Combating Rose Rosette Disease: Breeding for Resistance

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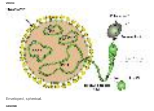
Introduction

In the past few decades, Rose Rosette Disease (RRD) has spread from its source in the Rockies, through the Mid-West to the East coast. It now threatens to decimate the US rose industry. Garden roses, which form the cornerstone of the multi-billion dollar landscape industry, annually generate wholesale US domestic bare root and container production valued at ~ $400 million. There is an urgent need to control RRD. Its cause, a novel plant virus, the Rose rosette virus (RRV) was first described in 2011 by the lab of Dr. Tzanetakis (Laney et al., 2011). It is transmitted by wind-blown eriophyid mites (Phyllocoptes fructiphilus). Unlike other rose diseases it kills a rose within two to three years.

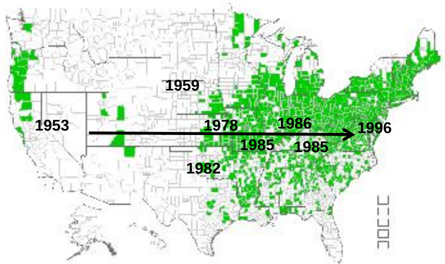
Virus, Vector, and Reservoir



Disease Symptoms Lead to Death

Distribution of Rosa multiflora and Movement of RRD

RRD moved from the western USA to the east coast over the last 60 years



Rosa multiflora is a large reservoir of the pathogen and the vector

Project Breeding Objectives

1. Phenotype for RRD resistance and horticultural traits
   a. 400 rose accessions
   b. Set of segregating rose populations
2. Create populations segregating for RRD resistance
3. Marker generation via genotyping by sequencing approach
4. Develop consensus map for the diploid rose
5. Identify markers associated with RRD resistance and horticultural traits using FlexQTL

Collaborators

Commercial Rose Breeders


Christian Bedard
Weeks Roses

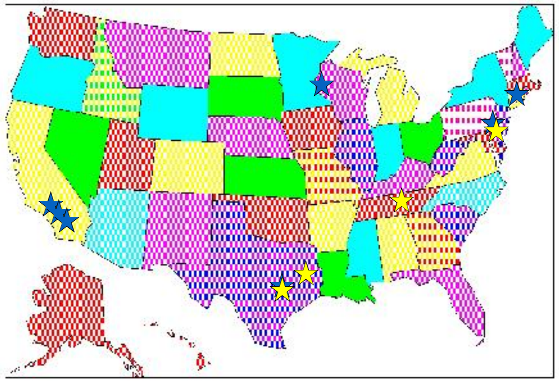

Ping Lim
Roses by Ping


Jim Sproul
Roses by Design


David Zlesak

Not pictured
Don Holeman


Michele Scheiber
NovaFlora



Plant Evaluators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FlexQTL – Pedigree-based analysis


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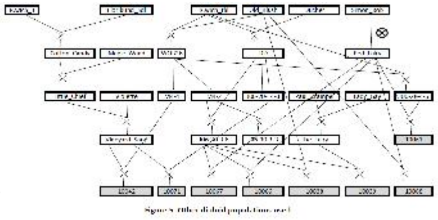
Advantages

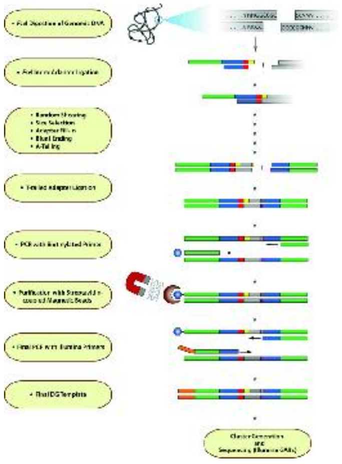
1. Designed for highly heterozygous crops
2. Analyses series of related populations
3. Marker-trait associations stable in wider germplasm base



Genotyping by Sequencing

Advantages

1. Deep multiplexing
2. Can target genic regions without repetitive DNA
3. Sequence based data
4. Redundancy and reproducibility
5. Ability to generate high numbers of markers inexpensively



Morishige et al., 2013. BMC Genomics 14: 448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Industry – Academic Collaborative Research

Interdisciplinary research: molecular genetics, plant breeding, plant pathology, plant physiology, statistics, plant production

Phenotyping

Measure the strength of resistance that a rose has to the disease organism.

QTL Analysis

Phenotype and marker data combined for identification of marker-trait associations with FlexQTL

Genotyping by Sequencing

Produce thousands of genetic tags or markers on rose chromosomes

Efficient introgression of RRD resistance and horticultural traits into new commercial roses

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