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PHYLOGENETIC COMPARISON OF SOME NEMATODE PARASITES OF *PERIPLANETA AMERICANA* BASED ON ELECTROPHEROGRAM AND SECONDARY RNA STRUCTURE

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ABSTRACT : Single stranded RNA molecules quickly fold due to hydrogen bonding mechanism if they are left in their environment. Helices which are made from the folding process known as stem. Only six (AU, GU, GC, UA, UG & CG) are stable to form base pairs among 16 possible ones. The nucleotide sequence of stems can vary and made variable RNA helical regions. The substitution of RNA bases are important in maintaining the secondary structure of RNA. DNA structure is not important to study the evolutionary models because that is double stranded due to which the base pairs in DNA does not give accurate results. So, secondary structure of RNA gives validate consequences in evolution of parasitic nematodes of *Periplaneta americana*.

Key words : Electropherogram, nematode, phylogenetic, secondary RNA structure.

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INTRODUCTION

Secondary structure models are taken for 18S rRNA of *Hammerschmidtiella indicus* and *Thelastoma icemi* 18S and 28S rRNA of *Leidynema appendiculata* and *Thelastoma icemi* 28S. Secondary structure of ribosomal RNA models support that it has been significantly conserved throughout evolution (Zwieb *et al*, 1981). In all living beings 18S gene is a part of ribosomal functional core and exposed to similar selective forces (Meyer *et al*, 2010). Bands of 18S and 28S are not clear in electrophoresis gel. The 28S and 18S ratio is 2:1 but actual ratio is 2.7:1. The secondary RNA structure is very useful in calculating the phylogenic inferences (Jow *et al*, 2002; Hudelot *et al,* 2003; Anonymous, 2003; Anonymous, 2020; Anonymous, 2020a). 28S rDNA sequences showed great resolution for *Schwenkiella icemi* (Pal and Singh, 2016). The sequences were aligned with the 28S rDNA genes and revealed clear differences in nucleotide sequences among different species. The sequences were aligning with the 18S rDNA genes revealed clear differences in nucleotide sequences among different species in comparison. rDNA is useful markers for distinguishing sister species and is helpful in discriminating species where there is species overlap and co-infection of the same definitive host especially when morphological differences are often difficult to determine (Pal and Singh, 2016; Pal and Neetu, 2017; Pal and Neetu, 2018). An electropherogram is a plot of DNA fragment sizes, typically used for genotyping such as DNA sequencing (Schwartz and Guttman, 1995). Such plots are often achieved using an instrument such as an automated DNA sequences. Such electropherograms may be used to determine DNA sequence genotypes, or genotypes that are based on the length of specific DNA fragments (*Karabiber*, 2013; Schwartz and Guttman, 1995). Evolution of rDNA is relatively independent of changes in its morphology and analyses of these have been shown to provide good phylogenetic resolution for molecular taxonomy (Pal and Singh, 2016; Pal and Neetu, 2017; Pal and Neetu, 2018; Nadler, 1992; Heise *et al*, 1995; Petrov *et al*, 2007). Several recent studies of eukaryotes used rDNA sequences make strong inferences in phylogenetic analyses of ancestor descendant