

Effect of Powdery Mildew Resistance on Phenolic Content of Inoculated *Vitis* Leaves

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Introduction

Genetic resistance to the economically damaging powdery mildew (*Erysiphe necator*) can improve the sustainability of viticultural control measures as demonstrated through the Ren3 and Ren9 resistance genes. These resistance genes trigger a hypersensitive response in tissues affected by powdery mildew.⁶ The hypersensitive response also causes changes in the expression of phenolic biosynthesis genes.² Phenolics are defensive compounds that may prevent the spread of powdery mildew in vines.¹ The rate of phenolic expression is in part determined by the resistance genes.² This experiment explored how the resistance genotype relates to the post inoculation phenolic content.



Figure 1. Powdery Mildew³

Materials and Methods

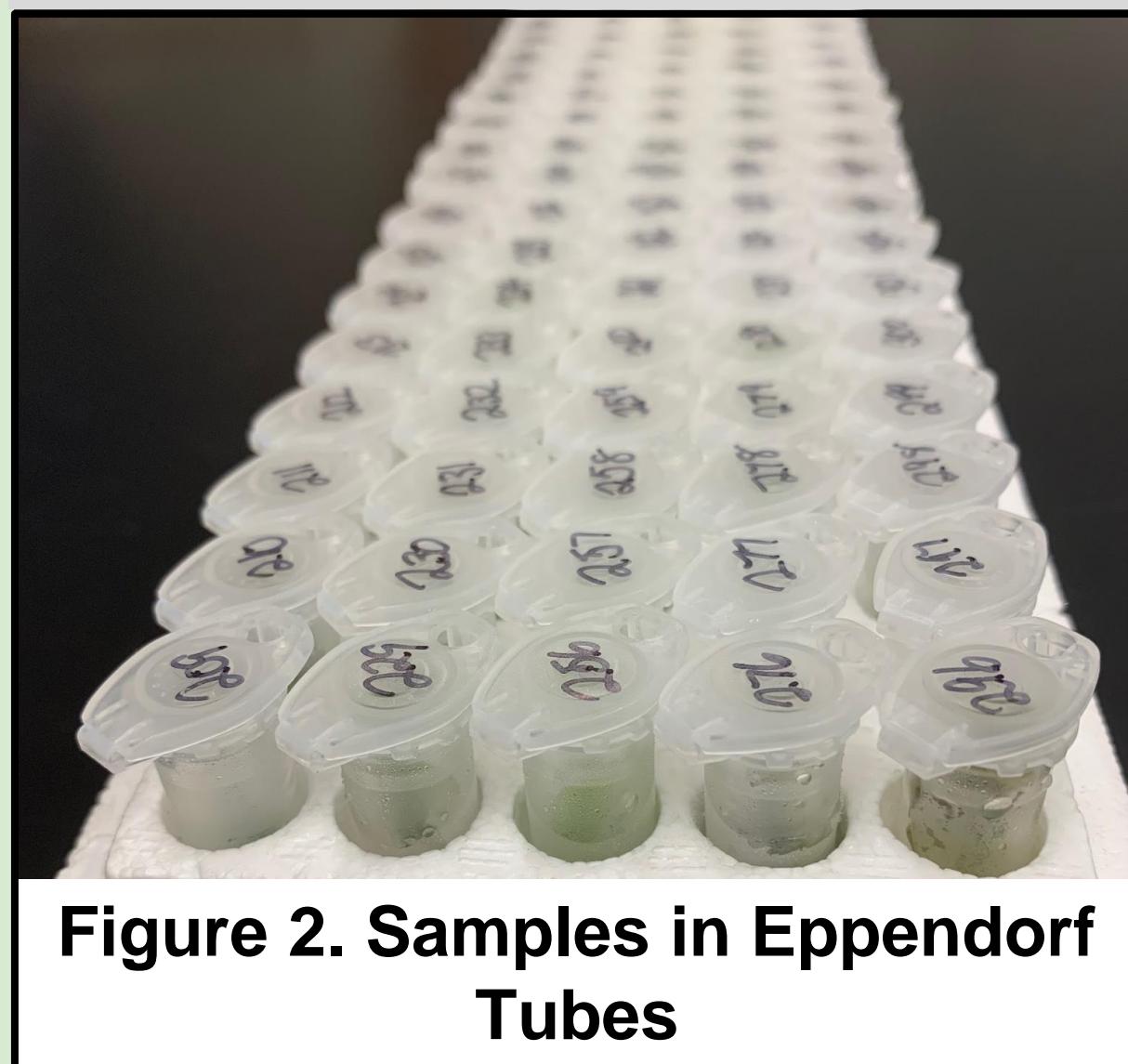


Figure 2. Samples in Eppendorf Tubes

Sample Collection

- The population of 103 individuals was divided into having both, either, or neither of the genotypes.
- Samples of analyzed leaves were taken at 8 days post inoculation (dpi) in duplicate with 2-3 leaf discs in each tube.



