

**MOLECULAR CHARACTERIZATION OF ANTI-
FUNGAL PRODUCING BACTERIA FROM BAMBOO
ROOT**

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ABSTRACT

MOLECULAR CHARACTERIZATION OF ANTI-FUNGAL PRODUCING BACTERIA ISOLATED FROM BAMBOO ROOT

A major challenge currently faced by agriculture is the fungal disease. A 16s rRNA is useful in order to identify the molecular characterization of its gene sequences and to study the phylogenetic tree and taxonomy. This project aimed to identify the sequence of strain A1 that was previously isolated from bamboo root by using the PCR amplification technique and to analyse the molecular characteristics based on the homology sequence, multiple alignment sequence and also to construct the phylogenetic tree by using the sequence analysis. The identification of previously isolated bamboo root strain A1 was streaked on nutrient agar to observe the morphological characteristics and was grown in nutrient broth for further storage. The quality and purify of DNA was observed under 1% (w/v) agarose gel. By using 16srRNA primers, strain A1 was successfully amplified by PCR and sequenced. Based on homology sequence analysis, strain A1 was proposed to be *Aeromonas* sp. Multiple sequence alignment showed strain A1 was highly conserved with *Aeromonas* sp. The phylogenetic tree analysis also showed that strain A1 was located in ancestot with the *A.caviae*, and clearly different from outgroup *Vibrio* sp. In conclusion, using the technique of 16s rRNA PCR amplication, it is a successful way to identify a bacteria developing an anti-fungal. The DNA sequencing of the 16S rRNA gene was used as an effective tool to study and detect bacterial phylogeny and taxonomy relationships between bacteria.