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**Lead author is a graduate student.*

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**Lead author is a graduate student.*

**Stem rust in the presence of barberry**

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*Puccinia graminis* is the causal agent of stem rust on cereals, a disease that has been known and feared for centuries. In Sweden, a law for removal of barberry was implemented from 1918 until 1994. Since then, the occurrence of barberry has increased, as well as stem rust on cereals and grasses. Our studies have shown that barberry is an important part of the disease cycle in Sweden and genetic variation in the pathogen is high, both within and between infested fields. Until now, only oats, rye and some wild grasses are infected by *P. graminis*. We found clear genetic and morphological differentiation between *P. graminis* isolates infecting rye and oats. Why wheat is not affected remains a question to be answered, since most Swedish wheat cultivars are susceptible to *P. graminis* f. sp. *tritici*.

## Surveying stem rust and barberry in South America

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The discovery of Ug99 stem rust with virulence on most widely grown wheat cultivars worldwide triggered substantial new research on host resistance genes and associated virulence dynamics in the pathogen. Ug99 is mutating and migrating, with eight variants presently known, and has spread throughout eastern Africa, across the Red Sea to Yemen and Iran, and to South Africa. It has been speculated that further movement of Ug99 spores from South Africa to South America could happen on prevailing winds that occur about eight days per month on average. While Ug99 is not yet present in South America, this is a critical entry point into the Western Hemisphere as demonstrated by introduction of soybean rust to Paraguay in 2001. Thus, work was initiated to engage countries in South America to participate in monitoring for its occurrence. Stem rust surveys are currently conducted in Argentina, Brazil, and Uruguay on a regular basis. Each country has a national agricultural institute with adequate to good capacity to perform pathotyping work, but have limitations due to inadequate greenhouse cooling. We will present the current virulence dynamics of *Pgt* in each country. In addition to surveys for rust, we searched for the presence of *Berberis* spp. in Brazil. *Berberis laurina* was abundantly distributed in the Rio Grande du Sul state near the city of Caçapava. Leaves sampled in October displayed low to moderate aecial infections. Determination of the pathogen species infecting *B*. *laurina* is currently being determined by physiologic and molecular methods.

**Development of a web-based geospatial database for sharing historic United States barberry eradication records**

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*Puccinia graminis* f. sp. *tritici* (*Pgt*), cause of black stem rust, is a destructive pathogen of wheat and barley. *Pgt* is heteroecious and in North America completes its life cycle primarily on common barberry, *Berberis vulgaris*, and other susceptible *Berberis* or *Mahonia* species and their hybrids (*Mahoberberis sp.*). The United States Barberry Eradication Program (BEP) began in 1918 with 17 northern-tier wheat-producing states participating, and ended in 1981 with over 400 million barberry bushes destroyed. Data from the BEP was recorded on paper records; United States Department of Agriculture Form L. Retrieving data from Form L records is cumbersome and no consistent effort was made to archive them when the BEP ended. The objective of this project was to digitize remaining Form L data and develop a web-based geospatial database for sharing it. Over 32,000 BEP Form L records were obtained for the states of Idaho, Oregon, Montana, South Dakota, Washington, Wisconsin and Wyoming, scanned as .jpg images, and coded by state and county using US FIPS codes and accession numbers for collection sites. About 13,000 records have been entered into the database to date. Each record was entered by locating it on a map using a variety of current geospatial data and the address of the historic record. The data are served via a web-based mapping application with each record represented by a single point. Users can select individual points to access information about the collection site including the number of barberry bushes present. Ultimately, users will be able to access an image of the Form L for each collection site. This tool will allow users to visualize current and historic patterns of disease outbreaks relative to locations of past or current barberry bushes, identify areas of pest risk or hazard, and assist in optimizing survey and control resources.

**Detection and phylogenetic relationships of *Puccinia emaculata* and *Uromyces graminicola* affecting switchgrass (*Panicum virgatum*) in New York State using rDNA sequence information**

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Several species of rust fungi infecting switchgrass (*Panicum virgatum*) in North America have been described; *Puccinia emaculata* and *Uromyces graminicola* are documented throughout the north central and eastern U.S. Although morphological characteristics of telia and teliospores have been used to differentiate the two species, morphometric analyses alone have been inadequate in assessing their phylogenetic relationships. Leaf rust commonly occurs on switchgrass late in the growing season in bioenergy feedstock systems in New York; however, the rust species responsible for inciting disease have remained unclear. In the present study, we extracted fungal DNA from single-sori (uredinia or telia) and, using PCR and Sanger sequencing, selectively amplified and sequenced the nuclear ribosomal internal transcribed spacer (nrITS) region. Infected leaves were obtained in 2011-2013 from different switchgrass ecotypes and localities including multiple sites in New York as well as individual collections from Alabama, Iowa, Nebraska, Pennsylvania, South Dakota, and West Virginia. Maximum likelihood, maximum parsimony, and Bayesian analyses demonstrated two monophyletic clades. Clade I consisted of *P. emaculata* and included the majority of rust isolates from each state except Iowa. Clade II was sister to *P. emaculata*, suggesting a shared common ancestry, and included multiple isolates from Iowa, Nebraska, and New York. Nucleotide identity and genetic distances between isolates in Clade I and II were also significantly different. Morphological analyses of the teliospores supported the phylogenetic results as distinct taxa with Clade I, i.e, *P. emaculata*, possessing only two-celled teliospores, and Clade II possessing only one-celled teliospores. No *U. graminicola* sequences exist in GenBank to compare with our Clade II isolates; however, based on teliospore morphology, the putative identity of Clade II is *U. graminicola*.