Figure 3. Vials Prepared for Extraction

HPLC Preparation

- These samples were
 - frozen in liquid nitrogen,
 - powderized,
 - suspended in a 1.5 mL solution of acidified methanol,
 - and filtered into amber vials for HPLC analysis.

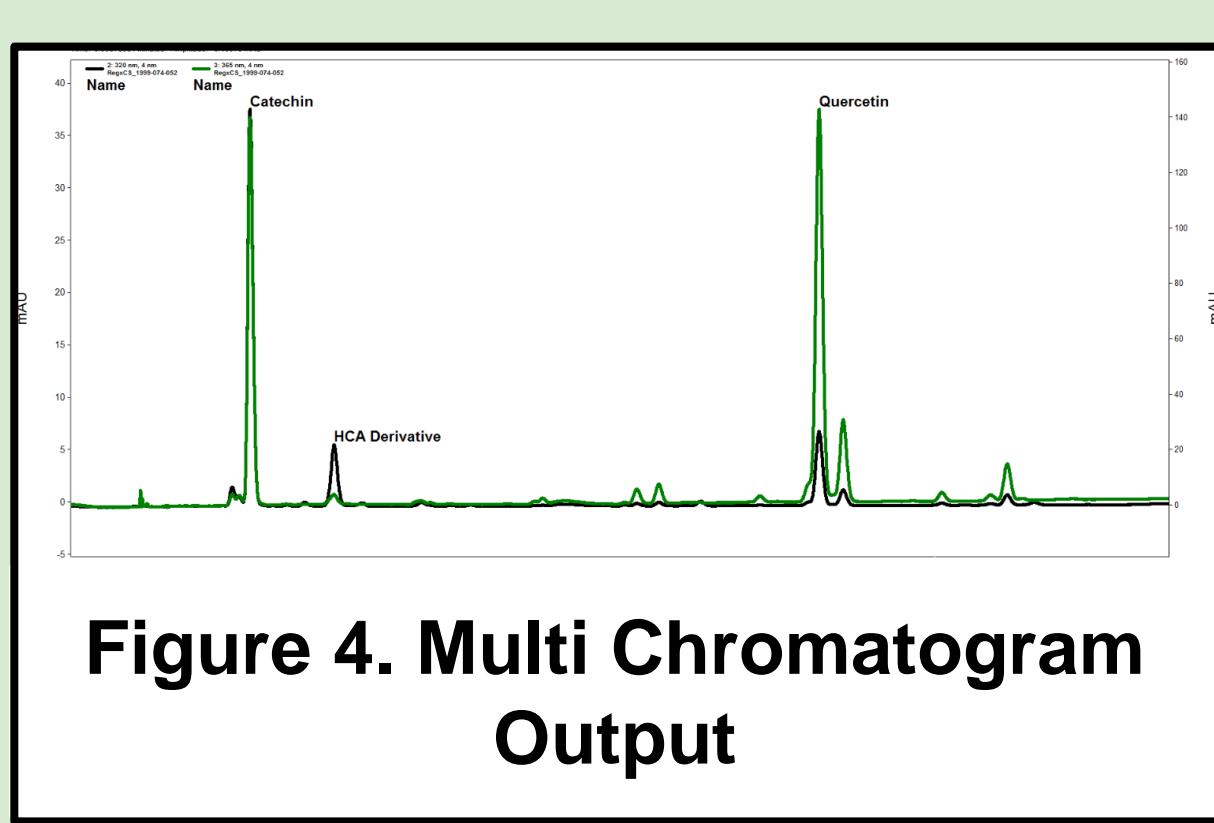


Figure 4. Multi Chromatogram Output

Analysis

- The major peaks found in the Multi Chromatogram were identified and quantified by peak area (mAU) and retention time.

References

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Acknowledgments

We are grateful to Benjamin Gutierrez, Lance Cadle-Davidson, and Daniel Zendler who supported and made this project possible and to the Cornell Geneva Summer Scholars Program partially funded by the N.J. Shaulis Advancement of Viticulture Fund, INC. for providing financial support to Lindsay Brown.

