Genetic Diversity of *Phoma sclerotioides* Isolates from Minnesota

Claudia V. Castell-Miller, Melinda R. Dornbusch and Deborah A. Samac
USDA-ARS-Plant Science Research Unit, St. Paul, MN

Phoma sclerotioides causes brown root rot in alfalfa (*Medicago sativa*) and root rot of several other legumes and winter wheat (1,2). Symptoms appear as dark, depressed lesions in taproots and secondary roots, sometimes accompanied by dark margins. Complete decay of the root system has been observed. The fruiting bodies of the fungus (beaked pycnidia) are frequently present in advanced lesions. The disease is widespread in the northern tier states of the U.S. and southern provinces of Canada where it contributes to winter injury and stand loss.

Previously, a multilocus phylogenetic analysis suggested that at least three subtypes of *P. sclerotioides* are present in North America (3). We used molecular population genetic tools to understand the relationships and the population structure of *P. sclerotioides* isolates of the Central subtype recovered from two production fields in Minnesota in 2007. Portions of three genes of 18 isolates, the internal transcribed spacers of the rDNA (ITS; 497 bp), chitin synthase (CHS; 300 bp) and glyceraldehyde-3-phosphate dehydrogenase (G3PD; 526 bp) were analyzed. Preliminary results of DNA polymorphism and haplotype diversity are depicted in Table 1.

Table 1. Sequence DNA polymorphisms of the internal transcribed spacers of the ribosomal DNA (ITS), chitin synthase (CHS) and glyceraldehyde-3-phosphste dehydrogenase (G3PD) from *Phoma sclerotioides* isolates.

	ITS*	CHS	G3PD
Polymorphic inv/var/inf. sites	482/13/1	295/5/2	519/5/2
θ_w (per site/sequence)	0.0076/3.78	0.0048/1.45	0.0039/2.035
No. of haplotypes	3	4	4
Nucleotide diversity (π)	0.0036	0.0041	0.0028
Nucleotide differences (k)	1.78	1.23	1.45
Total No. of mutations (η)	14	5	7
Haplotype diversity	0.451	0.686	0.529

* Sequences analyzed corresponds to ITS1, ITS2 and 5.8S

Within a location distinct haplotypes were recovered, but overall diversity is low to intermediate. AMOVA test indicates that there is not population differentiation by collection site using sequences of the genes individually (ITS F_{ST}=0.05 *P*-value=0.28; G-3-DP F_{ST}=0.00 *P*-value=0.65; CHS F_{ST}=0.00 *P*-value=0.57).

Preliminary results using a parsimony analysis support separation of isolates from Minnesota from the Western and Eastern subtypes. This may indicate limited gene flow among regions. These results indicate that disease resistance breeding and disease management efforts need to consider regional difference in the pathogen population.

References

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