



Phylogenomic resolution of the eriophyoid position among Acari and symbiotic bacteria of the gall-inducing mite *Fragariocoptes setiger* (Eriophyoidea)*

PAVEL B. KLIMOV^{1,2*}, PHILIPP E. CHETVERIKOV³, SAMUEL J. BOLTON⁴ & ANDREY V. TOLSTIKOV²

¹Department of Biological Sciences, Purdue University, 915 W State St., #G-225, West Lafayette, Indiana, 47907 USA

✉ pklimov@purdue.edu; <https://orcid.org/0000-0002-9966-969X>

²X-BIO Institute, Tyumen State University, Tyumen, 625003, Russia ✉ atolus@yahoo.com; <https://orcid.org/0000-0002-8537-038X>

³Saint-Petersburg State University, 199034, St. Petersburg, Russia ✉ f.chetverikov@spbu.ru; <https://orcid.org/0000-0003-1300-1486>

⁴Florida Department of Agriculture and Consumer Services, Gainesville, Florida, USA

✉ samuel.bolton77@googlemail.com; <https://orcid.org/0000-0002-5807-8519>

*In: Zhang, Z.-Q., Fan, Q.-H., Heath, A.C.G. & Minor, M.A. (Eds) (2022) *Acarological Frontiers: Proceedings of the XVI International Congress of Acarology (1–5 Dec. 2022, Auckland, New Zealand)*. Magnolia Press, Auckland, 328 pp.

Eriophyoid mites are ancient and widely distributed microscopic plant symbionts, with 4,400 nominal species. Some eriophyoid mites can induce galls in their plant hosts, but the mechanism of gall induction is not well understood. One hypothesis suggests that associated bacteria may enhance the production of phytohormones by gall-inducing arthropods. The phylogenetic position of Eriophyoidea is also a contentious issue. In the literature, eriophyoids have been placed near Nematalycidae (Acariformes: Endeostigmata) or within Eupodina (Trombidiformes) (Bolton *et al.*, 2017; Zhang *et al.*, 2011). Here, we sequenced and assembled the whole genome of the gall-inducing mite *Fragariocoptes setiger* and characterized its microbiome composition from two independent samples. We then inferred a phylogenomic tree of acariform mites, including Nematalycidae and Eupodoidea. To identify a potential bacterial gall-inducer, two independent metagenomes of *F. setiger* were analyzed using Gall-ID (comparison with known gall-inducers), Kraken (k-mer-based classification using nearly the entire GenBank nucleotide data), SingleM (comparison with 14 single-copy bacterial genes), and BLAST (classification of the intersection of the two metagenomic assemblies). Our metagenomic results suggested that *Wolbachia* supergroup Q was the only abundant OTU shared across the two samples. The substantial abundance of this bacterium points to its functional importance for its mite, however, *Wolbachia* is not known to induce galls. Another symbiotic bacterium, *Agrobacterium tumefaciens*, was also detected, however, it lacked the complete Ti plasmid and, therefore cannot be responsible for gall-formation. We also detected an array of plant pathogens that may be vectored by the mite (e.g., *Xanthomonas campestris*) and a mite pathogenic virus, *Betabaculovirus*, a double-stranded DNA virus, that may have a potential use in the control of agricultural pests. The mite genomic assembly was 40.9 Mb in size, had 3,581 contigs (N50=31,600) and 3,056 predicted genes. Our phylogenomic analysis showed strong support for Eriophyoidea being part of Endeostigmata (SH-aLRT support=100%, bootstrap support=99%). Particularly, Eriophyoidea was sister to Nematalycidae (100, 100%), a group of deep-soil, vermiform mites belonging to Endeostigmata. This result provides nearly decisive evidence for the long-standing controversy about the phylogenetic position of Eriophyoidea, providing the stability for the higher-level classification of acariform mites (Klimov *et al.*, 2022).

PBK was supported by the Ministry of Science and Higher Education of the Russian Federation within the framework of the Federal Scientific and Technical Program for the Development of Genetic Technologies for 2019–2027 (agreement №075-15-2021-1345, id: RF 193021X0012) to A. V. Lisitsa.

Keywords: Acariformes, phylogenomics, position of Eriophyoidea, gall-inducement, eriophyoid metagenomics

References

- Bolton, S.J., Chetverikov, P.E. & Klompen, H. (2017) Morphological support for a clade comprising two vermiform mite lineages: Eriophyoidea (Acariformes) and Nematalycidae (Acariformes). *Systematic & Applied Acarology*, 22 (8), 1096–1131.
- Klimov, P.B., Chetverikov, P.E., Dodueva, I.E., Vishnyakov, A.E., Bolton, S.J., Paponova, S.S., Lutova, L.A., Tolstikov, A. V. (2022) Symbiotic bacteria of the gall-inducing mite *Fragariocoptes setiger* (Eriophyoidea) and phylogenomic resolution of the eriophyoid position among Acari. *Scientific Reports*, 12 (1), 3811.
- Zhang, Z.-Q., Fan, Q.-H., Pesic, V., Smit, H., Bochkov, A.V., Khaustov, A.A., Baker, A., Wohltmann, A., Wen, T., Amrine, J.W., Beron, P., Lin, Ji., Gabrys, G. & Husband, R. (2011) Order Trombidiformes Reuter, 1909. *Zootaxa*, 3148, 129–138.