Primary and Secondary Structures of Internal Transcribed Spacer 2 Region of a Strepsipteran Insect, *Stylops mellitae*

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Strepsipterans are a comparatively small group of insects with a very specialized life history and peculiar morphology. Their larvae are free living in the first instar and develop thereafter into apodous endoparasites of other insects. There have been much argument on the phylogenetic position of the order Strepsiptera because of these unique features. Its small subunit ribosomal RNA (SSU rRNA) is over 3000 bp in length, which is dramatically expanded compared to those of other organisms (usually 1800bp-1900bp). According to the recent publication, large subunit ribosomal RNA (LSU rRNA) showed also dramatic expanded pattern. Here, for the first time, we report primary and secondary structures of internal transcribed spacer 2 (ITS2) region from a strepsipteran insect, *Stylops mellitae*. The total length is ca. 877bp, which is not only the longest ITS2 among invertebrates but also longer than those of any other organisms except that of human.. It has highly biased AT composition. Its secondary structure construction showed that all the expanded sequences form quite stable helices. This result will be helpful for elucidating evolution mechanism of rDNA spacer region and phylogenetic relationship of the related taxa.