A new non-destructive process for the *Brachycera* identification via DNA Barcoding

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In a subproject (FKZ: 22019814) of the BMEL/FNR project “prospective risk management of biotic pests in forests to maintain sustainable forestry” the impact of helicopter-applied insecticides for flies (*Brachycera*) was examined. Several flies are known pine insect pest antagonists and therefore relevant non-target organisms. The maggots and adults of several families have parasitoid (e.g. Tachinidae) or predatory (e.g. Asilidae) modes of life.

Morphological identification of families and species is supplemented by DNA Barcoding, because of the high number of individuals and the limited taxonomical expertise. To accomplish maximum yield DNA templates, destructive DNA extraction is regularly performed and the cytochrome c oxidase subunit is amplified and sequenced. To preserve the morphology of individuals the performance of non- or semi-destructive DNA extraction is a requirement to enable a later morphological identification. The stability of the wing membrane can be challenging and pre-trials showed that the loss of pigments and dorsal thorax bristles take place with established non-destructive methods related to commercial kits.

We modified an established non-destructive DNA extraction from mycology avoiding usage of proteinase. With this method DNA can be isolated from flies of laboratory insect rearing, commercial insects rearing and parasitoids hatched from subfamily Enonominae (Lepidoptera, Geometridae) and subfamily Diprioninae (Hymenoptera, Diprionidae) cocoons without impairing morphological traits. The non-destructive DNA extraction shall prospectively be considered for field ecological examinations. The potential application spans from biodiversity research to analysis of insect pest antagonistic complexes to studies about insecticide impacts on *Brachycera*.