Desert Durum Wheat and Barley Disease Surveys [1]

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Introduction

Several diseases occur on barley and durum wheat including seedling diseases (*Rhizoctonia*, *Pythium*), smut diseases (common bunt, loose smut, dwarf bunt, Karnal bunt), rust diseases (leaf rust, stripe rust, stem rust), bacterial streak, barley yellow dwarf, and wheat streak mosaic. Arizona's dry weather in most parts of the state has kept fungal and bacterial disease levels low in desert durum wheat and barley. Local disease outbreaks may occur and severely impact the yield and quality of grains in some years when weather conditions are favorable for disease development. For example, Fungal leaf blight is severe in barley fields in Gila Bend. Seed-borne diseases such as smut, Karnal bunt, leaf stripe, and bacterial blight present in a field to exceed the established tolerance for certification are cause for rejection and losses.

Disease surveys are a useful means to provide information on emerging or re-emerging diseases on cereal crops, their distribution in space and over time (years), according to their incidence and severity. The information generated from surveys can be utilized to determine disease resistance levels of cultivars or land races. The type of disease that is most common (seed-borne, straw-borne or air-borne) and their association may help in formulating the management practices needed for growers. Disease surveys will be conducted in Arizona to identify the most common diseases of wheat and barley and to help establish diagnostic capability to support our grower's needs for disease identification.

The goal of this survey project is to take proactive actions to present spread of economically important diseases in barley and wheat. Specific objectives are to: (i) survey Arizona wheat and barley fields for the presence of in-season diseases; (ii) build disease diagnostic capacity to support our pest control advisor and growers and provide the industry with an updated assessment of the distribution of major diseases in Arizona.

Materials and Methods

Field scouting for diseases. We plan to inspect wheat and barley fields across the state from November to May. Tissue samples were collected from fields with visible symptoms of rust, smut, seedling diseases, yellowing, wilting, and stunting. One to five samples were collected from each selected field and placed in a zip-lock bag and transported back to the laboratory in Tucson for further analysis.

Pathogen isolation and characterization. To identify the race of stripe rust, leaf samples suspected of stripe rust were sent to the USDA ARS Laboratory of the Wheat Genetics, Physiology, Quality, and Disease Research Unit at Pullman, WA. Fungal pathogens were isolated on the PDA medium. Briefly, small tissue fragments (3 × 3 mm) were cut from the margin between affected and healthy tissues and surface sterilized by soaking in 75% ethanol for 5 s, 1% sodium hypochlorite for 60 s, copiously rinsed with sterile distilled water, and dried on sterile filter paper in a laminar hood. Single-spore cultures were established for a putative isolate. The identity of fungi was determined based on morphology and DNA sequences of ITS and TEF1α genes. Bacteria were isolated using King's B and nutrient agar. Barley yellow dwarf virus-MAV (BYDV-MAV) and PAV strains were tested using commercial ELISA kits from Agdia (Agdia Inc.).

Pathogenicity test. The pathogenicity experiment was performed in a greenhouse. Fresh 1-week-old *Pyrenophora graminea* cultured on PDA media were used to inoculate barley seeds. Briefly, ten barley seeds were placed on *P. graminea* culture in the refrigerator for 3 days, ten barley seeds were placed on water agar as control. *P. graminea* -inoculated seeds and control seeds were then planted in a half-gallon pot. Disease incidence and severity were evaluated 2 weeks after inoculation.

[1] The authors would also like to thank the Arizona Grain Research and Promotion Council for supporting this research. This is the final project report.

