



Identification of Genetic Diversity in *Bactrocera* spp. from Minahasa Regency Based on COI Barcode

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Abstract : Fruit flies are one of the most important insect pests in agricultural crops, especially in horticultural crops because they cause significant damage and losses to agricultural cultivation systems. To date, about 1400 species of fruit flies have been identified. The speed and accuracy of identification and characterization of fruit fly types is one of the keys to the success of controlling fruit flies in agricultural crops. DNA Barcode technology is one of the most widely used genetic diversification techniques currently available because it provides accurate analysis results and can distinguish organisms to the species level. This study aims to analyze the genetic diversity of mitochondrial COI genes in several types of *Bactrocera* associated with fruit and vegetable crops in Minahasa Regency and *Drosophila* sp. as an outgroups. The results showed that in the five species of *Bactrocera* there were an average difference of 75 nitrogen bases. The smallest amount of nitrogenous bases, as many as five nitrogen bases, were found in *B. albistrigata* and *B. fraunfeldi*, whereas the largest difference of 104 nitrogen bases were found in *B.umbrosa* and *B. tau*. Genetic diversity analysis revealed 12.4% genetic differences among *Bactrocera* spp insects, the smallest manifestation (0.8%) between *B. albistrigata* and *B. fraunfeldi* and the greatest diversity between *B.umbrosa* and *B. tau* (15.8%).

Keywords : Bactrocera spp, COI DNA Barcode, PCR

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