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Poster/Постер

MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF *Metaculus* ERIOPHYID MITES FROM *Rapistrum rugosum* AND *Isatis tinctoria* (Brassicaceae)

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In the past few decades, increasing interest in the use of eriophyid mites as biological control agents has been expressed, especially due to their high host specificity, high intrinsic rate of reproduction and damage frequently caused to reproductive plant parts. To date, three *Metaculus* species were registered as potential biological control agents and the necessity of more comprehensive understanding of taxonomic status of *Metaculus rapistri* has been emphasized (Vidović et al., 2015). Namely, *M. rapistri* was initially described by Carmona (1969) from samples of *R. rugosum* collected in Portugal. Thereafter, a supplementary morphological description of this species was provided by Monfreda and De Lillo (2012) from samples of *Isatis tinctoria* collected in Turkey. The goal of this study was to clarify the taxonomic status of mite species within the genus *Metaculus* that inhabit *R. rugosum* and *I. tinctoria*.

Plant samples of *R. rugosum* were from Portugal, while *I. tinctoria* were collected from Turkey and Germany. For the morphometric study, 28–30 females from each sample were examined in the dorso-ventral position. Twenty-two morphological traits of each individual were measured. The multivariate analysis of variance (MANOVA) and Canonical variate analysis (CVA) were used to examine morphological differences among groups.

DNA was extracted from 30 to 40 whole specimens using QIAGEN DNeasy Blood & Tissue Kit. Mitochondrial COI sequences were amplified using primers LCO1490/HCO2198. Uncorrected pairwise genetic distances were used to calculate the average genetic divergence between species with different host affiliations.

As evident from the CVA plot, the CV1 axis (accounting for 79.2% of variance) separated *M. rapistri* hosted by *R. rugosum* from *Metaculus* spp. hosted by *I. tinctoria*, while CV2 axis (accounting for 20.8% of variance) discriminated *Metaculus* sp. from *I. tinctoria* collected in Germany from *Metaculus* sp. from *I. tinctoria* collected in Turkey. The barcoding region of mtCOI gene indicated a genetic divergence between the analyzed populations of *M. rapistri* from *R. rugosum* and *M. rapistri* from *I. tinctoria* (7.7–11%). The genetic divergence was registered also between populations of mites from *I. tinctoria* from Turkey and the same plant species from Germany (12.3%). The results of our study showed that *M. rapistri* from *R. rugosum* is a distinct species and that could be two different taxa hosted by *I. tinctoria*.