Wisconsin Department of Agriculture, Trade and Consumer Protection

Wisconsin Pest Survey Report

EARLY SEASON SOYBEAN ROOT ROT SURVEY

Over the last 12 years Wisconsin soybean growing areas have experienced heavy rainfalls in spring causing prolonged saturation of soils and flooding, which created optimal conditions for soybean diseases caused by water molds (or oomycetes). The Wisconsin Department of Agriculture, Trade and Consumer Protection Pest Survey Program and the Plant Industry Bureau Laboratory tracked water molds in soybean fields from 2008 to 2020. This report focuses on Phytophthora species, which belong to this group of fungus-like organisms.

During this time frame we have documented six different species of Phytophthora in Wisconsin soybean fields. Maps on page 5 note the locations where all Phytophthora species were detected on soybean seedling roots based on our surveys.

Phytophthora sojae is a well-established species that causes damping-off and root rot disease in spring. Later in the season it causes characteristic brown lesions on the lower stem. *P. sojae* is found in all major soybean growing areas of Wisconsin. In addition to *P. sojae*, our annual survey identified five other species of Phytophthora on soybean seedlings. *Phytophthora sansomeana* was first detected in Wisconsin soybean in 2012. We encountered four more species that are not usually associated with soybeans: *P. pini* and *P. taxon personii* during the 2014 survey and *P. inundata* and *P. iranica* in 2015. All five species are first detections on soybean in Wisconsin. To the best of our knowledge, *P. taxon personii*, *P. inundata* and *P. iranica* are new reports for this state on any plant host. *P. pini*, previously called *P. citricola* has been observed as a pathogen of shrubs and trees in Wisconsin.

Methods - DATCP plant pathologists collected soybean seedlings from up to 55 fields, when soybeans were in the vegetative to early reproductive stages. From each randomly chosen field, seedlings were carefully dug up, selecting symptomatic plants or plants from areas prone to flooding or soil compaction. A combined sample consisting of 20 seedlings from each field was diagnosed by the Plant Industry Laboratory. Seedling roots were washed thoroughly before root tissue was tested using gene-based methods. DNA was amplified using *P. sojae* specific primers (Bienapfl et al. 2011) and starting in 2010 with *Phytophthora* genus specific primers from the cytochrome oxidase gene region (Martin & Tooley 2003). Subsequent sequencing allowed for fast and accurate identification to species level. The same gene-based methods supported morphological identifications of isolates from root samples. Isolates of new Phytophthora species were submitted to collections for further research.

Table 1. Phytophthora (P.) and Pythium Survey Summary 2008-2020											
Year	Survey Dates	Total Fields	P. sojae		P. sansomeana		P. pini	<i>P.</i> taxon <i>personii</i>	P. inundata	P. iranica	Pythium spp.
2008	6-23 to 7-17	50	12	24%	NA	NA	NA	NA	NA	NA	NA
2009	7-9 to 7-17	50	9	18%	NA	NA	NA	NA	NA	NA	NA
2010	6-16 to 7-9	45	17	38%	0	0	0	0	0	0	NA
2011	6-14 to 7-14	15	2	13%	0	0	0	0	0	0	13 (87%)
2012	5-29 to 7-2	49	8	16%	3	6%	0	0	0	0	49 (100%)
2013	6-17 to 7-18	52	7	14%	5	10%	0	0	0	0	49 (94%)
2014	6-6 to 7-16	57	26	49%	4	7%	1 (2%)	1 (2%)	0	0	57 (100%)
2015	6-2 to 6-30	50	19	38%	2	4%	0	0	1 (2%)	1(2%)	50 (100%)
2016	6-7 to 7-13	53	20	38%	1	2%	0	0	0	0	NA
2017	6-9 to 6-30	55	13	24%	1	2%	0	0	0	0	53 (96%)
2018	6-11 to 7-7	54	25	46%	3	5%	0	0	0	0	52 (96%)
2019	6-21 to 7-10	52	20	38%	0	0%	0	0	0	0	52 (100%)
2020	6-8 to 7-3	50	23	46%	3	6%	0	0	0	0	43 (86%)
The total number of fields in 2013 and 2014 included two and four corn fields respectively, which had a											
history of <i>P. sansomeana</i> on a prior soybean crop. The percentage of <i>P. sojae</i> positive fields is based on											
the number of soybean fields (50 in 2013 and 53 in 2014). In 2010 testing for <i>P. sojae</i> was expanded to											
include all Phytophthora. Pythium screening started in 2011.											

