Determining the Host Range of *Cytospora* spp.

- Understanding the host range for different *Cytospora* spp. can be important for management
- The host range can be determined by performing artificial inoculations
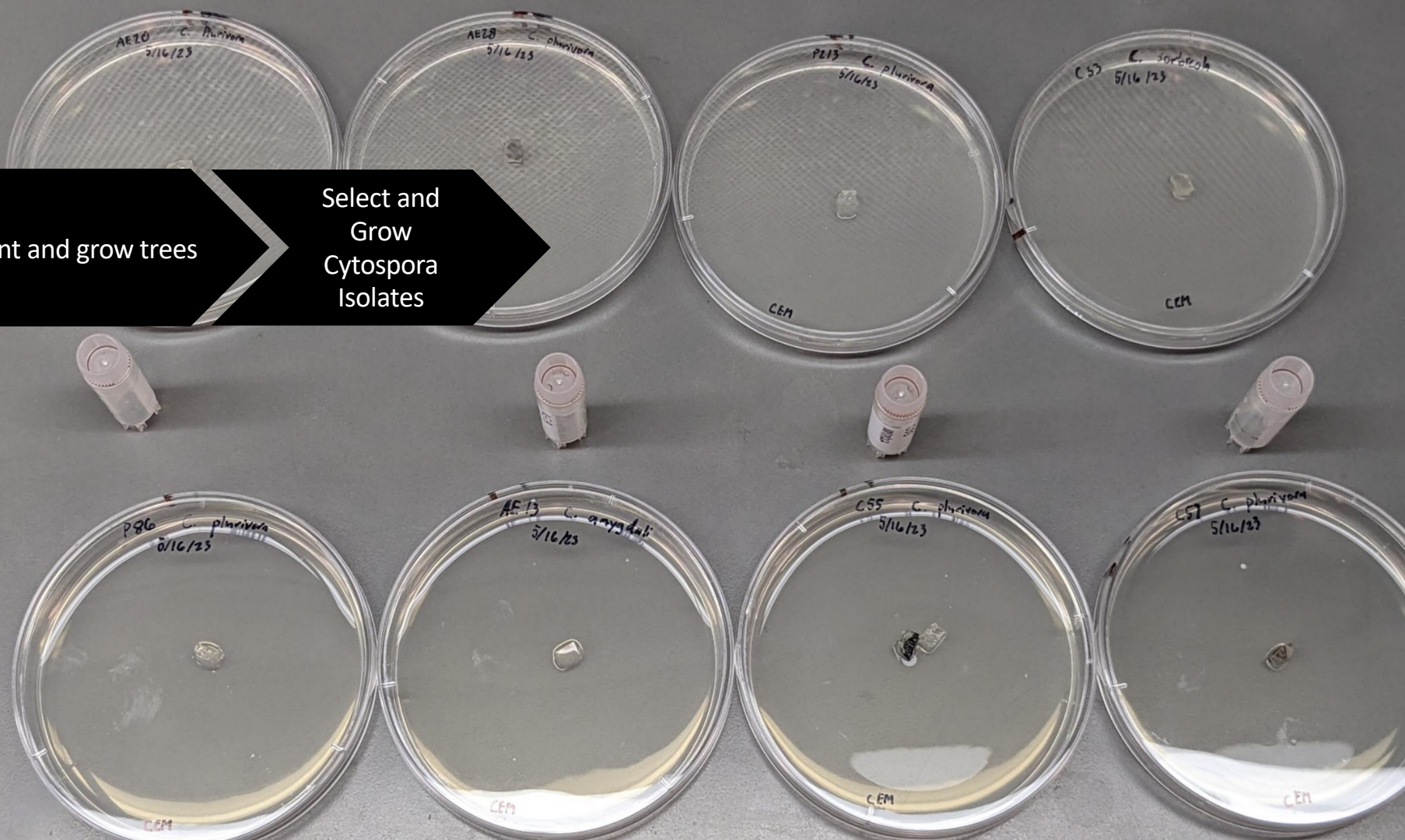
Plant and grow trees

