

comparison to the control ( $R^2 = 0.14\text{--}0.18$ ,  $P < 0.001$ ). The untreated controls had a high prevalence of *Peltaster fructicola*, which was absent in most treated samples. Species within the genus *Sporobolomyces* were abundant across treatments. There was a high prevalence of the genus *Alternaria*, a post-harvest rot, regardless of treatment. Also, *Botrytis cinerea* populations were enriched in the pulp of fruits treated with synthetic fungicides, highlighting the need for further understanding of fungicide resistance in agricultural microbiomes.

#### **Seedling reaction to leaf rust in spelt wheat (*Triticum spelta* L.) collection**

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Spelt wheat (*Triticum spelta* L.) is an ancient cereal that is gaining small grain growers' attention under an organic setup due to its high protein content, high fiber, and other health benefits. Spelt wheat, like common wheat, also succumbs to leaf diseases, including leaf rust. Leaf rust is a significant yield-limiting disease of wheat worldwide, especially in the U.S. Great Plains region. Identification of disease resistant spelt genotypes could be valuable for spelt production under organic management. In this study, 108 spelt accessions (National Small Grain Collection) from 20 countries were screened against leaf rust at the seedling stage in the greenhouse. The genotypes exhibited varying response ranging from susceptible ( $n = 49$ ), to moderately susceptible (39), moderately resistant (17), and resistant (3). All 108 genotypes were also characterized for tan spot (race 1 and race 5) and spot blotch. Spelt accessions resistant to leaf rust and leaf spots will be further evaluated for the agronomic traits in the field and results will be shared with the growers to assist in selection of superior spelt genotypes.

#### **Root-knot nematode survey of Asian vegetable farms in Hillsborough County, Florida**

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Root-knot nematodes (RKNs) are the most economically important plant-parasitic nematodes with broad host ranges that include many Asian vegetables. Sixteen RKN species have been reported in the Florida. There are over 40 Asian vegetables grown on more than 4,000 ha in Florida and the industry is growing rapidly. No information on RKNs is available from Asian vegetables in Florida, and most growers are unaware of their existence. During June 2020–January 2021, a RKN survey was conducted on seven Asian vegetable farms in Hillsborough County, FL. RKNs were present on all farms. Severely galled roots were found on luffa, sweet potato, basil, pumpkin, bitter melon, Malabar spinach, amaranth, perilla, jute, golden egg, and Indian cream melon. RKN species were identified through primers TRNAH/MRH106 and MORF/MTHIS, followed by restricting PCR products of TRNAH/MRH106 using *Hinf*I and *Mnl*I enzymes. The RKN species were confirmed by species-specific primers Far/Rar, Me-F/Me-R, and MI-F/MI-R. Four RKN species were found, *Meloidogyne arenaria*, *M. enterolobii*, *M. haplanaria*, and *M. incognita*. *M. enterolobii* was found in six out of seven farms on sweet potato, Thai basil, pumpkin, luffa, jute, Malabar spinach, golden egg and perilla. Our survey indicated that RKNs are likely cause significant yield loss in Asian vegetable production in Florida. Especially the concern of high prevalence of *M. enterolobii*, as it breaks down the RKN-resistance of several crops, and is currently considered a major threat to the sweetpotato and vegetable industry in the southeastern U.S.

#### **A transcriptomic analysis of wheat lines that are resistant and susceptible to tan spot (*Pyrenophora tritici-repentis*) disease**

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Tan spot (TS), causal agent *Pyrenophora tritici-repentis* (*Ptr*), is a major threat to wheat production due to the lack of resistant cultivars. In our previous work, we identified MAGIC population parental lines exhibiting TS resistance and susceptibility, namely Robigus and Hereward, respectively. To understand the mechanisms underlying these phenotypes, we performed RNA-seq analysis of leaves before and during *Ptr* interaction. Principal component analysis suggested that infection of Hereward resulted in major shifts in the transcriptome but only minor changes were observed in the resistant line. When comparing mock- and *Ptr*-inoculated samples, differentially expressed genes (DEGs) were identified with DESeq2, leading to the targeting of 15,193 DEGs. Functional annotation showed the pathways enzyme classification, solute transport, RNA biosynthesis, protein modification and homeostasis represented 49.5% of DEGs in Robigus. Cellular metabolism pathways were induced, as well as vesicle trafficking, actin polymerization and cellulose. The upregulation of these cell wall related genes along with microscopic data suggested that barrier defense is a major feature of TS resistance in Robigus. Conversely, photosynthesis was the top fifth pathway in Hereward, totaling 389 repressed genes (12.63%). Photosynthesis collapse was linked to the activation of oligosaccharide metabolism and suppression of glycolysis, TCA cycle and amino acids degradation. This may reflect mobilization of host nutrients to *Ptr*. Our observations could inform wheat-breeding programs targeting TS resistance.

#### **Two-year survey of *Diaporthe* species in soybean across Delaware and Maryland**

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The *Diaporthe* disease complex in soybean (*Glycine max* (L.) Merrill) can cause significant quality and yield losses. Soybean diseases caused by the multiple *Diaporthe* species involved include stem canker, pod and stem blight, and Phomopsis/Diaporthe seed decay. Surveys were conducted across Delaware and Maryland in 2019 and 2020 to determine which species are most prevalent in the region. Survey locations included 60 fields in 2019 and 45 in 2020. Symptomatic plants identified through field scouting were brought back to the lab for fungal isolation from stem pieces. Four *Diaporthe* species, *D. longicolla*, *D. aspalathi*, *D. sojae*, and *D. ueckerae*, were identified across the two seasons. Among the 24 *Diaporthe* isolates collected in 2019, 88% were *D. longicolla*, 8% *D. aspalathi*, and