Results and Discussion

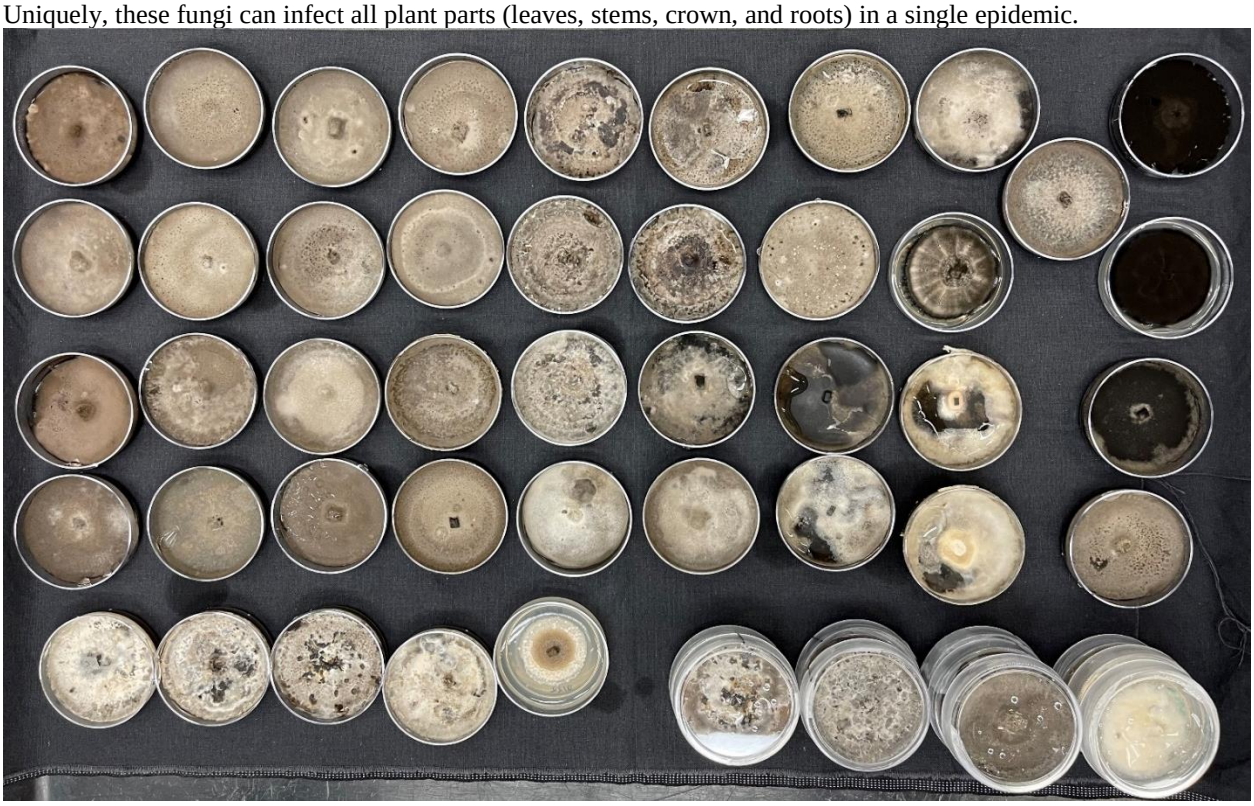
A total of more than 90 commercial fields were inspected for barley and wheat diseases in seven counties. Stripe rust, barley yellow dwarf virus, and bacterial leaf streak were not detected on barley and wheat in any of the fields visited. However, a number of foliar fungal diseases were detected in barley (see table below). In some cases, significant yield loss was expected.

Pathogens	Diseases	County (# isolates)
Puccinia striiformis f.sp. *tritici*	Wheat stripe rust	Not detected
Puccinia striiformis f.sp. *hordei*	Barley stripe rust	Not detected
Ustilago nuda	Barley loose smut	Maricopa (6)
Ustilago avenae	Oat loose smut	Yuma (1), Pinal (2)
Pyrenophora graminea	Barley/wheat striping	Maricopa (9)
Stemphylium vesicarium	Barley leaf blight	Maricopa (6), Pinal (13)
Exserohilum rostratum	Barley leaf blight	Maricopa (6), Pinal (13)
Alternaria sp.	Barley leaf blight	Maricopa (6), Pinal (13)
Cuvularia sp.	Barley leaf blight	Maricopa (6), Pinal (13)
Cladosporium allicinium	Barley leaf blight	Maricopa (6), Pinal (13)
Pythium aphanidermatum	Stunted wheat/barley/oat	Yuma (2), Pinal (4), Cochise (2)
P. spinosum	Stunted wheat/barley/oat	Yuma (2), Pinal (4), Cochise (2)
P. vanterpoolii	Stunted wheat/barley/oat	Pinal (1), Graham (1)
BYDV	Barley yellow dwarf virus	Not detected