Results

- The major peaks include a catechin (A), a hydroxycinnamic acid derivative (B), and a quercetin (C).
- Ren3 had the highest overall phenolic content and Susceptible had the lowest.
- There is a strong correlation (>0.5) between the peak areas and the genotypes, respectively.

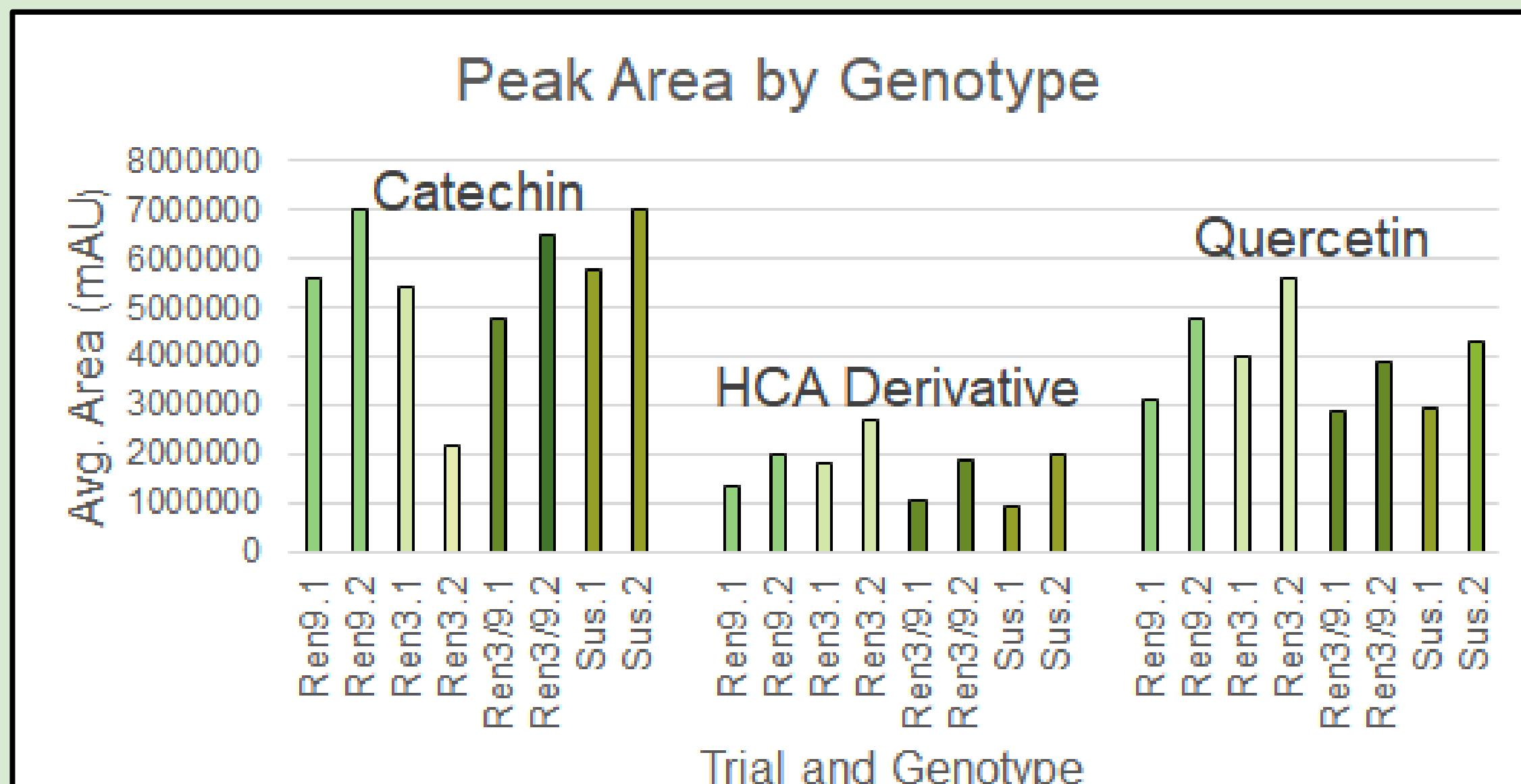
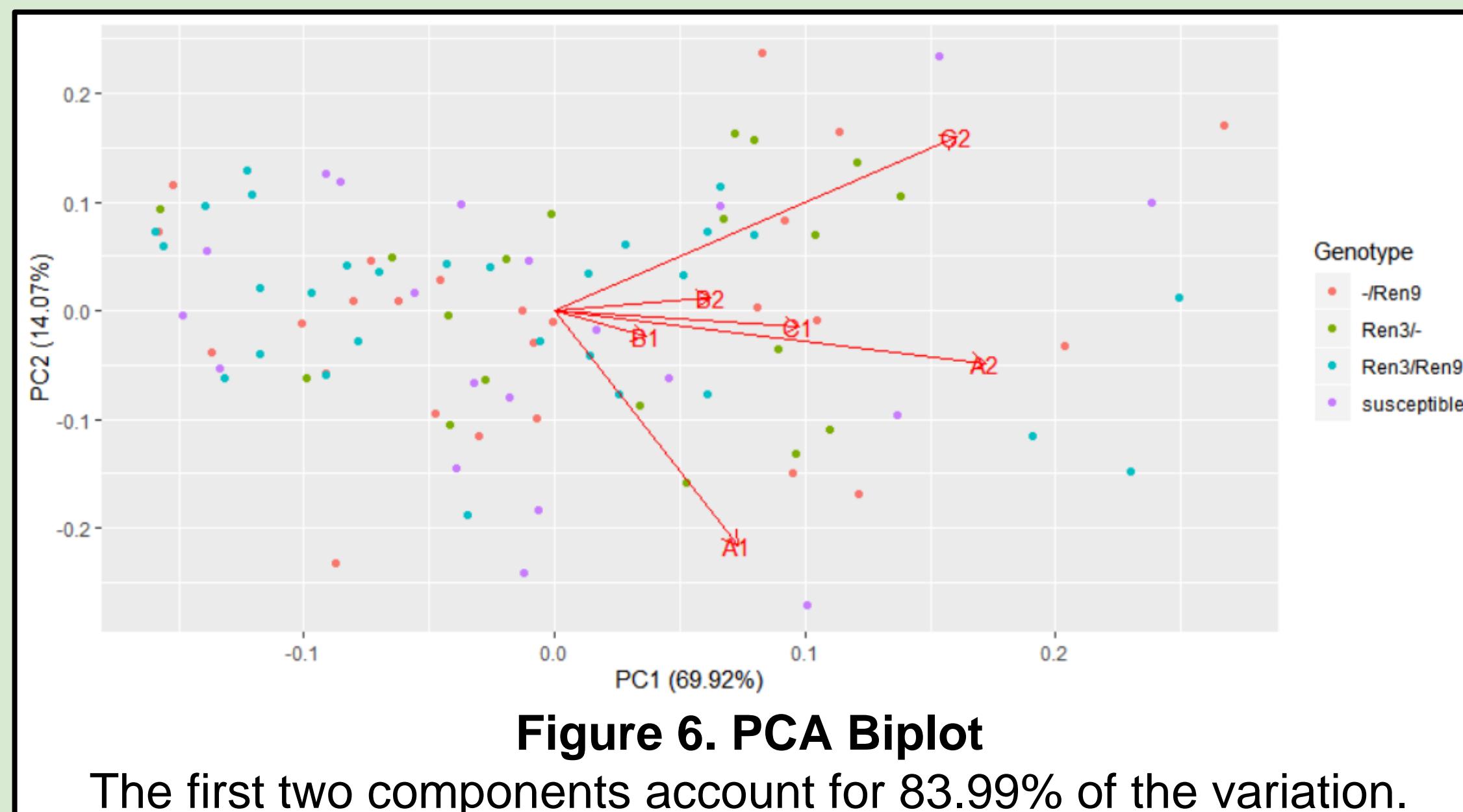


Figure 5. Area Comparison between Trials and Genotypes



The first two components account for 83.99% of the variation.

Discussion

- There was a stronger correlation within the trials than between them as can be seen in the PCA Biplot.
- The phenols found in these samples are produced and used as a defense response to the inoculum.
 - The expression of phenolic biosynthesis genes peaks at 12 hours post inoculation (hpi).
 - By 8 dpi, the concentration of these compounds could have decreased as they were used for disease prevention.
 - Thus, the phenolic concentrations present in these samples can either be indicative of the production or usage heightened by the resistance genotype.²

Conclusions

- An experiment with samples taken at 0 hpi, 12 hpi, 24 hpi, 72 hpi, and 120 hpi would encompass the most variation in the phenolic levels to fully demonstrate the impact of the genetic differences.
 - This would demonstrate endogenous differences, and the peak and decline of phenolic concentration.²