Results - Table 1 shows the number of fields and percentage of fields infected with Phytophthora and Pythium from 2008 to 2020. Table 2 shows GenBank accession numbers of select isolates included in this survey.

Root rot caused by *P. sojae* was identified in 13% to 49% of fields surveyed from 2008 to 2020. *P. sojae* caused seedling disease usually appears after one to two weeks of continuous moisture with temperatures of 60-65°F.

P. sansomeana showed up in 0% to 10% of samples from 2010 to 2020. *P. pini, P.* taxon *personii* and *P. inundata* and *P. iranica* were each only found once. Pythium another water mold was present in almost all surveyed soybean fields. A separate detailed report on "Pythium Species Associated with Soybean Seedlings" can be found on this website.

P. sansomeana symptoms observed on soybean seedlings consisted of lesions on tap and lateral roots, and decaying fine roots. The brown stem lesions characteristic for *P. sojae* are not associated with *P. sansomeana*. Unlike *P. sojae* which is specific to soybeans, *P. sansomeana* can infect multiple hosts including corn.

Our survey detected *P. sansomeana* on corn in Sheboygan Co. in 2013 but there were no disease symptoms associated with the infected corn roots. The corn field where it was found had a history of *P. sansomeana*-infected soybeans. In a corn-soybean crop rotation this pathogen could build-up over time in the soil. We believe 2013 was the first detection of *P. sansomeana* on corn in Wisconsin.

Researchers first reported *P. sansomeana* on corn in Ohio, soybeans in Indiana, Douglas fir seedlings in Oregon, and weeds in New York (Hansen et al 2009). Significant losses of soybean caused by *P. sansomeana* have been reported from China (Tang et al 2010). An extensive study of oomycetes in soybeans (Rojas et al 2017) reported *P. sansomeana* throughout the Midwest (Illinois, Iowa, Kansas, Michigan, Minnesota and Nebraska) and Ontario, Canada. This study showed that *P. sansomeana* was very aggressive at warmer temperatures. It caused almost 95% disease severity in a soybean seed-rot assay at 68°F and 59% at 55°F.

On soybean *P. sansomeana* has been found in 15 Wisconsin counties: Calumet, Dane, Dodge, Dunn, Eau Claire, Fond du Lac, Green, Green Lake, Jefferson, Marathon, Outagamie, Rock, Sheboygan, Walworth and Winnebago. Three of these counties (Fond du Lac, Green Lake, and Walworth) were new detections in 2020. This species was first detected in Wisconsin on Fraser and balsam fir in 2011. It is present in Christmas tree plantations in six Wisconsin counties (Clark, Jackson, Lincoln, Manitowoc, Marathon and Price). Combining Christmas tree and soybean survey data reveals that *P. sansomeana* is present in 20 Wisconsin counties.

P. pini (formerly called *P. citricola*) is a known pathogen of shrubs and trees. The organism survives well in surface waters and could inadvertently be introduced by flooding or irrigating with pond or river water. *P. pini* was isolated from an Eau Claire Co. soybean sample that was also infected with *P. sansomeana*.

P. taxon *personii* is new to science and has yet to be formally described. It was originally found in rivers and wetland soils in Australia, where it also affects horticultural crops. *P. taxon personii* was isolated from Winnebago Co. soybean roots that also tested positive for *P. sojae*.

