

Introducing a novel 28S rRNA marker for improved assessment of coral reef biodiversity

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Abstract

Biodiversity monitoring based on DNA metabarcoding depends on primer performance. Here, we develop a new metabarcoding primer pair that targets a ~ 318 bp fragment of the 28S rRNA gene. We validate the primer pair in assessing sponges, a notoriously challenging group for coral reef metabarcoding studies, by using mock and natural complex reef communities to examine its performance in species detection, amplification efficiency, and quantitative potential. Mock community experiments revealed a high number of sponge species ($n = 94$) spanning a broad taxonomic scope (15 orders), limited taxon-specific primer biases (only a single species exceeded a two-fold deviation from the expected number of reads), and its suitability for quantitative metabarcoding – there was a significant relationship between read abundance and visual percent coverage of sponge taxa ($R = 0.76$). In the natural complex coral reef community experiments, commonly used COI metabarcoding primers detected only 30.9% of sponge species, while the new 28S primer increased detection to 79.4%. These new 28S primers detect a broader taxonomic array of species across phyla and classes within the complex cryptobiome of coral reef communities than the Leray-Geller COI primers. As biodiversity assessments using metabarcoding tools are increasingly being leveraged for environmental monitoring and guide policymaking, these new 28S rRNA primers can improve biodiversity assessments for complex ecological coral reef communities.

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