Barley leaf blight. was a common and potential yield-limiting disease in the Gila Bend area. The initial disease symptoms started at the end of January when leaves are covered with morning dew for a prolonged period. Individual leaves generally start dying back from the tip (Fig.1), and uniform lesions affecting the entire leaf blade may develop. When leaf lesions are present, they are dark brown and circular to elliptical. These spots enlarge into bigger lesions that girdle the leaf and cause it to become chlorotic and die.

Isolation results indicated that several fungal species including *Alternaria* sp., *Stemphylium vesicarium*, *Curvularia* sp., *Exserohilum rostratum*, and *Cladosporium alliciniumwere* were associated with barley leaf blight. Theses graminicolous species of *Helminthosporium* have been segregated into four genera, namely *Bipolaris*, *Curvularia*, *Pyrenophora* (synonym: *Drechslera*), and *Exserohilum*. These genera are characterized as being dark-pigmented and share overlapping conidia characteristics which previously resulted in the erroneous assignment of generic names. All of our isolates were confirmed by obtaining ITS sequences. These fungi share similar asexual life cycles. Conidia

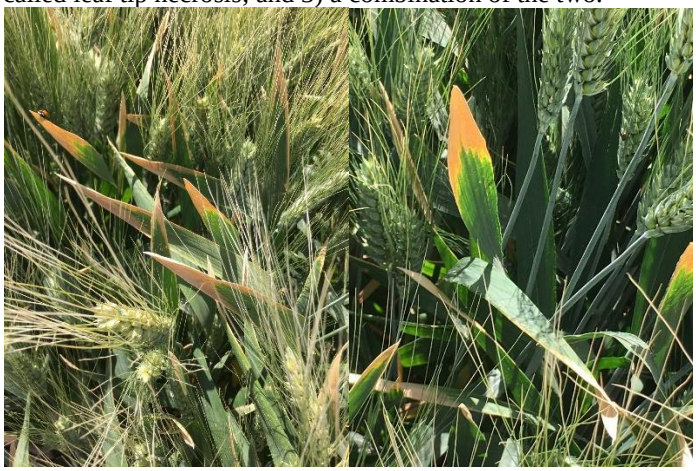
(asexual spores) are considered the primary inoculum source, inciting polycyclic diseases on barley and grasses. Uniquely, these fungi can infect all plant parts (leaves, stems, crown, and roots) in a single epidemic.



Barley leaf stripes. This disease was detected in several barley fields in Buckeye areas. Long pale or yellow stripes become darker as the fungus sporulates on the leaf. The fungal pathogen was identified as *Pyrenophora graminea* based on morphology and ITS DNA sequences. Pathogenicity testing results indicated that *P. graminea* was pathogenic to barley. This finding is the first account of barley leaf stripes in Arizona.

In addition, other foliar fungal diseases including loose smut of barley (*Ustilago nuda*) were also found in several fields. Pythium root rot caused by three Pythium species (*Pythium aphanidermatum*, *P. spinosum*, *P. vanterpoolii*) was detected on barley and oat seedlings.

Under certain conditions, necrotic areas on wheat flag leaves can look like a severe disease outbreak: The flag leaf dies back, starting at the tip and moving toward the base of the leaf. We did not detect any bacterial or fungal pathogens in symptomatic leaves. This symptom is likely due to: 1) hot, dry and windy weather; 2) a physiological phenomenon called leaf tip necrosis; and 3) a combination of the two.



Barley leaf blight and leaf stripes have the potential of causing significant yield losses under favorable weather conditions, especially in Gila Bend and Buckeye grain-producing areas. Both diseases were caused by closely-related fungal pathogens. The disease can be seed-borne. It is important to quantify yield loss by working with growers and determine whether seed treatment with fungicides is adequate in reducing disease severity and protecting yield loss. A replicated field trial that includes foliar fungicide spray and yield monitoring is needed to determine whether the economic benefit of additional foliar fungicide spray is justified.

