QTL Mapping of Botrytis bunch rot Resistance in a *Vitis aestivalis*-derived ‘Norton’-based Population

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Norton has been grown in Missouri for over 160 years, but little is known about the genetics of its disease resistance, cold hardiness and berry quality.

Vitis aestivalis-derived ‘Norton’
State Grape of Missouri
Genetics of Norton (Missouri State) Grapes

Norton has naturally evolved resistance to:
1. Powdery mildew
2. Downy mildew
3. Berry rot complex including *Botrytis*
   - Bunch rot, Bitter rot and Black rot
4. Insect Phylloxera
5. Cold hardiness
Norton vs Cabernet Sauvignon

**Vitis aestivalis**-derived ‘Norton’
Cold hardy and Resistant to most fungal pathogens
Good wine quality

**Vitis vinifera** ‘Cabernet Sauvignon’
Cold sensitive and Susceptible to most fungal pathogens
Great wine quality

A need exits to breed for grapevines that would combine the superior wine quality of *V. vinifera* with the disease resistance and cold hardiness of Norton.
Marker Development (PCR & DNA Sequencing)

1. Restriction Fragment Length Polymorphism (RFLP)
2. Random Amplified Polymorphic DNA (RAPD)
3. Amplified Fragment Length Polymorphism (AFLP)
4. Simple Sequence Repeats (SSRs)
5. Single Nucleotide Polymorphism (SNP)

- More than 1,000 SSR markers available in grape society
- Grape with a high level of “Heterozygosity”; SSR marker “Transferability” between populations
Genotyping
Norton Linkage Map Construction

1. 1,157 SSR markers were tested on the parents (Norton & Cabernet Sauvignon) and 4 progenies for polymorphism
2. 414 polymorphic markers were identified and screened through a 182 genotype population
3. 411 markers clustered in 19 linkage groups
There are 26 gaps larger than 10 cM.
**VitisGen I&II Project (2011-Present)**

- A 10-year project funded by the USDA-National Institute of Food and Agriculture (NIFA) Specialty Crops Research Initiative
- Combines the expertise of breeders, geneticists, pathologists, physiologists, chemists, enologists, computational biologists, sociologists, economists, and the grape industry
- 12 research institutions

**Participants:**
- Dr. Bruce Reisch
- Dr. Lance Cadle-Davidson

**Institutions:**
- USDA
- United States Department of Agriculture
- Agricultural Research Service
- Oklahoma State University
- Oklahoma City University
- Cornell University
- Cooperative Extension
- FAMU
- Florida Agricultural and Mechanical University
- Missouri State University
- University of Minnesota
- SDSU
- University of California
- Dalhousie University
- Inspiring Minds
VitisGen I Project

Genotyping

Genotyping-by-Seqencing (GBS)

Single Nucleotide Polymorphism (SNP)

A consensus map of 3,825 SNPs
A consensus map of 411 SSRs

Integration of Genetic Maps to construct a high-resolution map with both SSR and SNP markers using JoinMap 4.1 software
JoinMap 4.1

Norton Haploid Map (407 SSRs + 1665 SNPs)

There are only 4 gaps larger than 10 cM.

Theoretical and Applied Genetics (2019) 132: 137
Phenotyping
Botrytis Bunch Rot

*Botrytis cinerea*

Cabernet Sauvignon

Norton
# Botrytis Bunch Rot

*Botrytis cinerea*

## Table 1. Average disease incidence and severity between two grape cultivars; Norton and Cabernet Sauvignon (CS) under different stages.

<table>
<thead>
<tr>
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<tbody>
<tr>
<td></td>
<td>Norton</td>
<td>CS</td>
<td>Norton</td>
<td>CS</td>
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<tr>
<td>E-L Stage 36</td>
<td>4.2</td>
<td>100.0</td>
<td>8.3</td>
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<td>83.3</td>
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<td>91.7</td>
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<td>E-L Stage 40</td>
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<td>100.0</td>
<td>10.0</td>
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</table>

Values are mean for five replicates for each stage between two cultivars for both years. Significant differences (two-sampled t test) are designed at P>0.05.
Botrytis Bunch Rot

<table>
<thead>
<tr>
<th>Population Size</th>
<th>158</th>
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<tr>
<td>Repetitions</td>
<td>8</td>
</tr>
<tr>
<td>Duration</td>
<td>10 DAI</td>
</tr>
</tbody>
</table>

Disease Severity (%)
Genotypes
Year 2015

Disease severity (%)
Genotypes
Year 2016
Botrytis Bunch Rot Resistance

*LOD value of 7.5 explaining 20.4% of the total phenotypic variation flanked by markers VMC6F1 (36.8 cM) and VMC3B10 (44.4 cM) which are 7.6 cM apart.

*Five SNP-trait association were detected between the two flanking SSR markers, further reducing the interval distance to 0.8-2.1 cM.
Summary

1. GBS data can be used to saturate the grape genome with SNPs in a Norton x Cabernet Sauvignon mapping population.

2. SNPs and SSRs can have complementary roles: first, to identify genome regions associated with traits of interest using SNPs, and second, to perform marker-assisted selection using SSRs.
Summary
The overall goal of this program is to provide molecular genetic support to expedite grape breeding effort with the ultimate goal of improving viticultural performance and enological quality with new grape cultivars well adapted to Missouri conditions.
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