

Outlineoffungi.org - Note 819 *Nothopucciniastrum*

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Nothopucciniastrum P. Zhao & L. Cai

Based on analysis of ITS and LSU sequence data, Zhao et al. (2022) introduced *Nothopucciniastrum* to accommodate *N. tiliae* (Miyabe) P. Zhao & L. Cai (\equiv *Pucciniastrum tiliae* Miyabe) as the type. Nine other species of *Nothopucciniastrum* were previously included within *Pucciniastrum*. *Nothopucciniastrum tiliae* was described as a rust pathogen on the leaves of *Tilia cordata* var. *japonica* (\equiv *T. japonica*) and *T. miqueliana* from Japan (Miyabe in Hiratsuka 1897). The other nine species were transferred from *Pucciniastrum* and they were originally described in Japan, found on a variety of host plants. *Nothopucciniastrum* is autoecious and known to produce spermogonia, aecia, uredinia and telia on a broad range of host plants within the families *Actinidiaceae*, *Clethraceae*, *Cornaceae*, *Fagaceae*, *Malvaceae*, *Sapindaceae*, *Styracaceae*, *Theaceae*, *Urticaceae* and *Viburnaceae*. The genus is characterized by group 1 (type 2 and 3) spermogonia, peridermium-type or milesia-type aecia, milesia-type uredinia with well-developed ostiolar cells, and subepidermal telia that are one spore deep and consist of laterally adherent, aseptate or multiseptate teliospores. Previous studies have shown that the resolution of some phylogenetic lineages of rust fungi remains poor, especially for *Pucciniastrum* and the *Pucciniastraceae* (Aime & McTaggart 2020). Phylogenetic evidence from the analysis of ITS and LSU sequence data by Zhao et al. (2022) showed that *Pucciniastrum* is polyphyletic and formed a well-supported clade containing ten species, was defined as the new genus. Consequently, Zhao et al. (2022) clearly places *Nothopucciniastrum* in the newly described family *Nothopucciniastraceae* (*Melampsorineae*, *Pucciniales*, [Pucciniomycetes](#), [Basidiomycota](#)). Unfortunately, because Zhao et al. (2022) failed to provide registration numbers issued by a recognized repository for *Nothopucciniastrum* and for the new combinations made within this genus, all the new names are invalid (Turland et al. 2018).

References

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