

## Accelerating Breeding for Pestalotia Resistance II

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### Summary

The UF Strawberry Breeding Program is prioritizing resistance to *Neopestalotiopsis* sp. Last year's project focused on incrementally increasing tolerance throughout the breeding program. This year's project focused on discovering a chromosome region behind strong resistance. We also released a new advanced selection FL 20.80-4 that is more resistant than current varieties and will be trialed with growers during the 2023-24 season. If all goes well, this new variety can be planted at commercial scale in Fall, 2024.

### Introduction

A new strain of *Pestalotia* caused by a species of *Neopestalotiopsis* has become a primary focus of the UF Strawberry Breeding Program. Current UF varieties do not have the resistance or tolerance needed to prevent plant and yield losses when plants come infected from nurseries. In the near-term, the program is working to increase incremental levels of tolerance. At present, many crosses are being made with strong resistance sources that were discovered in the previous year's project.

The breeding program currently uses DNA technology to predict the performance of seedlings before they are planted in the field, screening about 50,000 seedlings each year for multiple disease resistance and fruit quality traits. The remaining 15,000 seedlings are to be moved to the breeding nursery and ultimately to the fruiting field. We must now develop the same kind of tools to predict *Pestalotia* resistance, and we must do it as quickly as possible.

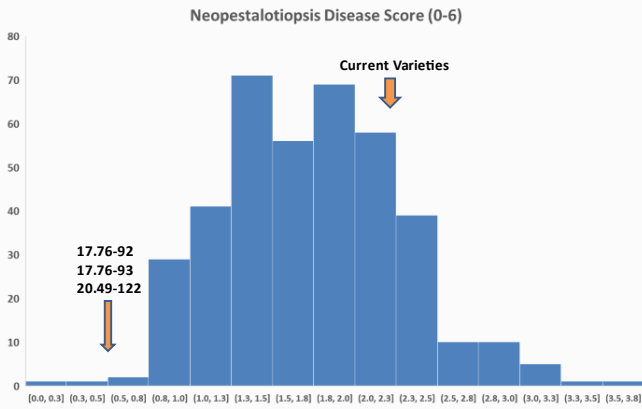
### Methods

The methods for this project are briefly summarized as follows:

1. More than 50 different crosses were made between elite UF varieties and selections and individuals in the breeding program with much stronger resistance compared to current varieties.
2. A subset of crosses and selections were inoculated with *Pestalotia* in the field, genotyped for 50,000 chromosome locations with DNA sequence variations or "markers", and subject to genome-wide association analysis (GWAS) to identify chromosome locations associated with strong resistance.
3. A DNA genotyping methodology for 500 chromosome locations developed in the previous year's project was utilized to select for 5,000 additional seedlings to select for increased resistance.

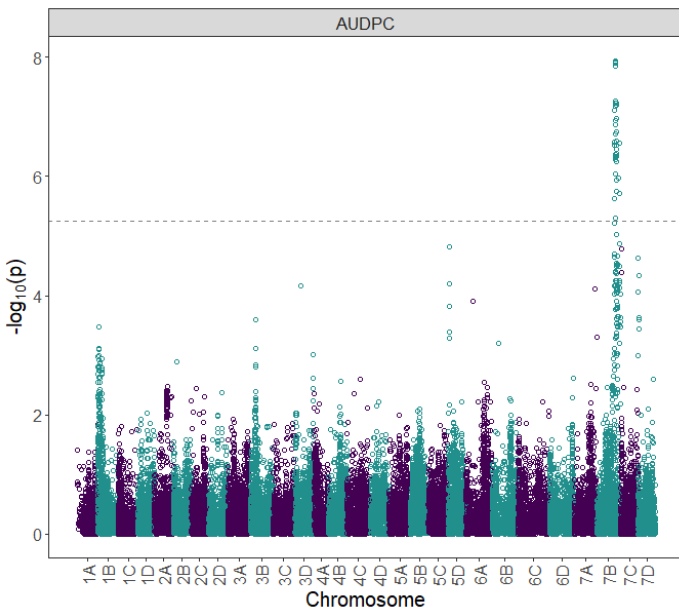
### Results

Inoculation of selections in the field over the last two years has shown that many selections in the breeding program currently have better tolerance than the commercial varieties. Fig. 1 shows the wide distribution of results across nearly 500 advanced selections, including a limited number of highly resistance selections (left side).



**Figure 1.** A wide distribution of tolerance and resistance among UF strawberry varieties and advanced selections.

The results of the GWAS analysis identified chromosome-locations (markers) that are associated with strong resistance (Fig. 2).



**Figure 2.** A GWAS analysis shows a strong peak on Chromosome 7B, indicating a gene for strong resistance at this location.

Some of these markers were incorporated into our newest genotyping panel, and approximately 2,100 seedlings from crosses with highly resistant material were selected so that only the most resistant 500 seedlings were sent to the summer nursery.

## Immediate and Long-Term Impacts

During the 2023-24 season, highly resistant seedlings from these crosses will be identified by inoculations, and candidates for cultivar release will be identified. Meanwhile, these resistant seedlings will also be crossed to material with the best yield and fruit quality, to further spread resistance into the entire breeding program.

## Takeaways

Selection FL 20.80-4 with incrementally improved resistance compared to Brilliance, Sensation and Medallion has been released and will be trialed with growers this fall. The commercial availability of this selection will be Fall, 2024. In the meantime, new selections have been made using DNA markers that will have much stronger resistance, with the hope that more resistant cultivars can be quickly identified.

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