DNA BARCODE IN CHIRONOMID CLASSIFICATION

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DNA barcode was recently used to classify Chironomids (Ekrem, Willassen & Stur, 2007), but at present results are below expectation. The most striking problem is that often species belonging to different genera or tribes are clustered together. Different DNA regions were used (COX1, COX2, CYTB, 18S, 28S RNA etc.), but different species were tested with different regions so the results often cannot be compared; 1811 Chironomids accession numbers are at present available in GenBank. Samples analysed with the same gene were selected and analysed using Matlab R2009a Bioinformatics toolbox. In the present example 97 partial cox1 sequences (Ekrem, Willassen & Stur, op. cit.) are discussed. The sequences belong to six genera belonging to the tribe of Tanytarsini (*Micropsectra, Parapsectra, Tanytarsus, Cladotanytarsus, Paratanytarsus* and *Rheotanytarsus*). Samples belonging to the same species cluster together as do species belonging to the same species groups as but there are many misclassifications with species belonging to different genera clustering together (*M. pallidula* for example clusters with *Tanytarsus* species) and the three *Micropsectra* species groups (*attenuata, notescens* and *atrofasciata*) are not reproduced. Even worse results were obtained using 28S and 18S RNA probes. The present data analysis suggests that DNA barcode is at present unable to give a reconstruction of phylogenetic relationships within the family Chironomidae. Chironomids have the advantage to be holometabolous insects, with 4 semaphoronts (adults males and females, pupae and larvae) available, each with a well defined morphology rich in characters useful for diagnostic. This allows a good classification well supported by many characters; DNA barcode at present can only aid in separating populations belonging to the same species or sister species not separated by morphological characters, in this sense DNA barcode goes in the same direction of salivary gland polythene chromosomes which are still used to separate *Chironomus* species.