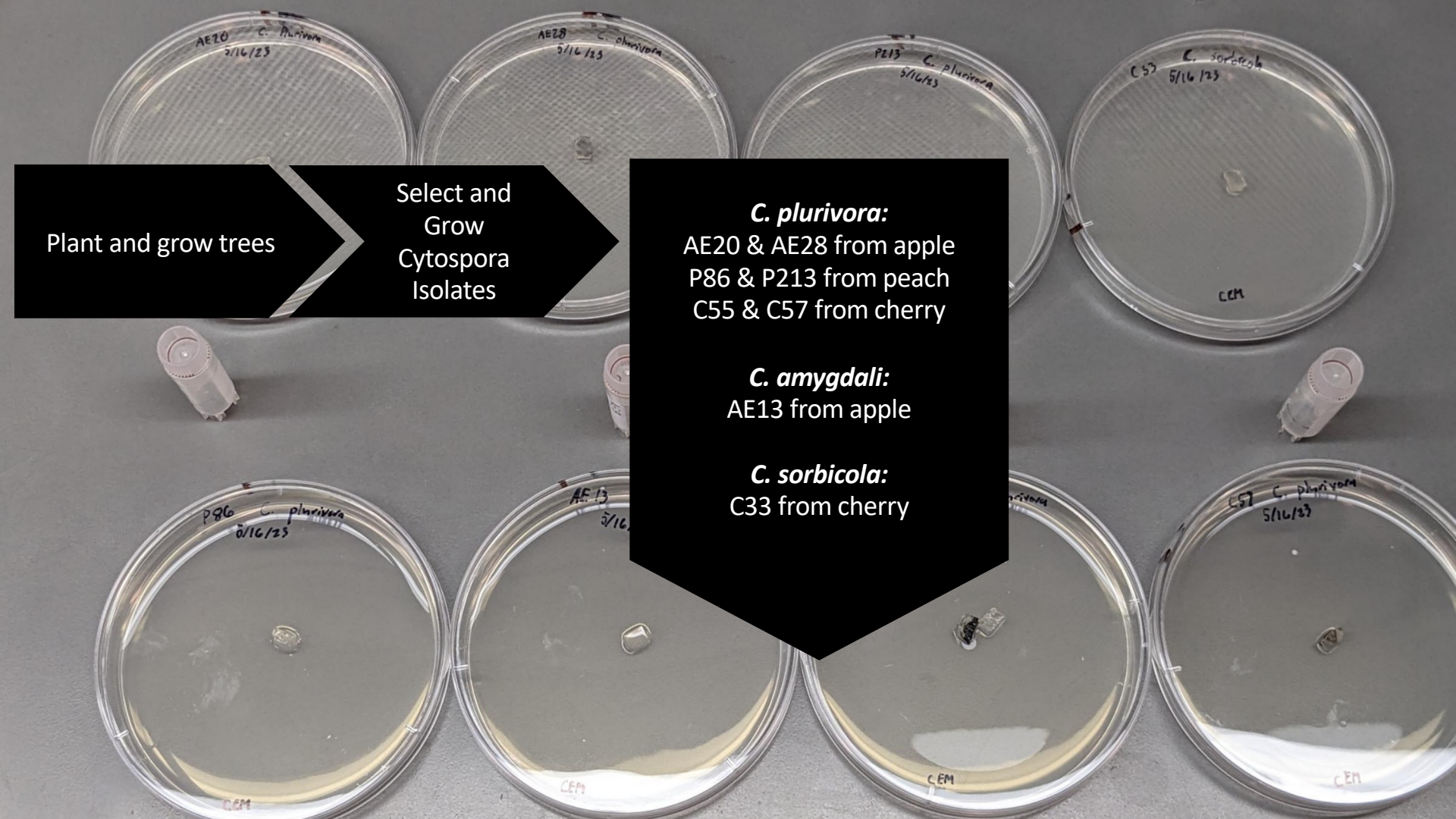Plant and grow trees

Peach:
Redhaven & Crest Haven

Cherry:
Bing & Rainier

Apple:
Honeycrisp

Plant and grow trees

Select and Grow Cytospora Isolates

Plant and grow trees

Select and Grow Cytospora Isolates

C. plurivora:
AE20 & AE28 from apple
P86 & P213 from peach
C55 & C57 from cherry

C. amygdali:
AE13 from apple

C. sorbicola:
C33 from cherry

Plant and grow trees → Select and Grow Cytospora Isolate → Wound and Inoculate Trees

Plant and Grow Trees → Select and Grow Cytospora Isolate → Wound and Inoculate Trees → Care for Trees and Look for Lesions

Plant and Grow Trees

Select and Grow Cytospora Isolate

Wound and Inoculate Trees

Care for Trees and Look for Lesions

Harvest Branches, Measure Lesions

```python
                'C. amygdali', 'C. sorbicola']
trees = ['Pink Lady', 'Honey Crisp', 'Bing', 'Rainier', 'Red Haven', 'Cresthaven']
