



Molecular identification of hard ticks (Ixodes sp.) infesting rodents in Selangor, Malaysia

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ABSTRACT TOOLS

SHARE METRICS

ABSTRACT

This study aims to identify hard ticks (Ixodes sp.) infesting rodents in three different sites in Selangor, Malaysia using a molecular approach. A total of 11 individual ticks infesting four different host species (Rattus tiomanicus, Rattus ratus, Maxomys surifer and Sundamys muelleri) were examined based on its morphological features, followed by molecular identification using mitochondrial 16S rDNA gene. Confirmation of the species identity was accomplished by using BLAST program. Clustering analysis based on 16S rDNA sequences was carried out by constructing Neighbour-joining (NJ) and Maximum parsimony (MP) tree using MEGA 7 to clarify the genetic identity of Ixodes sp. Based on morphological features, all individual ticks were only able to be identified up to genus level as most of the samples were fully engorged, damaged and lacked morphological characters. However, molecular analysis of samples revealed 99% similarity with Ixodes granulatus from the GenBank database. Thus, the result of this study showed that all these ticks (Ixodes granulatus) were genetically affiliated to a monophyletic group with highly homogenous sequences.

