Screening for Anthracnose Stem Dieback Susceptibility in Florida Blueberry Cultivars

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Summary

Anthracnose, caused by fungal pathogens of the *Colletotrichum* genus (Figure 1), is typically associated with postharvest fruit rots, but can also produce stem lesions and dieback in susceptible cultivars (Figure 2). This disease has recently been reported on two southern highbush blueberry (SHB) cultivars ('Flicker' and 'Scintilla') grown primarily in central Florida, and is sufficiently serious that it has led to a reduction in new plantings of these cultivars. The degree of susceptibility of other cultivars is currently unknown. The pathogen species has been identified as *Colletotrichum gloeosporioides*. The objectives of this research are to screen several SHB cultivars commercially grown in Florida for susceptibility to anthracnose, and develop a small scale laboratory assay that could be used to rapidly screen breeding selections. For the assay development, a whole plant protocol will be compared to a detached stem protocol. A future step will be to identify molecular markers associated with this susceptibility. This will allow for identification and selection of parents that are not susceptible to anthracnose stem dieback.

Screening Material and Methods

Vegetative material

- SHB cultivars: 'Chickadee', 'Emerald', 'Farthing', 'Flicker', 'Jewel', 'Kestrel', 'Rebel', 'San Joaquin', 'Springhigh', and 'Star'

Inoculum concentration

- 10^5 conidia/ml

Plant tissue

- Stems (whole plants and detached stems)

Experimental design

- RCBD, ten cultivars as treatments, ten replications, performed twice

Incubation

- Plastic bags for 16 h after spray inoculation, tubes for stems as a humid chamber, to maintain moist environments for infection (Figures 3, 4)

Assessment

- Disease incidence, lesion length on stems 7 days after first appearance of symptoms

Data analysis

- Cultivar susceptibility was analyzed by one-way ANOVA, and means compared by Tukey's HSD test at *alpha=0.05*

Figures

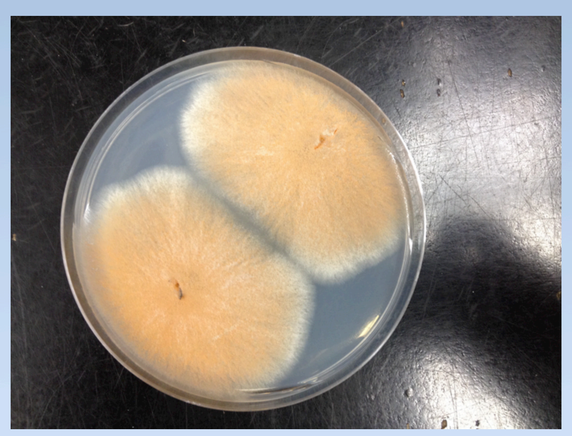

Figure 1 – *C. gloeosporioides* colonies

Figure 2 – Anthracnose stem lesion

Figure 3 – Whole plant incubation

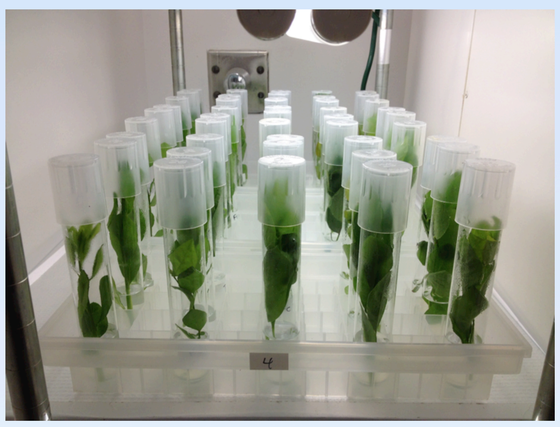

Figure 4 – Detached stem incubation

Preliminary Results

Table 1. Cultivar susceptibility – whole plants

Cultivar	Mean # Lesions	Std. Error # Lesions	Mean Lesion Length (mm)	Std. Error Lesion Length (mm)	Mean Separation (# and Length)
Chickadee	0.0	0.0	0.0	0.0	b
Emerald	0.0	0.0	0.0	0.0	b
Farthing	0.1	0.1	0.5	0.5	b
Flicker	1.5	0.5	8.8	3.5	a
Jewel	0.1	0.1	0.5	0.5	b
Kestrel	0.0	0.0	0.0	0.0	b
Rebel	0.1	0.1	0.5	0.5	b
San Joaquin	0.2	0.1	1.0	0.7	b
Springhigh	0.0	0.0	0.0	0.0	b
Star	0.1	0.1	0.5	0.5	b

Table 2. Cultivar susceptibility – detached stems

Cultivar	Mean # Lesions	Std. Error # Lesions	Mean Lesion Length (mm)	Std. Error Lesion Length (mm)	Mean Separation (Length)
Chickadee	0.1	0.1	1.5	1.5	ab
Emerald	0.0	0.0	0.0	0.0	b
Farthing	0.0	0.0	0.0	0.0	b
Flicker	0.9	0.3	11.5	3.5	a
Jewel	0.2	0.1	7.9	5.3	ab
Kestrel	0.1	0.1	0.8	0.8	b
Rebel	0.2	0.1	2.7	1.8	ab
San Joaquin	0.3	0.2	8.6	4.4	ab
Springhigh	0.0	0.0	1.5	1.5	ab
Star	0.1	0.1	2.4	2.4	ab

Note: Detached stem assay may be skewed by wounding on stems; will redo detached stem experiment.

Mean separation by Tukey's HSD at *alpha=0.05* are indicated by different letters in the same column.

Preliminary Conclusions

Based on data from the whole plant assay, 'Flicker' was the only cultivar with significantly different means (number of lesions and lesion length). Therefore, of the tested cultivars, only 'Flicker' appears to have a unique level of susceptibility to stem lesions caused by *C. gloeosporioides*. The data from the detached stem assay was possibly skewed due to blueberry gall midge damage, allowing infection by both *Colletotrichum* and other pathogens and thereby increasing lesion length, so this assay will be repeated and the new data used in the final analysis. This will determine whether the detached stem assay is a viable screening method for future use.

Future Steps

1. Repeat detached stem inoculation experiment with unwounded tissue
2. Population inoculations (with and without susceptible parents) to determine segregation
3. Genotype segregating populations to identify single nucleotide polymorphism (SNP) molecular markers
4. Perform Genome Wide Association study (GWAS)
5. Mapping of linkage groups identified via GWAS and QTL analysis