colors = ['seagreen', 'seagreen', 'firebrick', 'firebrick', 'orange', 'orange']
for x, trt in enumerate(trts):
    avgs = [0] * 6

    ctl_mean = [0] * 6
    ctl_err = [0] * 6
    # new_tree_data = {'Tree mean':[0] * 6, 'Tree control mean':[0] * 6}
    # new_err = {'Tree stdev':[0] * 6, 'Tree control stdev':[0] * 6}

    for key, value in tree_data.items():
        if 'Control' in key:
            this_tree = ' '.join(key.split(' ')[2::]) # this g
            tree_index = trees.index(this_tree)
            ctl_mean[tree_index] = value[0]
            ctl_err[tree_index] = value[1]
            # new_tree_data['Tree control mean'][tree_index] = value[0]
            # new_tree_data['Tree control stdev'][tree_index] = value[1]
        elif trt in key:
            this_tree = ' '.join(key.split(' ')[2::]) # this gets the tree name
            tree_index = trees.index(this_tree)
```
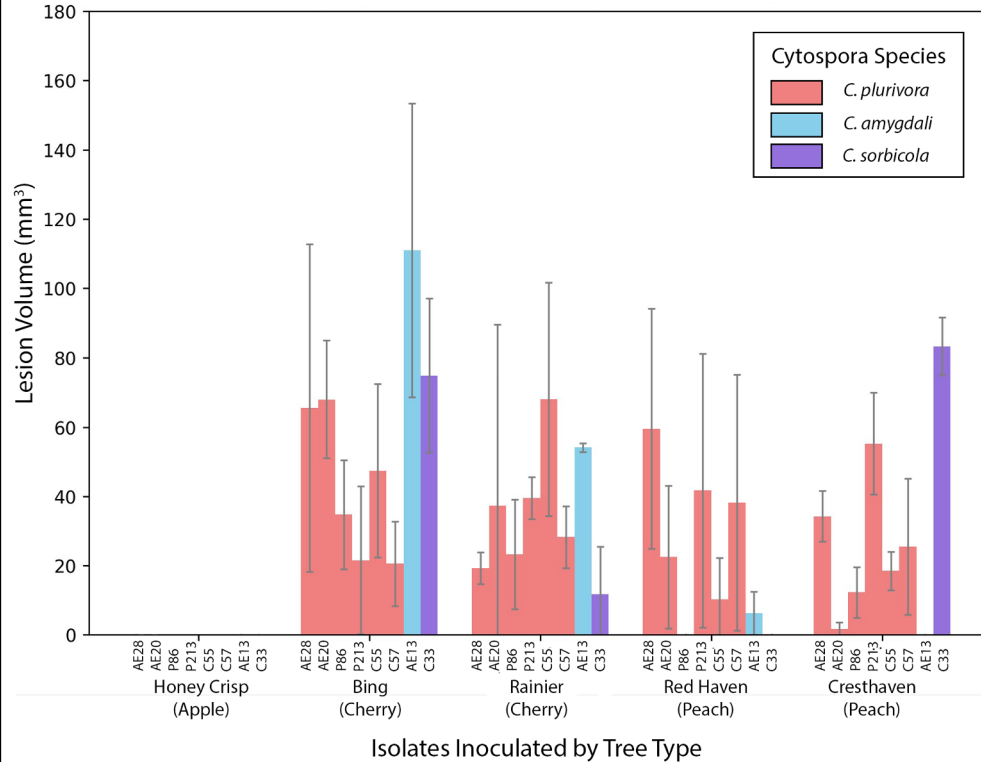
Plant and Grow Trees

