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MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF ERIOPHYID MITES *Aculodes* sp. ON *Taeniatherum caput-medusae* AND *Bromus tectorum* (Poaceae)

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All mites in the family Eriophyidae are obligate herbivores. Many of them are crop pests, some of which can transmit viruses, while others are associated with weeds and have high potential as classical biological control agents. Several eriophyid species have been released as biological control agents but to date, none of them had impact in control of grass targets. So far, about 30 species have been described in the genus *Aculodes*, out of which most were recorded from grasses (Poaceae). *Aculodes altamurgiensis* was described by de Lillo & Vidović (2018) from samples of *Taeniatherum caput-medusae* collected in Italy. Thereafter, cryptic populations of mites from *Bromus tectorum* were found. The purpose of this study was to clarify the taxonomic status of mites within the genus *Aculodes* from different host plants.

Plant samples of *T. caput-medusae* were collected from Italy and those of *B. tectorum* were collected from Serbia and Bulgaria. For the morphometric study, 23 morphological traits were measured on 25-27 females of mites from each sample. The multivariate analysis of variance (MANOVA) and Canonical variate analysis (CVA) were conducted to examine morphological differences between them.

Pooled samples of 15-20 whole mites were processed as one sample for DNA extraction, using the Dneasy Blood and Tissue Kit (Qiagen, Hilden, Germany). The barcoding region of the mitochondrial cytochrome oxidase subunit I gene was amplified by polymerase chain reaction (PCR) using a pair of primers LCO1490/HCO2198. Uncorrected pairwise genetic distances were employed to calculate the average genetic distance between species with different host affiliations.

The results of our morphometric analyses showed general inter-population differences although *A. altamurgiensis* from *T. caput-medusae* diverged the most from *Aculodes* sp. hosted by *B. tectorum*. Pairwise comparison of the COI distances indicated approximate to 18% of genetic divergence between analyzed populations. These data provide evidence to support the hypothesis that mites associated with *T. caput-medusae* and *B. tectorum* are two distinct species.