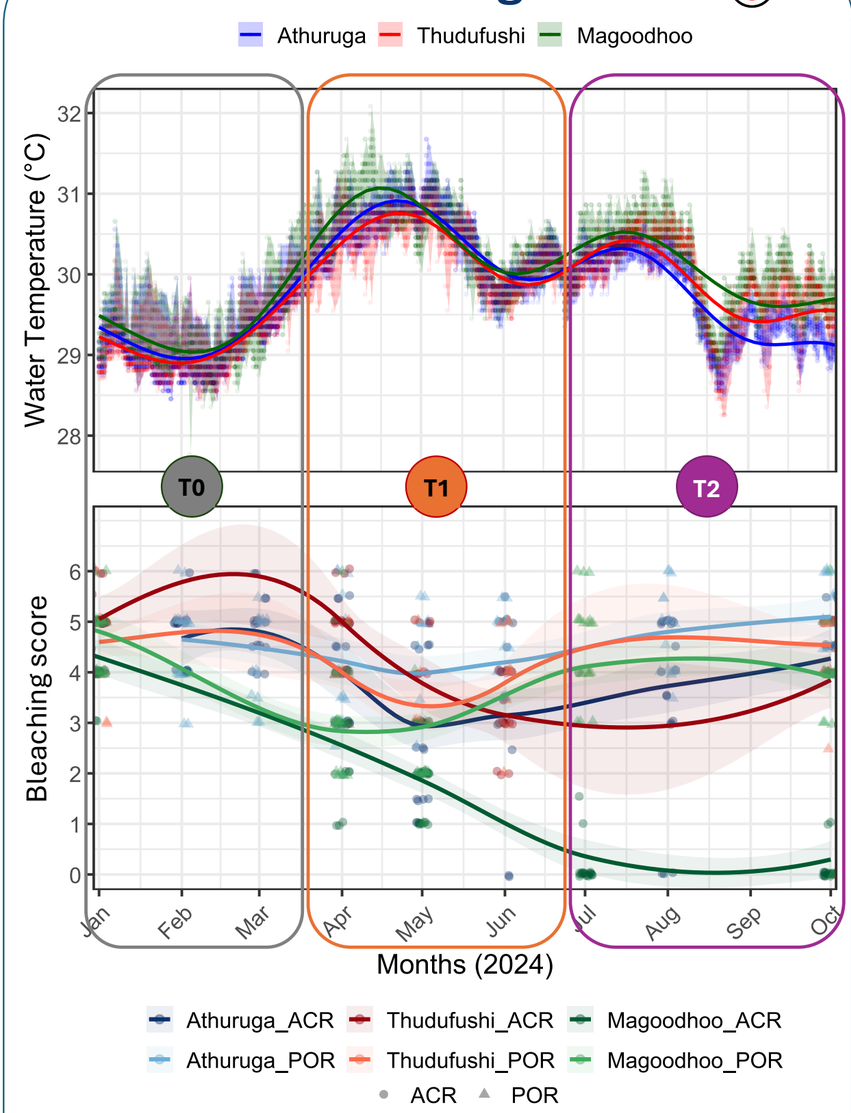
Aim

This study characterises the spatiotemporal dynamics of **Symbiodiniaceae** and **bacterial** communities in *Acropora muricata* and *Porites lutea* across **three** Maldivian reef sites (**Athuruga**, **Thudufushi** and **Magoodhoo**), sampled **before (T0) Jan-Mar**, **during (T1) Apr-Jun**, and **after (T2) Jul-Oct** the **2024 bleaching event**, to identify microbial signatures associated with differential bleaching outcomes.

Sampling design



Water temperature and bleaching score



Magoodhoo experienced the highest temperatures, lowest bleaching score and highest mortality compared to the other locations

	Death %	Death %	MAX
Mean Overall	40 %	2 %	31.2 °C
Athuruga	10%	0%	31.7 °C
Thudufushi	15%	0%	31.2 °C
Magoodhoo	85%	5%	32.1 °C
	Bleached % → 42 %	Fully recovered % → 39 %	