Select and Grow Cytospora Isolate

Wound and Inoculate Trees

Care for Trees and Look for Lesions

Harvest Branches, Measure Lesions

Analyze Data

Data Analysis

- The volume of each lesion was calculated
- Volumes were then averaged
- The average of each treatment was calculated
- The control mean was subtracted from the treatments
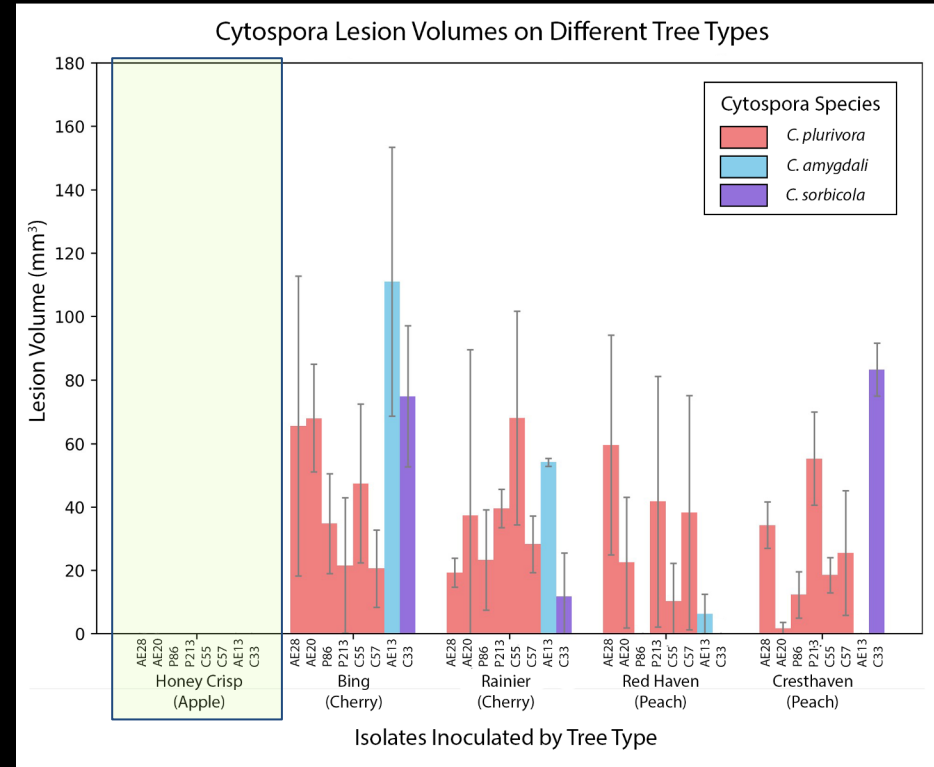- The data was then plotted using Python

Results

Cytospora Lesion Volumes on Different Tree Types

No *Cytospora* spp. caused significant lesions on apples

- There were no significantly large lesions on apples
- This trial is being repeated in the greenhouse to confirm these results

