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SHORT COMMUNICATION

Population Diversity of *Puccinia graminis* is Sustained Through Sexual Cycle on Alternate Hosts

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Abstract

A high degree of virulence diversity has been maintained in the population of *Puccinia graminis* f. sp. *tritici* (*Pgt*) in northwestern United States. Although *Berberis vulgaris* is present in the region and *Pgt* has been isolated from aecial infections on *B. vulgaris*, the population is too diverse to be explained by the limited presence of *B. vulgaris* alone. Since 2008, we have isolated *P. graminis* from aecial infections on fruits of *Mahonia repens* and *Mahonia aquifolium* from northwestern United States. These two native woody shrub species, widely distributed in western North America, were once classified as resistant to *P. graminis* based on artificial inoculations. By isolating *P. graminis* from aecia, we established that *M. repens* and *M. aquifolium* along with *B. vulgaris* (*albeit* infrequent) serve as the alternate hosts of *P. graminis* in the region. The isolates of *P. graminis* from Mahonia of North America had diverse virulence patterns and most of the isolates could be differentiated on Morocco, Line E, Chinese Spring, Little Club, LMPG-6, Rusty, and other genotypes that are considered to be universally susceptible to most *Pgt* isolates. This discovery explained the persistence of virulence diversity of *Pgt* observed in isolates derived from uredinia on cereal crops in the region. In addition to cereal crops, uredinial stage of the *P. graminis* population is sustained by wild grasses, especially *Elymus glaucus*, a native grass sharing the same habitat with the rusted *Mahonia* spp. Although virulence to some important stem rust resistance genes was observed in some isolates derived from Mahonia of North America when tested against single stem rust resistance gene stocks, the overall virulence is very limited in these isolates. This is likely a result of limited selection pressure on the rust population. In contrast to northwestern United Sates, the *Pgt* population in east of the Rocky Mountains of North America has declined steadily with a single race, QFCSC, being predominant in the last decade. This decline is likely due to a combination of factors, of which a lack of sexual recombination in the region is perhaps the most important one.

Key words: *Puccinia graminis* f. sp. *tritici*, wheat stem rust, alternate host, *Mahonia aquifolium*, *M. repens*, *Berberis vulgaris*

INTRODUCTION

In the region east of the Rocky Mountains of North America, the population of *Puccinia graminis* f. sp. *tritici* (*Pgt*) has steadily declined over several decades (Roelfs 1982). A single race, QFCSC, predominated in the pathogen population in the last decade. Stem rust is rarely observed in wheat production fields, even on susceptible cultivars, in a vast wheat production region where the environments are usually favorable for stem rust development. This decline, both in virulence diversity and population size, strongly indicated the presence of a bottleneck for the survival of the *Pgt*

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population in the region. Among factors contributing to the decline discussed by Kolmer *et al*. (2009), a lack of sexual recombination in the region was perhaps the most important one (Jin 2010). In contrast, a high degree of virulence diversity has been observed in the *Pgt* population in northwestern United States (Roelfs and Groth 1980). Although *Berberis vulgaris* is present in the region and *Pgt* has been isolated from aecial infections on *B. vulgaris*, the population is too diverse to be explained by the limited presence of *B. vulgaris* alone. Studies were undertaken to investigate the causes that may have contributed to, and sustained, the *Pgt* diversity.

RESULTS AND DISCUSSION

By isolating *P. graminis* from aecia on *Mahonia repens* and *Mahonia aquifolium*, we established that *M. repens* and *M. aquifolium*, along with *B. vulgaris* (*albeit* infrequent), serve as the alternate hosts of *P. graminis* in northwestern United States. The virulence frequencies of 62 isolates derived from aecia to various wheat differentials and other lines ranged from 0 to 95% (Fig.). Virulence to some important stem rust resistance genes was observed in some isolates when tested against stocks of single stem rust resistance genes. This may explain the persistence of virulence diversity of *Pgt* observed in isolates derived from uredinia on cereal crops in the region. However, the overall virulence to cereals is very limited in these isolates, which may be a result of limited selection pressure on the rust population. Most of the isolates could be differentiated on Morocco, Line E, Chinese Spring, Little Club, LMPG-6, Rusty, and other genotypes that are considered to be universally susceptible to most *Pgt* isolates. Avirulence on most of the "universal susceptible" wheat lines, which serve as the background for many single stem rust resistance genes, renders race identification to be less informative. Common wheat genotype Line E and durum genotype Rusty appeared to be more susceptible than other wheat lines. In order to investigate the interactions between specific *Sr* genes and these avirulent isolates, new stocks of differential genes, perhaps in Line E background, need to be developed. Low frequency of isolates with virulence to Prolific rye, a rye genotype susceptible to *P. graminis* f. sp. *secalis* (the rye stem rust pathogen), was observed. Compared to the limited compatibility with wheat and rye, the set of isolates appeared to be highly compatible (producing high infection types) with the barley genotype, Hypana. The differential host genotypes used in this study could not differentiate the population readily into recognizable subgroups.

