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Abstract Title: Switchgrass leaf rust in U.S. caused by two genetically and morphologically distinct, yet, closed-related fungi

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Abstract (250 words or less): The identity and diversity of rust fungi (Pucciniales) inciting disease on switchgrass (*Panicum virgatum*) grown in bioenergy systems across the north-central and eastern United States remain unclear. In the present study, the species number and phylogenetic relationships of rust isolates affecting switchgrass were examined in 2011–2013 at two sites in New York as well as selected sites in Alabama, Iowa, Nebraska, Pennsylvania, South Dakota, and West Virginia using ribosomal RNA gene data (partial internal transcribed spacer [ITS] 1, complete 5.8 subunit [S] and ITS2, and partial 28S). Uredinia and teliospore morphology were also utilized to determine taxa. Maximum likelihood, maximum parsimony, and Bayesian analyses demonstrated two monophyletic clades. Clade I consisted of *Puccinia emaculata* and included the majority of isolates across sites, whereas, Clade II included multiple isolates from Iowa, Nebraska, and South Dakota. Uredinia of Clade I and II isolates were morphologically indistinguishable. Teliospores for isolates assigned phylogenetically to *P. emaculata* (Clade I) were two-celled, brown to chestnut-brown, and oblong to ellipsoid averaging $35.4 \pm 0.6 \times 18.0 \pm 0.2 \mu\text{m}$ in length and width, respectively. Clade II isolates also possessed ellipsoid, brown to chestnut-brown teliospores; however, these teliospores were only one-celled and significantly smaller in length ($26.1 \pm 0.4 \times 17.5 \pm 0.3 \mu\text{m}$) in comparison to *P. emaculata*. Therefore, Clade II isolates were diagnosed to *Uromyces graminicola* according to previously published species descriptions. Results demonstrated that *P. emaculata* and *U. graminicola* are closely-related phylogenetically, yet, can be readily delimited via molecular or morphological analysis.