Cytospora Lesion Volumes on Different Tree Types

The Specialist: *C. amygdali*

- *C. amygdali* caused the largest lesions on both cherry cultivars
  - 111.04mm³ on Bing
  - 54.17mm³ on Rainier
- Only caused small lesions on Red Haven peaches; no significant lesions on Cresthaven peaches
- Likely a host specific pathogen
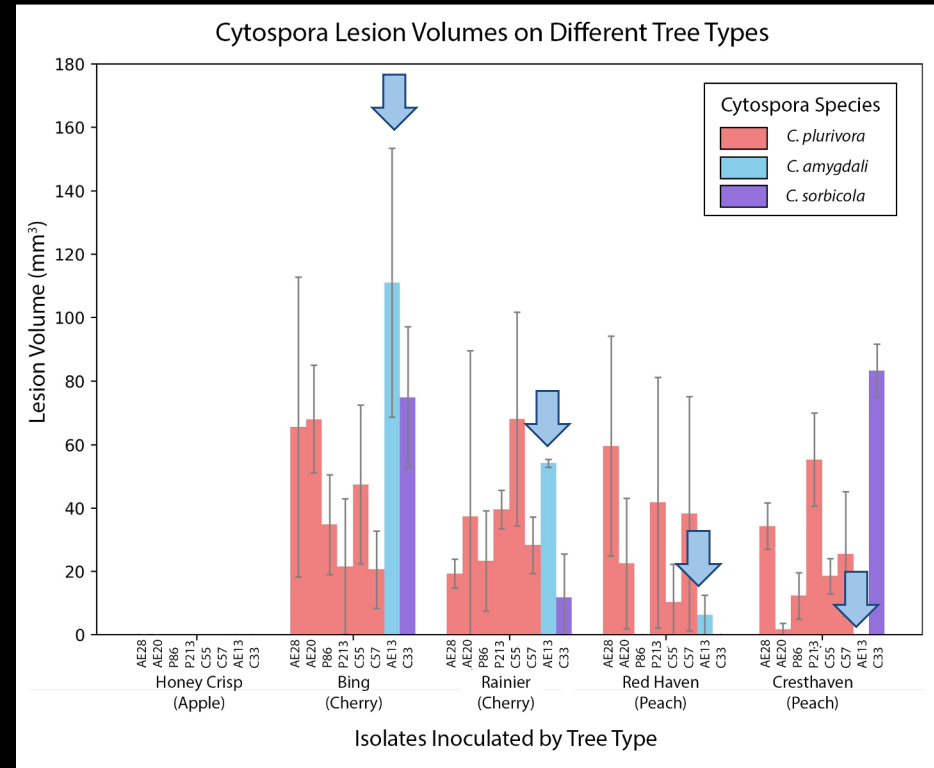
The Generalist: *C. plurivora*

