Identifying the genetic basis of local adaptation in natural populations of Pocillopora spp

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Résumé

Coral reefs face severe vulnerabilities to environmental fluctuations and are poised to endure adverse consequences amid escalating climate change impacts. However, current research remains confined to localized contexts, failing to provide a comprehensive understanding of how various coral species and reef ecosystems respond to these global stressors across macrogeographic scales. This knowledge gap inhibits a nuanced grasp of the broader ecological and evolutionary dynamics at play. During the TARA Pacific expedition from 2016 to 2018, we conducted an extensive study involving the collection of _˜300 samples of *Pocillopora* spp. from 32 Pacific islands. Employing a multibiomarker methodology, our research delved into diverse phenotypic expressions, including metrics such as animal and symbiotic dinoflagellate biomass, metabolic indicators, and redox status. Furthermore, we amassed comprehensive genome-wide and environmental data, facilitating the identification of genes and genetic regions pivotal to the adaptive response of these organisms to environmental fluctuations throughout the distribution area, as elucidated through Genetic Environment Association (GEA) and Genome-Wide Association Study (GWAS) analyses. Our investigation unveiled genotypes associated to fluctuations in sea surface temperature and unusual environmental conditions or to physiological conditions associated to these fluctuations. By exploring the allelic diversity associated with each coral phenotype and its responsiveness to environmental cues, we pave the way for tailored conservation strategies aimed at safeguarding this species within the Pacific Ocean.

Mots-Clés: Corals, phenotype, genotype, environment, GWAS, GEA

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