

ABSTRACT

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Extreme upwelling in Alor Kecil waters causes a drastic temperature decrease that triggers environmental stress and the emergence of various fish species in an unconscious condition on the surface. This study aims to identify fish species found during the upwelling phenomenon using DNA barcoding technique with 12S rRNA marker, analyze the phylogenetic relationships of fish species, and examine the relationship between the upwelling phenomenon and the fish species findings. A total of 31 fish samples were collected during the upwelling event. Identification was conducted through morphological and molecular analysis, including DNA extraction, PCR, sequencing, BLAST analysis, and phylogenetic tree reconstruction using Neighbor-Joining method with MEGA X. The research results identified 19 genera from 31 samples, with 25 samples identified to 19 species dominated by reef fish and one sample that experienced sampling errors. The phylogenetic tree shows the closest kinship relationship between the genera *Taeniamia* and *Ostorhinchus*, and the farthest genetic distance between *Gymnothorax* and *Zanclus* genera. Analysis revealed that upwelling not only causes temperature shock in reef fish, but also brings deep-sea species to the surface. The research proves that DNA barcoding technique with 12S rRNA gene marker is effective for revealing the diversity and phylogenetic relationships of fish species affected by extreme upwelling phenomenon in Alor Kecil waters.

Keywords: *Alor Kecil, DNA barcoding, 12S rRNA gene, upwelling*