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Spider mites (Acari: Tetranychidae) are among the most dominant and destructive plant-feeding mites worldwide. Despite their economic impact in agriculture, data on biodiversity are scarce in some regions of Europe, as for example in Serbia as well as in the Balkans. According to the Spider Mites Web database (<http://www1.montpellier.inra.fr/CBGP/spmweb/>), fifteen known species from six genera were until now reported from Serbia. This is a relatively small number of spider mites considering the whole country area, and the geographic and the floral diversity. To improve our knowledge on mite diversity of this region we conducted a survey on 97 different localities in Serbia during three growing seasons (2013-2015). Samples were collected in different habitats: forests, agricultural areas and urban landscapes, as well as in protected natural areas like national parks, nature parks, special and protected areas. We collected samples from 82 different host plants and among these 47 were wild and weed plants and 35 were cultivated plants or plants that are economically important agricultural crops. Species identification was done by using morphological criteria. A total of nine new spider mites species for Serbia were uncovered. These are *Eotetranychus rubiphilus*, *Eotetranychus pruni*, *Eotetranychus fraxini*, *Eotetranychus carpini*, *Eotetranychus aceris*, *Panonychus citri*, *Tetranychus evansi*, *Schizotetranychus garmani* and *Bryobia praetiosa*. While some information does exist of other four genera and six species in Serbia, but without precise information and published data available. These are *Oligonychus* sp., *Tetranychopsis* sp. (*T. horridus*), *Neotetranychus* sp. (*N. rubi*), and *Eurytetranychus* sp. (*E. buxi*), and also *Eotetranychus tillarium* and *Eotetranychus coryli*. The work here presented is the first faunistic study in Serbia conducted on spider mites sampled over the whole country. It represents a valuable first step to better know the biodiversity and distribution of Tetranychidae mites in the Balkans.

First molecular phylogeny of the tribe Typhlodromini (Phytoseiidae) inciting a taxonomic reassessment

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One of the main goals of taxonomic classification is to improve predictive power on different aspects of a particular taxon based on known traits of closely related taxa; therefore it is especially useful if based on the evolutionary relationship among organisms. Predatory mites of the family Phytoseiidae consist in the main group of biological control agents on plants; three subfamilies are recognized in this family. In the Typhlodrominae subfamily, the Typhlodromini Wainstein tribe includes three genera: *Typhlodromus* Scheuten, *Neoseiulella* Muma and *Typhloseiulus* Chant & McMurtry. The most numerous genus *Typhlodromus* (454 spp.) is currently divided in two subgenus T. (*Typhlodromus*) Scheuten and T. (*Anthoseius*) De Leon. Phylogenetic relationships in the tribe Typhlodromini are herein firstly investigated based on four DNA molecular markers which have been defined as informative for supra-generic, generic and specific taxonomic levels in the Phytoseiidae, being three mitochondrial: COI mtDNA (790 bp), CytB mtDNA (428 bp), 12S rRNA (457 bp); and one nuclear ITSS (699 bp). Sequences of specimens from 58 populations from Spain (6 peninsular provinces, Canary Islands and Ibiza), France (Corsica and Reunion Island), Portugal (Azores), Russia, Iran, and USA belonging to at least 25 species in the three Typhlodromini genera and two outgroups tribes (Paraseiulini and Metaseiulini) were obtained. Sequences available in public database (GenBank) were recovered and included in the datasets. Data were analysed using Parsimony and Bayesian approaches, markers were analysed separately as well as combined. *Neoseiulella* genus and T. (*Anthoseius*) subgenera showed to be paraphyletic. Occurrence of cryptic species was observed among populations preliminarily identified as T. (*Anthoseius*) *rhenanoides* Athias-Henriot and *Neoseiulella litoralis* (Swirski & Amitai). Phylogenetic value of morphological traits is discussed.