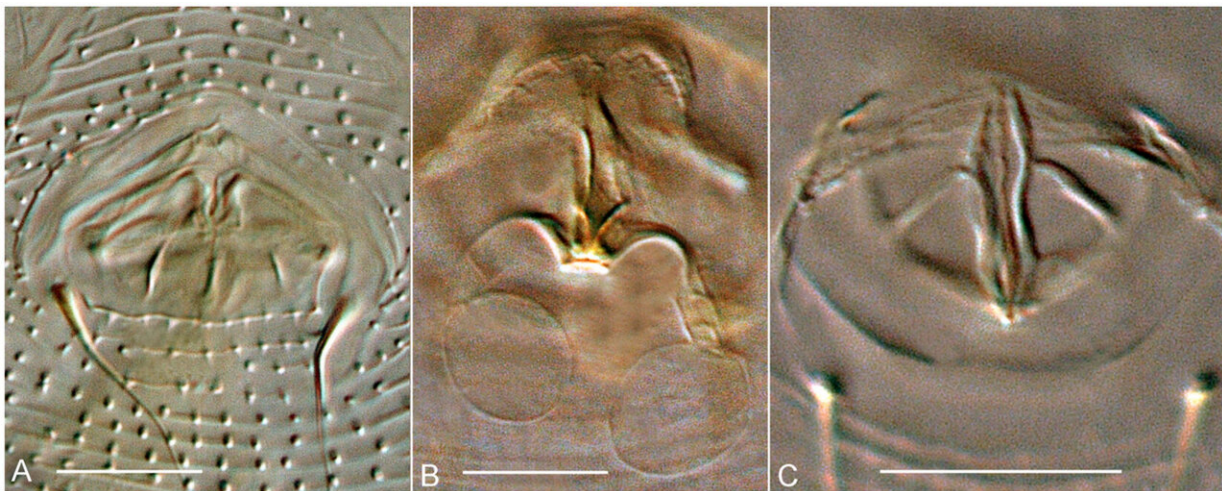


A new species of Canadian gall mite challenges current classification of a major lineage

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Microphotographs of male and female genital structures of *Setoptus tsugivagus*.
Credit: Chetverikov et. al / Systematic and Applied Acarology, 2019

A new species of gall mites (*Setoptus tsugivagus*) associated with the Western hemlock (a common coniferous tree at the west coast of North America) has been described by a group of scientists from Russia, Serbia and the U.S. The researchers believe that the current classification of the *Setoptus* mites and other groups should be reconsidered, because species that were previously considered as closely related do not have a common ancestor. The results of the study were

published in *Systematic and Applied Acarology*.

About one-third of microscopic phytoparasites (400 species out of 5000) are gall mites that inhabit coniferous plants. They lack two back pairs of legs and belong to the superfamily of *Eriophyoidea* (four-legged mites). The group has three families—*Eriophyidae*, *Diptilomiopidae* and *Phytoptidae*, and the latter include a group called *Nalepellinae*. This group was divided into three subgroups (tribes): *Pentasetacini*, *Nalepellini* and *Trisetacini*. However, molecular and [genetic analyses](#) show that the tribe *Pentasetacini* is not related to *Nalepellini* and *Trisetacini*. Instead, the *Pentasetacini* was elevated to a separate family, *Pentasetacidae*, and *Nalepellini* and *Trisetacini* were placed in the family *Phytoptidae*.

The *Nalepellinae* are characterized by long, recurved spermathecal tubes. This group inhabits *Pinaceae*, *Cupressaceae*, and *Taxaceae* trees. The *Nalepellinae* are found in North America, Eurasia, and Eastern Asia, which are the areas with the largest diversity of coniferous plants.

A team of scientists from Saint Petersburg State University, the Institute of Zoology of the Russian Academy of Sciences, Tyumen State University, and other universities with their colleagues from the U.S. and Serbia organized an expedition to the conifer forest on the Pacific coast of Canada and studied mites associated with *Tsuga heterophylla*. The samples included gall mites that were identified as distinct species of *Nalepellinae* and the genus *Setoptus*—*Setoptus tsugivagus* (the species was named for the host plant). The scientists also collected [species](#) of the *Nalepella* genus to analyze the two groups.

The team compared the morphological features of the mites and carried out molecular and [genetic analysis](#) to find evolutionary resemblances. They analyzed a DNA gene fragment encoding ribosomal RNA (rRNA). Because rRNA is important for accomplishing a major cellular function, protein biosynthesis, this gene is evolutionarily conservative, usually

accumulating only a few changes over millions of years of evolution. It is commonly used to infer relationships between different groups.

"The results of phylogenetic analysis suggest that the genera *Setoptus* and *Nalepella* are polyphyletic groups, i.e., they might have different ancestors. Therefore, the whole classification of the *Nalepellini* group should be reconsidered," said Philipp Chetverikov.

"It also would be interesting to apply a molecular clock analysis to this system to see whether the divergence patterns of mites temporarily coincide with those of their conifer hosts, i.e., if mites and plants co-evolved with each other. We are planning this analysis in the future pending additional [mite](#) taxa from various continents to be sequenced," said project participant, Pavel Klimov.

More information: Philipp Chetverikov et al. The description and molecular phylogenetic position of a new conifer-associated mite, *Setoptus tsugivagus* n. sp. (Eriophyoidea, Phytoptidae, Nalepellinae), *Systematic and Applied Acarology* (2019). [DOI: 10.11158/saa.24.4.13](https://doi.org/10.11158/saa.24.4.13)

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