

Accelerating Breeding for Pestalotia Resistance

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Summary

The UF Strawberry Breeding Program is prioritizing resistance to a new strain of Pestalotia that is impacting our industry. Numerous crosses have been made between elite UF varieties and selections and resistant germplasm. Chromosome locations that increase tolerance were identified. A custom panel of DNA markers was developed and utilized for 5,000 seedlings to select the 500 that are predicted to be the most tolerant. These seedlings will be evaluated in the field in the coming season.

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 tolerance needed to prevent plant and yield losses when plants have been infected from nurseries. In the near-term, the program is working to increase incremental levels of tolerance. In the long-term, elite UF materials are being crossed with materials outside the program that are highly resistant.

The breeding program currently uses DNA technology to predict the performance of seedlings before they are planted in the field, screening about 60,000 seedlings each year for multiple disease resistance and fruit quality traits. The 15,000 remaining seedlings move 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 40 different crosses were made between elite UF varieties and selections and individuals in the breeding program with increased tolerance compared to current varieties.
2. At the same time, crosses were made with highly resistant germplasm that originated outside the UF breeding program.
3. 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 that confer increased tolerance.
4. A DNA genotyping methodology was developed called SeqSNP for 500 chromosome locations that can be used to predict Pestalotia tolerance in larger numbers of seedlings.
5. The SeqSNP method was utilized to screen 5,000 seedlings

Results

Inoculation of selections in the field showed 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).

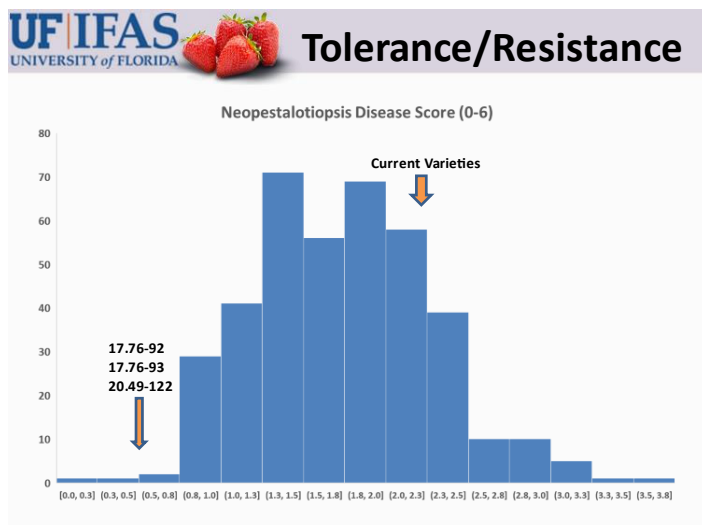


Figure 1. A wide distribution of tolerance and resistance among UF strawberry varieties and advanced selections.

The results of the GWAS analysis identified chromosome-locations (markers) that confer increased tolerance to Pestalotia (Fig. 2).

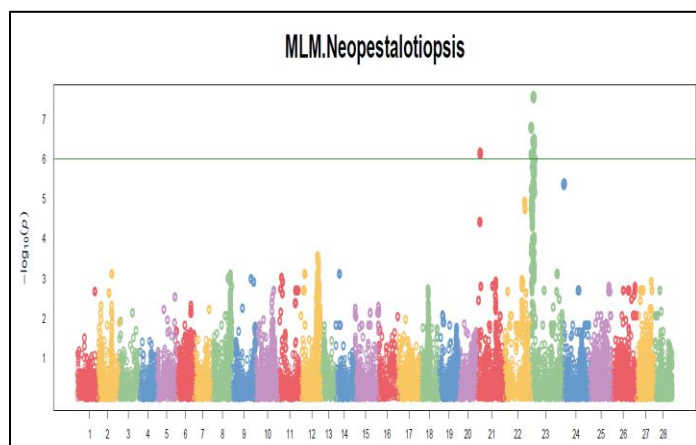


Figure 2. A GWAS analysis shows significant peaks indicating chromosome locations that increase tolerance to Pestalotia.

Finally, the DNA genotyping method called SeqSNP was applied to 5,000 seedlings, and 500 were retained that were predicted to have the highest tolerance to the disease. The remaining 4,500 were discarded. These 500 seedlings will be tested for fruit quality and yield traits in the upcoming season.

Immediate and Long-Term Impacts

The selection of 500 seedlings with increased Pestalotia tolerance is an immediate impact of this work. Additional trials and genotyping in the upcoming season will provide further evidence for tolerance loci and potentially allow the development of a smaller number of high-throughput markers to make this process even more efficient. Meanwhile the genetic basis of the strong resistance will also be studied in the upcoming season toward the development of genetic tools for high resistance levels.

Thank You

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