

## Standing genetic variation of coral populations under changing environments

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How genetic diversities affect ecosystem functions is one of key questions to understand the maintenance of genetic diversities and their roles in ecosystem. To evaluate the functional genetic diversities of corals which are main composers of coral reefs, I genotyped 20 colonies (collected in front of Sesoko Station) of *Acropora digitifera* which is one of dominant coral species around the Ryukyu Archipelago where is the northern peripheral area of coral reefs, and performed common garden experiment using five clonal fragments from each colony (to reduce accidental response in each genotype) to estimate variations of growth and photosynthetic efficiencies among colonies, namely, genotypes. Genotyping was performed with microsatellite markers for coral host and ITS2 direct sequencing for symbiotic algae, indicating that all host colonies were genetically distinct and belonging to major populations around the Ryukyu Archipelago and mainly maintaining clade C symbionts which are dominant around this region. In common garden experiment, all colonies showed different growth patterns whilst the photosynthetic efficiencies showed similar optimal peaks among colonies. The experimental approach above suggests that there are standing genetic variations in host itself of *A. digitifera*, which might guarantee the adaptive potential of coral population for future global warming in northern peripheral reef area. These genetic variations might also contribute to the change of material cycles in future coral reefs.