- Almost all *C. plurivora* isolates caused significant lesions on both cultivars of peach and cherry
  - The only exceptions were:
  - P86 on Redhaven peaches
  - AE20 on Cresthaven peaches
- Likely a generalist pathogen
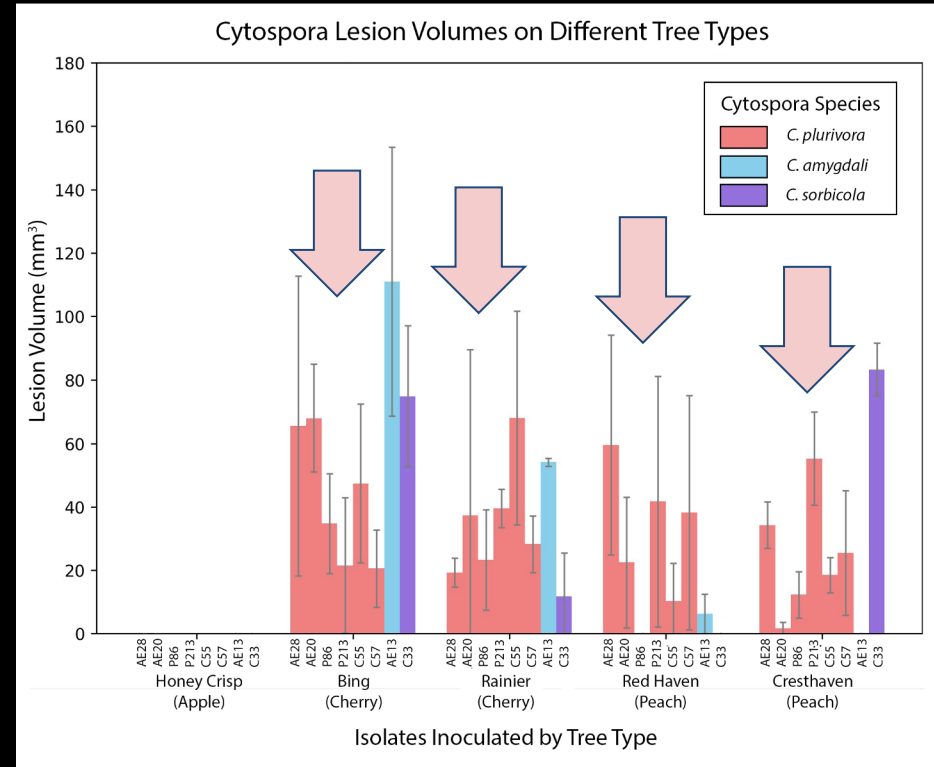
The Strange Case: *C. sorbicola*

- Produced large lesions on Bing cherries and Cresthaven peaches
- It also produced small lesions on Rainier cherries and no significant lesions on Red Haven peaches
- Could this be oddly host specific, or just a combination of errors?