Supplementary data

ITS sequence of *Pyrenophora graminea*

TTCATGGACGCGCGACCGCGGCTGGACAAGAGCGCAAATAATGTGCTGCGCTCCGAAACCAGTAGGC
CGGCTGCCAATGTTTTTAAGGCGAGTCTCGGGGGAGAGACAAAAGACGCCCAACACCAAGCAAAGCT
TGAGGGTACAAATGACGCTCGAACAGGCATGCCCTTTGGAATACCAAAGGGCGCAATGTGCGTTCAA
AGATTCGATGATTCACTGAATTCTGCAATTCACACTACTTATCGCATTTCGCTGCGTTCTTCATCGATGC
CAGAACCAAGAGATCCGTTGTTGAAAGTTGTAATTGATTACATTGTTTTGCTGACGCTGATTGCAATAA
AAAAAGGTTTGAATAAAGTCCAATTGGCGGGCGAGCCCGCCAAGGAAACAAGTAGTACGCAAAAGAC

ATGGGTGAATATGGCGCCAGAATGGGCAAACCCCCCAAAGCGGGGACTACCCAATCTGCCTTCATATT
TGTGTAATGAT

ITS sequence of *Ustilago nuda*
TCGTAACAAGGTATCTGTAGGTGAACCTGCAGATGGATCATTTCGATGAAAAACCTTTTTTCAGAGGT
GTGGCTCGCACCTGTCCAACTAAACTTGAGCTACCTTTTTCAACACGGTTGCATCGGTCGGCCTGTCAA
ACAGCGCGACGCAAGGAGAAAATCCTCGCGTCTGCTGGGCGACGGACAGACAATTTTATTGAACACTT
TTTGATGATCTAGGATTTGAAGGAGAAAAAGTCATTTTTACGAATGAAATCGGCTGGTAATGCGGTCG
TCTAATTTTAAAAACAACTTTTGGCAACGGATCTCTTGGTTCTCCCATCGATGAAGAACGCAGCGAATT
GCGATAAGTAATGTGAATTGCAGAAGTGAATCATCGAATCTTTGAACGCACCTTGCGCTCCCGGCAGA
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CATTTTATAGGCAAGACGGACGAAAGCTCGATTTTTGCTCTCTCTTCCCTGCCGGGTTTTGATACTATC
AGGACTTCGGAGAGGTTGAGATGGGTAGGAGCTCGACGCAACGGCTTGCTGTTTGGAGTGCTTCTGAA
ACCCGCCCATGCCGAGTTTTCTTTTAGAAAGCTAGGAAGGAATTTATAATAATTCATCGGCCTCAGATT
GGTAGGACTACCCGCTGAACTTAAGCATATCAATA

ITS sequence of *Alternaria alternata*
AGGTGAACCTGCGGAGGGATCATTACACAAATATGAAGGCGGGCTGGAACCTCTCGGGGTTACAGCC
TTGCTGAATTATTCACCCTTGTCTTTTGCGTACTTCTTGTTTCCTTGGTGGGTTCGCCCACCACTAGGAC
AAACATAAACCTTTTGTAATTGCAATCAGCGTCAGTAACAAATTAATAATTACAACTTTCAACAACGG
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GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTCGAGCGT
CATTTGTACCCTCAAGCTTTGCTTGGTGTTGGGCGTCTTGTCTCTAGCTTTGCTGGAGACTCGCCTTAAA
GTAATTGGCAGCCGGCCTACTGGTTTCGGAGCGCAGCACAAGTCGCACTCTCTATCAGCAAAGGTCTA
GCATCCATTAAGC

ITS sequence of *Stemphylium_vescarium*
TGAAGGCAGATTGGGTAGTCCCCGCTTTGGGGGGTTTGCCCATTMTGGCRMCWTATKCRCYSMTGTCY
TWWGCRTACWGTCGGSTGCCRATCATTTTAAGGCGAGTCTCGTGAGAGACAAAKACKCCCAACACCA
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GCTTTCA