Symbiodiniaceae community

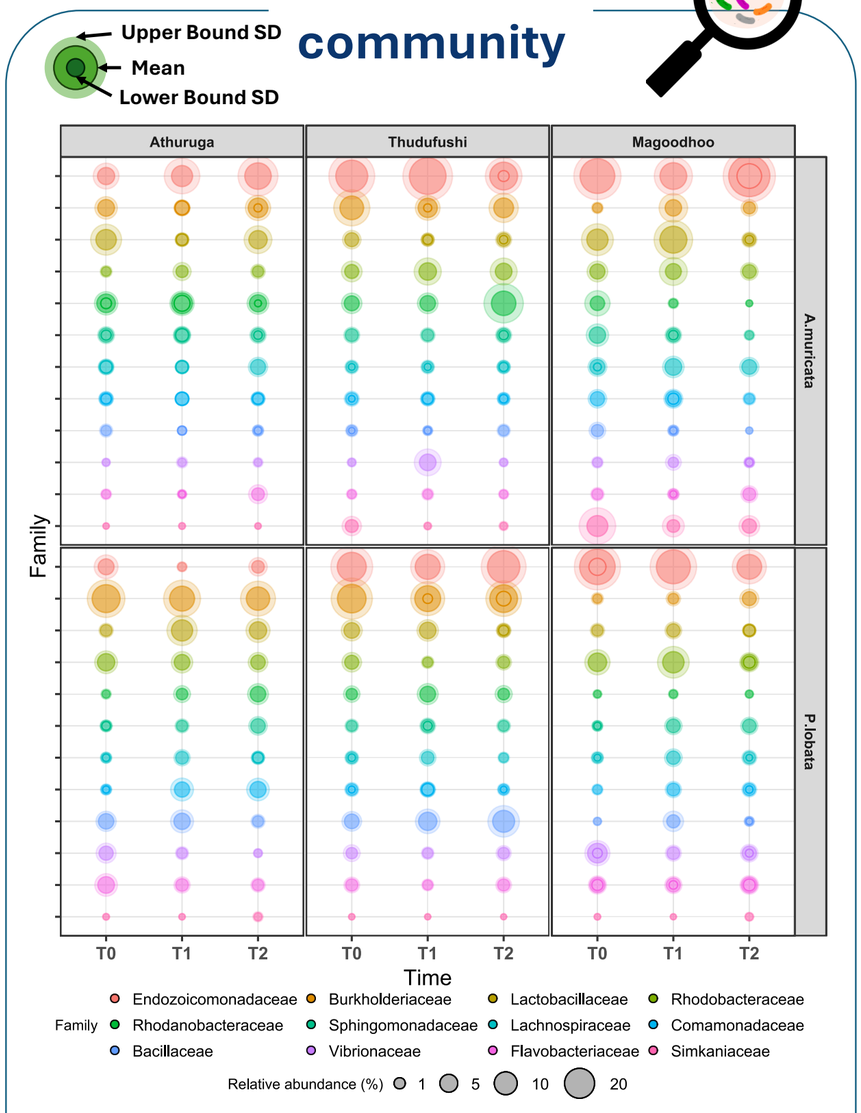
Symbiodiniaceae community **didn't change** over time
PERMANOVA $R^2 = 0.0093$, $p = 0.487$

Dominated by C3 ITS2 type profile (**85%**)

Dominated by C15 ITS2 type profile (**82%**)

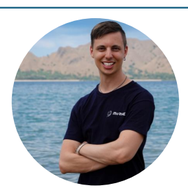
Increased susceptibility to bleaching and mortality in **Magoodhoo** could be linked to:
- Presence of A1-A1nu ITS2 type profile (*Symbiodinium spp.*)
- Near absence of D1 ITS2 type profile (*Durusdinium spp.*)

Bacterial community



Bacterial community shifts were more consistent with **stress-associated restructuring** than with a uniform time effect. Endozoicomonadaceae and Rhodobacteraceae relative abundances is maintained throughout the bleaching event, even at the bleaching peak (**T1**), while they are usually complementary [11]. Additionally, Vibrionaceae did not show a broad event-wide increase, remaining below 1% in most *A. muricata* samples, but site-specific enrichment at **Thudufushi** (4.1%) suggests that opportunistic taxa may emerge only under particular local conditions.

Magoodhoo has a distinct microbiome signature with higher Simkaniaceae in *A. muricata* (8.0% at T0, compared with ≤1.8%) and lower Bacillaceae in *P. lobata* (0.1–2.0%, versus up to 9.1%), alongside generally reduced Burkholderiaceae (0.5–4.0%, compared with 6–18%) and a contrasting Lactobacillaceae peak at **T1** (15.5%, compared to 1.3–8.3%). This suggests that the bleaching event interacted with local environmental conditions and host background to reshape the bacterial assemblage in a site-specific manner.

References

[1] Zahir et al., 2009; [2] Pisapia et al., 2016; [3] Perry & Morgan, 2017; [4] Montefalcone et al. 2026; [5] Coles & Brown, 2003; [6] Palumbi et al., 2015; [7] Torda et al., 2017; [8] Webster & Reusch, 2017; [9] Tracy et al., 2015; [10] Epstein et al., 2019; [11] Pootakham et al., 2018; [12] Maher et al., 2020; [13] Montaño-Salazar et al., 2023