## 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 moleculary based phylogenies (Sorensen et al., 1995; Campbell et al., 1995; Bourgoin et al., 1997, 1999, Ouvrard, 2000).

- Bourgoin Th., Chan K. L., Ouvrard D. & B. C. Campbell. 1999. Character analysis using ribosomal RNA secondary structure and its application to Hemiptera and Fulgoromorpha phylogeny. 10<sup>th</sup> Int. Auchenorrhyncha Congress, 6-10 sept. 1999. Abstract, Cardiff, Wales, UK.
- Bourgoin Th., Steffen-Campbell J. D. & B. C. Campbell. 1997. Molecular phylogeny of Fulgoromorpha (Insecta, Hemiptera, Archaeorrhyncha). The enigmatic Tettigometridae: evolutionary affiliations and historical biogeography. *Cladistics*, 13: 207-224.
- Campbell B. C., Steffen-Campbell, J. D., Sorensen, J. T. & R. Gill. 1995. Paraphyly of Homoptera and Auchenorrhyncha inferred from 18S rDNA nucleotide sequences. *Syst. Entomol.*, 20: 175-194.

Kjer K. M. 1995. Use of rRNA secondary structure in phylogenetic studies to identify homologous positions: an example of alignment and data presentation from the frogs. *Mol. Phyl. Evol.*, 4(3): 314-330.

Ouvrard D., Campbell B. C., Bourgoin Th. & K. L. Chan. 2000. 18S rRNA Secondary Structure and Phylogenetic Position of Peloridiidae (Insecta, Hemiptera). *Mol. Phyl. Evol.*, 16(3), 403-417.

Simon Ch., Frati F., Beckenbach A., Crespi B., Liu H. & P. Flook. 1994. Evolution, weighting and phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. Ann. Entomol. Soc. America, 87(6): 651-701.

Sorensen J. T., Campbell B. C., Gill R.J. & J. D. Steffen-Campbell. 1995. Non-monophyly of Auchenorrhyncha ("Homoptera"), based upon 18S rDNA phylogeny: eco-evolutionary and cladistic implications within pre-Heteropterodea Hemiptera (s.l.) and a proposal for new monophyletic suborders. *Pan-Pac. Entomol.*, 71(1): 31-60.

Van de Peer Y., Caers A., De Rijk P. & R. de Wachter. 1998. Database on the structure of small ribosomal subunit RNA. Nucleic Acids Research, 26(1): 179-182.