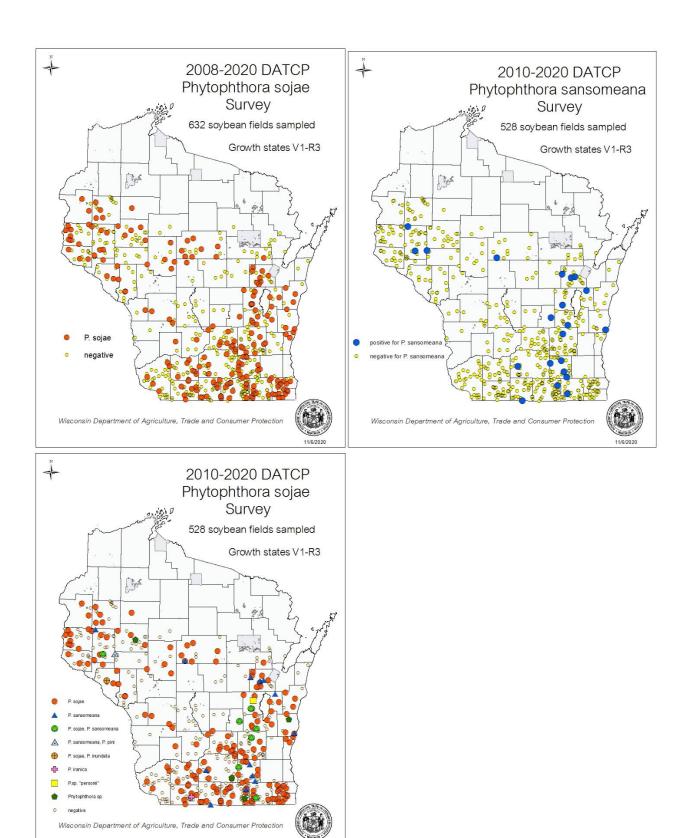
P. inundata was first described in 2003 (Brasier et al.) in wet or flooded soils in Europe and South America. It is associated with root and collar rots of hardwood trees and shrubs (horse chestnut, olive, willow and grape). In Wisconsin, *P. inundata* was detected in Buffalo Co., in a field where *P. sojae* was present as well.

P. iranica described in 1971 (Ershad, Park et al 2015), infects eggplant, potato, tomato, and sugar beet in Iran according to the USDA National Fungus Collections (Farr et. al 2018). In Wisconsin *P. iranica* was found in Lafayette Co.

At this point these four organisms are incidental finds and whether these pathogens have any significant effect on soybean production remains to be determined.

Accession No	Collected By	Collection Date	Location	Host	Isolation Source	Isolate	Dev. Stage	Phytophthora Species
MW160207	A. Barta	6/12/2012	Jefferson County, WI	Glycine max	soybean roots	2012P13	V1	P. sansomeana
MW221449	A. Barta	6/20/2012	Sheboygan County, WI	Glycine max	soybean roots	2012P23	V1	P. sansomeana
MW310398	A. Barta	6/24/2013	Sheboygan County, WI	Zea mays	corn roots	2013P12corn	V4	P. sansomeana
MW221450	A. Barta	7/10/2013	Dane County, WI	Glycine max	soybean roots	2013P25	V4	P. sansomeana
MW221451	A. Barta	7/11/2013	Outagamie County, WI	Glycine max	soybean roots	2013P28	R1	P. sansomeana
MW310399	A. Barta	7/11/2013	Outagamie County, WI	Glycine max	soybean roots	2013P30	V2	P. sansomeana
MW246830	J. Domino	6/24/2014	Winnebago county, WI	Glycine max	soybean roots	2014P16	VC	P. sp. 'personii'
MW246831	N. Clemens	7/1/2014	Eau Claire County, WI	Glycine max	soybean roots	2014P28	V2	P. pini
MW221452	N. Clemens	7/1/2014	Dunn County, WI	Glycine max	soybean roots	2014P29	V2	P. sansomeana
MW221453	J. Domino	7/1/2014	Jefferson County, WI	Glycine max	soybean roots	2014P38	V2	P. sansomeana
MW221454	A. Barta	6/2/2015	Jefferson County, WI	Glycine max	soybean roots	2015P02	V1	P. sansomeana
MW246832	A. Barta	6/9/2015	Lafayette County, WI	Glycine max	soybean roots	2015P20	V2	P. iranica
MW246833	A. Barta	6/16/2015	Buffalo County, WI	Glycine max	soybean roots	2015P27	V2	P. inundata
MW310400	J. Domino	6/16/2015	Dodge County, WI	Glycine max	soybean roots	2015P45	V2	P. sansomeana
MW310401	A. Barta	6/25/2018	Rock County, WI	Glycine max	soybean roots	2018P21	V3	P. sansomeana
MW221455	A. Barta	7/2/2018	Winnebago County, WI	Glycine max	soybean roots	2018P36	V1	P. sansomeana
MW221456	A. Barta	6/23/2020	Walworth County, WI	Glycine max	soybean roots	2020P39	R1	P. sansomeana

Table 2. GenBank accession numbers of select isolates from this survey.



1/6/202

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