

Studi keanekaragaman genetik bakteri dari usus ikan nila (*Oreochromis niloticus*) melalui teknik metagenom sequence-based

Adhitya Bayu Perdana, author

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Abstrak

Penelitian untuk mengetahui keanekaragaman genetik bakteri dari usus ikan nila melalui teknik metagenom sequence-based telah dilakukan. Hasil amplifikasi gen 16S rRNA dari usus sebesar 1550 pb, kemudian dilakukan sequencing pada isolat dari Kolam Laboratorium PTPP, Serpong (L1, L2); Tambak Ikan Nila Salin, Karawang (Mu, Pu); dan KJA Waduk Cirata, Purwakarta (A1, C1). Identifikasi ke-6 isolat bakteri berdasarkan BLAST menunjukkan bahwa terdapat similaritas terhadap 4 spesies bakteri dengan nilai max identity tertinggi.

Hasil analisis pohon filogenetik menggunakan metode neighbor-joining memperlihatkan bahwa isolat L1, L2 dan C1 diduga berkerabat dekat dengan bakteri *Ochrobactrum anthropi*, isolat A1 diduga berkerabat dekat dengan *Lysinibacillus boronitolerans*, isolat Pu diduga berkerabat dekat dengan *Stenotrophomonas maltophilia*, sementara isolat Mu diduga berkerabat dekat dengan *Cetobacterium somerae*. Berdasarkan hasil yang didapat, maka terbukti bahwa terdapat keanekaragaman gen 16S rRNA dari usus ikan nila yang dianalisis melalui teknik metagenom sequence-based.

.....Research to know the genetic diversity of intestinal bacterias in *Tilapia* gut had been done using sequence-based metagenome. 16S rRNA gene amplification produced PCR fragment with 1550 bp length, then followed by sequencing of isolates from Outdoor Laboratory, Serpong (L1, L2); Saline *Tilapia* Ponds, Karawang (Mu, Pu); and Cirata Reservoir, Purwakarta (A1, C1). Identification six bacteria isolates based on BLAST showed that there are 4 different species of bacteria with the highest value of max identity.

Phylogenetic analysis using neighbor-joining method showed that L1, L2, and C1 isolates is close relatives to *Ochrobactrum anthropi*, while A1 isolates is close relative to *Lysinibacillus boronitolerans*, Pu isolate is having close relationship with *Stenotrophomonas maltophilia*, and Mu isolates with *Cetobacterium somerae*. Thus, based on the results, it is proven that there is 16S rRNA gene diversity from *tilapia* intestines using metagenome sequence-based method.