

Supporting data

DNA barcoding and phylogeny of Acari species based on ITS and COI markers

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List of Supporting Information:

Table S1. List of all sequences used in this work.

Table S2. List of primers used to generate the 3' COI fragment, ITS1, ITS2 or whole ITS from either Phytoseiidae or Tetranychidae used in this work.

Table S3. New Acari mitochondrial COI sequences obtained in this work.

Table S4. New ITS sequences obtained in this work.

Table S5. Estimates of evolutionary divergence distance between Acari COI sequences.

This excel file contains several sheets, first one with interspecific distances \pm SE, and the others with intraspecific distances \pm SE (one sheet per species).

Table S6. Estimates of evolutionary divergence distance between Acari ITS sequences.

This excel file contains several sheets, first one with interspecific distances \pm SE, and the others with intraspecific distances \pm SE (one sheet per species).

Figure S1. Evolutionary relationships of Acari taxa based on 43 Acari Cytochrome C oxidase I (COI) fragment sequences inferred by BEAST (Bayesian analysis), including three different sequences from *Euseius nicholsi*.

Figure S2. Evolutionary relationships of Acari taxa based on 61 Acari Cytochrome C

29 oxidase I (COI) fragment sequences inferred by MEGA X (Kumar *et al.*, 2018), using the
30 Maximum Likelihood (ML) method.
31 **Figure S3.** Evolutionary relationships of Acari taxa based on 157 Acari Internal
32 Transcribed Spacer (ITS) fragment sequences inferred by MEGA X (Kumar *et al.*, 2018),
33 using the Maximum Likelihood (ML) method.