Cytospora Lesion Volumes on Different Tree Types
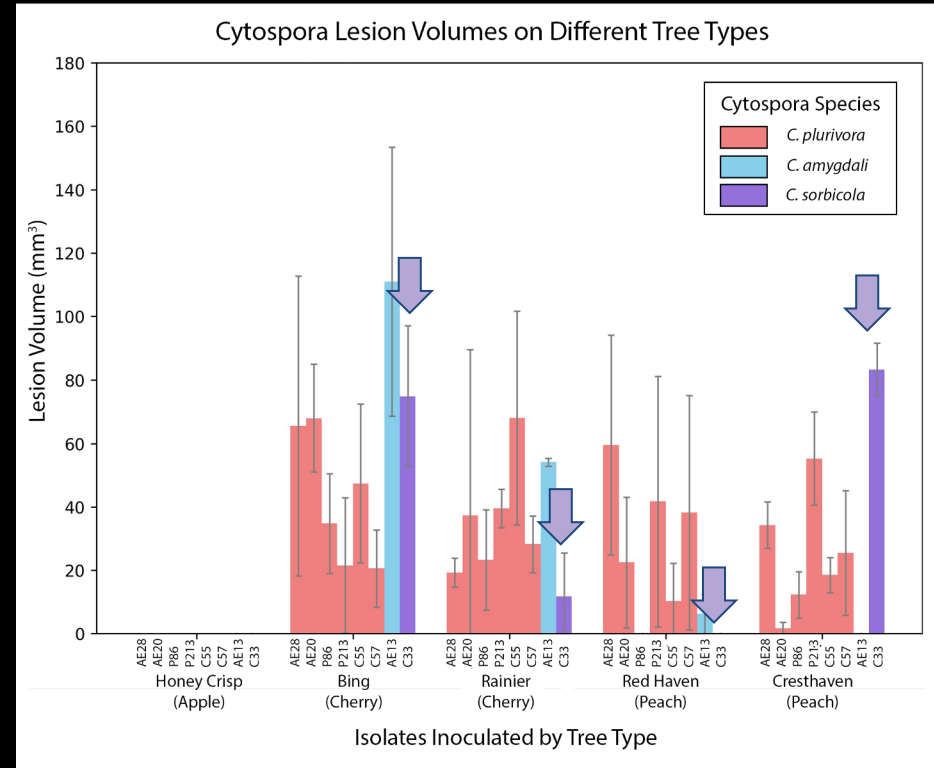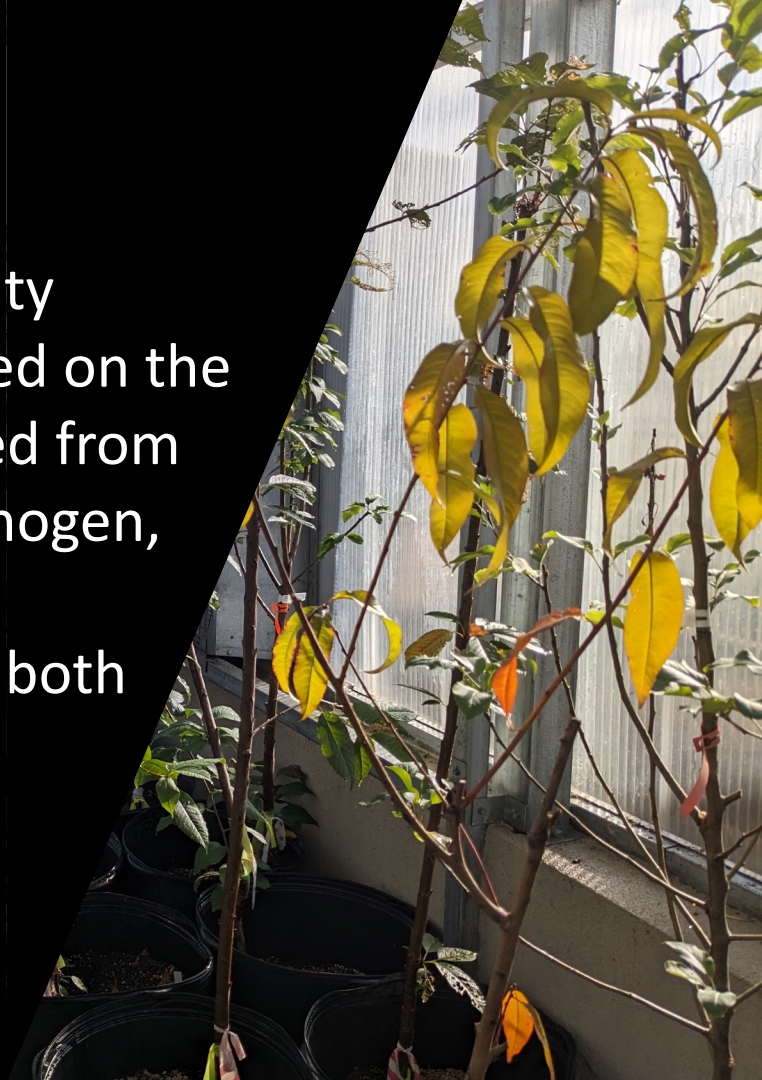
Potential Errors

- Japanese Beetles
- Uneven watering
- Agar plug selection

Conclusions

- There appears to be some host specificity among the *Cytospora* spp., but not based on the host species they were originally isolated from
- *C. amygdali* was the most selective pathogen, only impacting cherries
- *C. plurivora* was a generalist, impacting both peaches and cherries

Future Directions

- Redo inoculations to confirm that no isolates are pathogenic on apples

- Characterize the pathogenicity mechanisms of *Cytospora* species across host

- This work has already begun!

Acknowledgements

- Dr. Stewart and Dr. Ibarra Caballero for their mentorship
- Sal Greenberger for teaching me inoculation methods
- Stephan Miller for his help in data analysis
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