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Molecular Identification of Black Band Disease on *Pachyseris* sp in Spermonde Archipelago

Rahmi[12*], Jamaluddin Jompa[3], Akbar Tahir[3] & Alexander Rantetondok[3]

[1]Doctoral Program of Agricultural Science University of Hasanuddin MakassarJl. Perintis Kemerdekaan KM.10 Makassar 92045, Indonesia
[2]Faculty of Agriculture University of Muhammadyah Makassar Jl. Sultan Alauddin No. 259 Makassar 90221, Indonesia
[3]Faculty of Marine Science and Fishery, University of Hasanuddin Jl. Perintis Kemerdekaan KM.10 Makassar 92045, Indonesia

Abstract : This study aimed to identify species of isolated bacterial with the nitrogen base sequence analysis method on nucleotide constituents 16S rDNA genes of bacterial disease-causing Black band disease. Identification was done by isolatied the bacteria, based on the appearance of the morphology of the colony, five isolates bacterias isolated from healthy coral tissue infected with BBD (C, j, L and F) and four isolates bacterias found in the coral tissue associated with BBD (N, X, Z and H). The bacterial DNA was extracted and amplified on fragments of its 16S rDNA genes using Polymerase Chain Reaction instrument. Fragments of sequences of nucleotides on the nitrogen bases constituent fragments of the gene was amplifiedand analyzed and to be known as its homology with nitrogen bases gene fragment sequences 16S rDNA while other origin bacteria have been originated in BankGen by using a BLAST-N program. Local alignment analysis of Samples C, j, L and F of the Gen bank data base, overall sample C had a similarity with the *Halomonas* sp, the j sample has a similarity with *Pseudoalteromonas sp*, sample L has the highest similarity with *Thiobacillus denitrifican*, samples of F has similarities to score 100% identity with *Psychromonas ingrahamii*. The coral network associated with BBD i.e. N, X, Z and h. The results of the analysis of the local alignment (local alignment) (BLASTn) shows that the sample N can be identified as *Shewanella sp*, samples of X has a similarity with *Bacillus farraqinis*, samples of Z has a similarity with *flavobacterium* and sample H has a similarity with highest *Desulfovibrio salexigen.*

Keywords : Black Band Disease, Bacteria, 16 S rDNA, *Pachyseris* sp.

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