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Phylogeny and taxonomy of *Cronartium* and allied genera

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Purpose: The pine blister rust diseases, caused by the *Cronartium* species (*Basidiomycota*, *Pucciniales*), are one of the three most important forest diseases worldwide. Species in this genus usually infect two-needle or five-needle pines, and several species have been listed as quarantine pests in many countries because of their severe ecological damage and economic losses to forestry. However, relationship of genus *Cronartium* with other genera in rust fungi is still unresolved, and species delineation within genus is also in a state of disorder, which further hampered the pathogen recognition and disease control. This study was conducted to clarify the intergeneric relationships of the genus *Cronartium* with related genera and the interspecific relationship within genus.

Methods: 705 specimens were loaned from worldwide herbaria and they were used for molecular analyses and morphological examination.

Results and Conclusions: At the generic level, the monophyly of genus *Cronartium* and its relationship with related genera in families *Coleosporiaceae*, *Melampsoraceae* and *Pucciniastraceae* were confirmed. A novel genus, *Quasipucciniastrum*, typified by *Q. agrimoniae*, sp. nov., is proposed based on distinct morphological characters and phylogenetic placement. Within genus *Cronartium*, 18 species including three potential novel species were confirmed based on the association of morphological characteristics, geographic origins and host range with phylogenetic relationships. Host alternation of 9 *Cronartium* species were confirmed. Our morphological and molecular studies further emphasized the importance of several morphological characters in aecial stage for species recognition.