



## The Identification of Laor Worms (Polychaeta) in Marine Areas of Ambon Island, Mollucas Province, Indonesia Based on 16s rRNA Gene Sequence

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**Abstract :** The identification of Laor worms (Polychaeta) found in marine areas of Ambon Island has been done up till now based on phenotypic characters. The research goal is to find out the species of those worms and to determine their kinship relationship based on 16S rRNA gene sequences. The data were analyzed using sequencing scanner software (ABI) and multiple alignment was performed using *CLUSTAL W*, the phylogeny tree reconstruction based on nucleotide sequence was conducted using 5.03 MEGA program. The results of the research show that those Laor worm phenotype differs in body shape, color, and size. The results of the phylogenetic analysis based on the 16S rRNA gene sequences and the results of genetic distance and similarity analysis related show that the worm samples classified into 5 groups, namely group A (samples A2, A4, H1, H2, L3, and L4) identified as *Palola viridis*; group B (samples A5, L1, L2, L6, and L9) identified as *Eunice fucata*; group C (samples A7, H4, H5, L5, and L10) identified as *Eunice*; group D (sample A3) identified as *Lumbrineris magnidentata*; group E (samples H3, A1, A6, L7, and L8) identified as Nereidae. The value of NJ and ML *bootstrap* was 28-100% and 22-100% respectively. The genetic distance range between 0.03851 and 0.22936 with the highest and lowest similarity 96.14897% and 77.06362% respectively. The analysis results based on the 16S rRNA gene sequences of those worms were able to complement the identification phenotypically based on the number of antennas.

**Keywords:** Ambon Island; Laor Worm; Mollucas; Polychaeta; 16S rRNA gene.