Preliminary results from this study indicated that this aecial/telial host system of *Mahonia* spp. and *E. glaucus* sustained a native *P. graminis* population that may not depend on the presence of cereal crops in this region. Similar native rust populations are likely present in other regions where indigenous or naturalized aecial/telial hosts co-exist in close proximity. Non-native *P. graminis* forms, such as *Pgt*, could be incorporated into such a system if both the aecial hosts and the telial hosts are susceptible to the non-native *P. graminis*. In the case of the *Mahonia/Elymus* system in the northwestern United States, the presence of *P. graminis* f. sp. *tritici* in the system was evident by the isolation of a few typical *Pgt* races from *Mahonia* spp. and from *E. glaucus*, and by the presence of a large number of characteristically avirulent *Pgt* races isolated from infected barley and wheat crops in the region.

MATERIALS AND METHODS

Since 2008, we have isolated *P. graminis* from aecial infections on fruits of *M. repens* and *M. aquifolium* collected in northeastern WA where limited acreage of cereal crops is grown and natural vegetation is dominated by mixed coniferous forests. *Mahonia repens* and *M. aquifolium*, two native woody shrub species are major forest-floor vegetation components in the sampled region and are cultivated as ornamentals. These two species were once classified as resistant to *P. graminis* based on artificial inoculations (Whetstone *et al*. 1997). We also identified *Elymus glaucus*, a native grass sharing the same habitat with the rusted *Mahonia* spp., as the telial host of *P. graminis* from *Mahonia* spp. Other grasses with stem rust infections included *Agrostis alba*, *Elytrigia repens* and *Elymus canadensis*. Aeciospores were collected from aecia on fruits of *M. repens* and *M. aquifolium* and inoculated onto seedling plants of a set of cereal crop species,

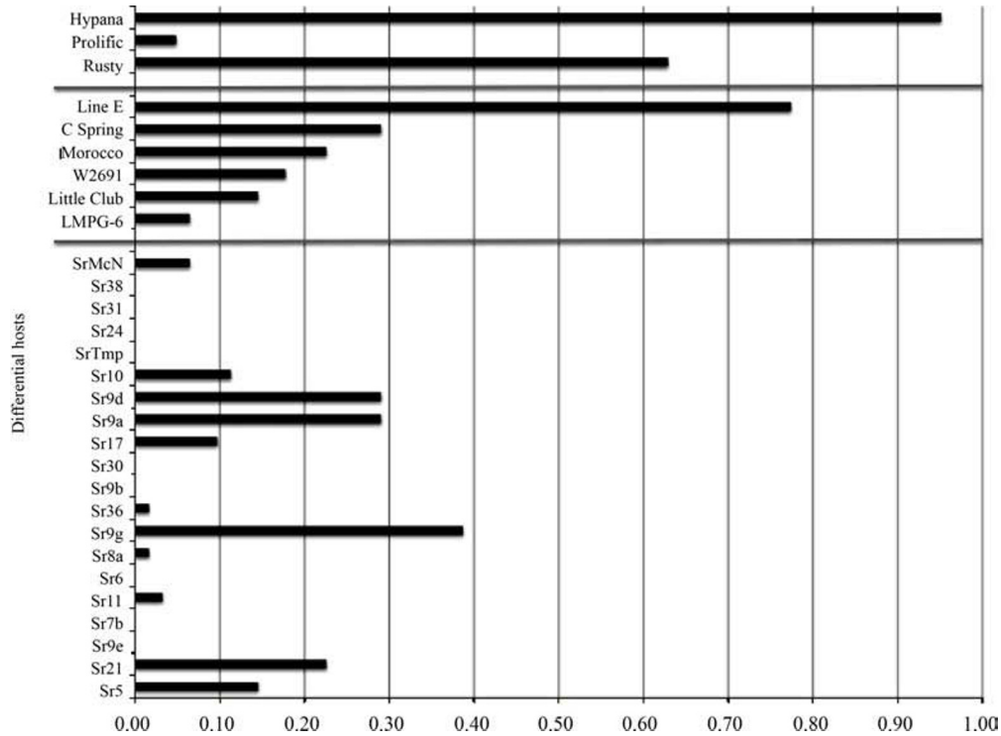

Fig. Virulence frequency of 62 isolates of *Puccinia graminis* derived from *Mahonia* spp.

including Morocco and Line E (wheat), Hypana and Hiproly (barley), Prolific (rye), and Marvelous (oats) that are used to differentiate major *P. graminis* subgroups (Jin *et al*. 2010) and *E. glaucus*. Inoculation of aeciospores on the cereal genotypes resulted in infection on all lines except on Marvelous (oat) although degrees of infection varied. To maximize the genotypic diversity, the first generation of urednia resulted from aeciospore inoculation were used to develop single-pustule isolates, i.e., each isolate representing an independent infection by an aeciospore. Single-pustule isolates were derived from each of the host lines except for rye. Single-pustule isolates were then evaluated against the wheat stem rust differential lines and additional genotypes of wheat and barley.

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