18S Ribosomal RNA patterns in Hemiptera with emphasis on Fulgoromorpha

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In molecular phylogenies, 18S rRNA is a privileged gene product. It is known to be homologous across all metazoan taxa and it is characterized by strong primary sequence and structural conservation which allow fruitful comparisons between distantly related taxa. This gene product has especially proven useful where attempts at using morphological characters in the past proved to be difficult or impracticable. However, importance of the secondary structure of 18S rRNA for accurate alignment of nucleotides has been stressed by several authors (reviewed in Kjer, 1995) and particularly in phylogenetic reconstruction of Hemiptera (Simon, & al., 1994; Bourgoin & al, 1999).

Using the 18S rRNA secondary structural model of Van de Peer & al. (1998) we have aligned about 2700 nucleotides of some 100 different Hemipteran taxa. Particular 'molecular signatures' forming short or longer paired base patterns (from few to several hundreds of nucleotides) for several major groups of taxa were identified. These autapomorphies are generally not detected by alignment programs. This underlines the problem of an automatic recognition of the primary homology between nucleotides (alignment of primary structures) in regions of non homologous RNA. How to take these 18S rRNA pattern data into account as characters for inferring a phylogeny, and preliminary results in inferring a phylogeny of Hemiptera and more particularly Fulgoromorpha, will be discussed and compared to other recent molecular based phylogenies (Sorensen et al., 1995; Campbell et al., 1995; Bourgoin et al., 1997, 1999, Ouvrard, 2000).


