

## Substrate as a driver of sponge distributions in mangrove ecosystems

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**Supplement.** Bacterial community analyses for various Caribbean sponges, and mangrove and reef habitat water samples

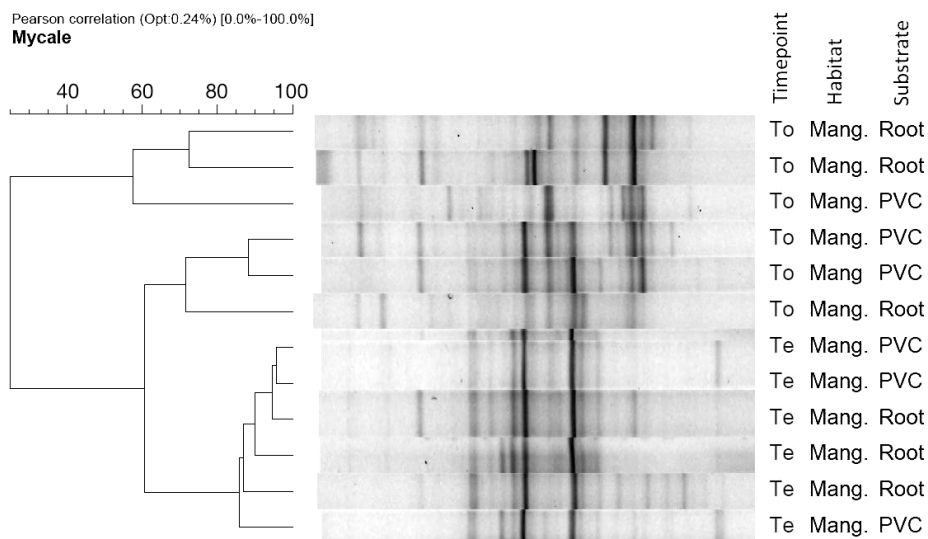


Fig. S1. Pearson's based cluster analysis of sponge-associated bacterial community composition of samples of *Mycale microsigmatosa* before ( $T_0$ ) and after ( $T_e$ ) transplantation

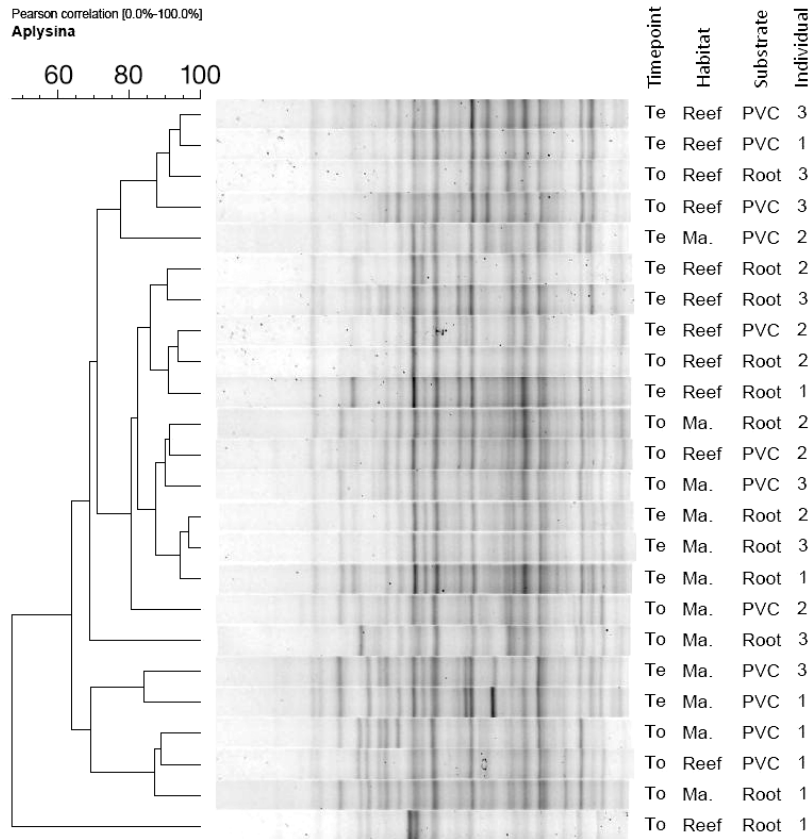


Fig. S2. Pearson's based cluster analysis of sponge-associated bacterial community composition of samples of *Aplysina archeri*, before ( $T_0$ ) and after ( $T_e$ ) transplantation

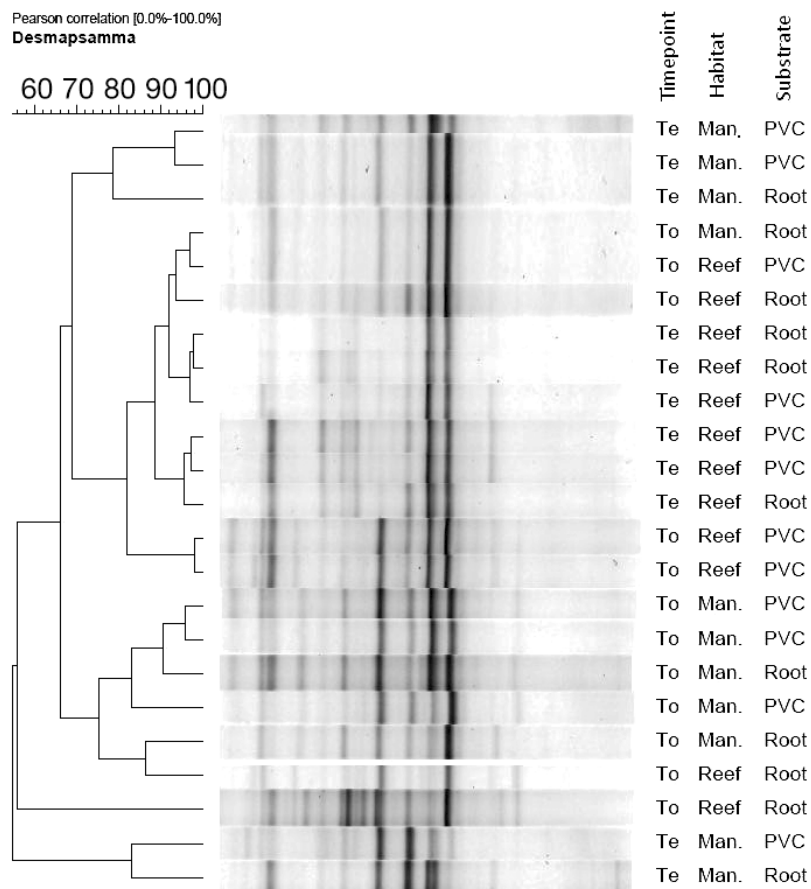


Fig. S3. Pearson's based cluster analysis of sponge-associated bacterial community composition of samples of *Desmapsamma anchorata* before ( $T_0$ ) and after ( $T_e$ ) transplantation

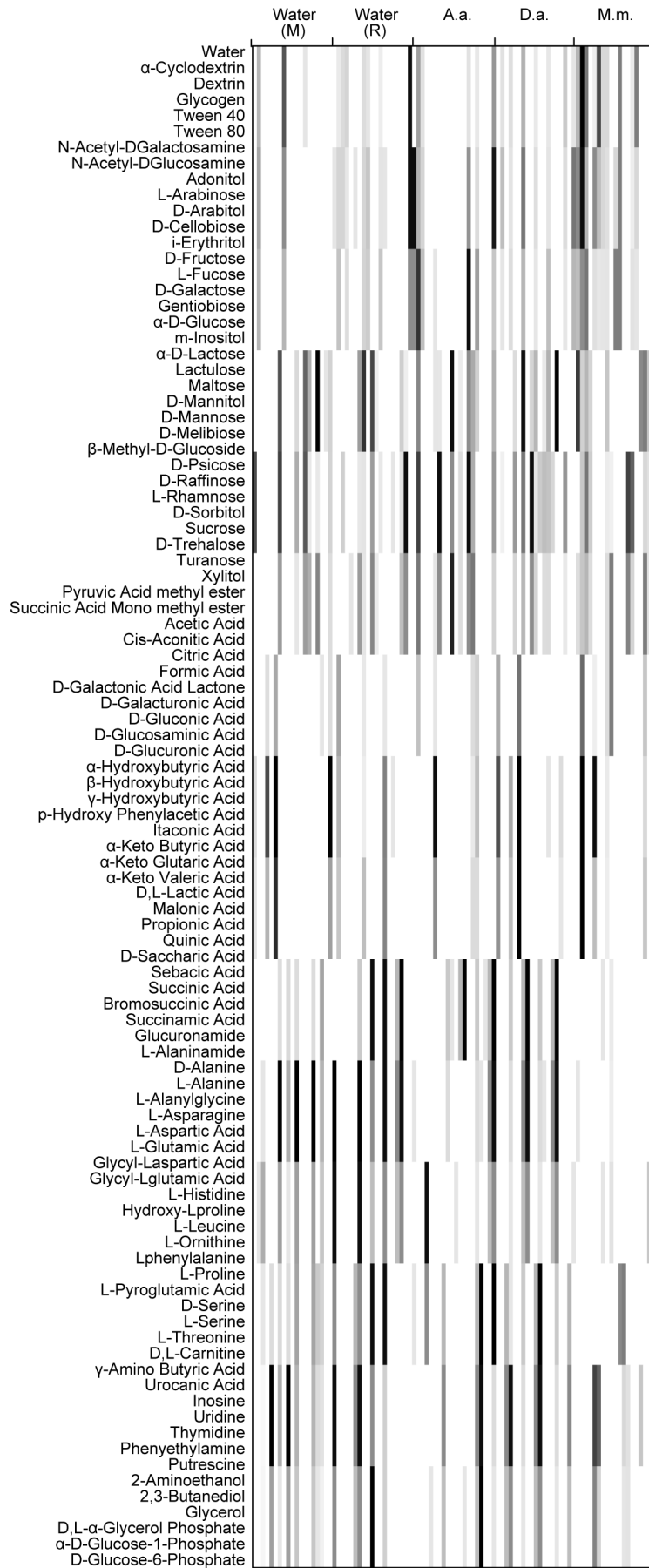


Fig. S4. Substrate utilization profiles (Biolog GN) of triplicate water samples of both study sites and the symbiotic bacteria isolated from triplicate sponge samples. M = mangrove site, R = reef site, A.a. = *Aplysina archeri*, D.a. = *Desmapsamma anchorata*, M.m. = *Mycala microsigmatica*. Grey-scale = relative activity