

**AGRICULTURAL RESEARCH FOUNDATION
INTERIM REPORT
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TITLE: Assessment of aphid resistance in black raspberry and development of trait-associated molecular markers for breeding improvement

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SUMMARY:

Black raspberry is a minor but lucrative crop with most of the acreage in the U.S. grown in Oregon. One of the challenges for black raspberry growers is the rapid decline of plantings resulting from aphid-borne virus infection. The North American large raspberry aphid is a vector of *Black raspberry necrosis virus* (BRNV) and other viruses in the *Raspberry mosaic virus* complex, to which all available cultivars are susceptible. BRNV spreads rapidly in the field resulting in plantings that decline in as few as two or three growing seasons. Aphid resistance was discovered in each of three separate wild black raspberry populations collected from Simcoe, Ontario, Canada (ON), Gardiner, Maine, USA (ME), and Bath, Michigan, USA (MI). The objective of this study was to study the inheritance of the aphid resistance from a bi-parental population, ORUS 4812, resulting from a cross between the susceptible cultivar Munger and the resistant selection ORUS 4310-2 from MI. We constructed a linkage map using single nucleotide polymorphisms (SNP) markers through genotyping by sequencing (GBS) for the parents and identified a single locus, R_{MI} , on *Rubus* Linkage Group (RLG) 6 that is associated with resistance. The loci for the resistance from ON (Ag_4), ME (Ag_5), and MI (R_{MI}) appear to be separate loci on the same linkage group, RLG6. Association analysis suggests that loci from 15 regions on the black raspberry genome sequence alignment are significantly associated with resistance. Markers will be developed from these loci and screened for usefulness in distinguishing the MI resistance source

OBJECTIVES:

1. Identify the genetic locus responsible for the Michigan (MI) source of aphid resistance, and
2. Develop molecular markers for detecting aphid resistance that can be used by breeding programs to develop cultivars that will improve the ability of Oregon growers to grow black raspberries profitably.

PROCEDURES:

Plant Material: One full-sib family: ORUS 4812 = Munger x ORUS 4310-2 (MI) (62 progeny).

Genotyping By Sequencing (GBS): The protocol described by Elshire et al. (2011) was used to discover single nucleotide polymorphic (SNP) loci in the three half-sib populations.

Genetic Linkage Mapping: JoinMap 4.1 (Van Ooijen, 2006) was used to construct linkage maps for the three populations.

Association Analysis: GBS data were filtered so that 80% of single nucleotide polymorphic sites were represented in each genotype with minor allele frequencies >5%. General Linear Model in TASSEL was used for genotype-aphid resistance association.

SIGNIFICANT ACCOMPLISHMENTS TO DATE:

- 1- Constructed linkage map using SNP markers for the parents and identified a single locus, R_{MI} , on RLG6 that is associated with resistance.
- 2- Consensus mapping across three bi-parental populations suggests the resistance loci for the ON (Ag_4), ME (Ag_5), and MI (R_{MI}) sources are separate and linked.
- 3- Association analysis suggests that loci from 15 regions of the genome are significantly associated with resistance.

ADDITIONAL FUNDING RECEIVED DURING PROJECT TERM:

- The Northwest Center for Small Fruit Research, the Oregon Raspberry and Blackberry Commission, the Washington Red Raspberry Commission, the North American Raspberry and Blackberry Association and the USDA-ARS-SCRI.

FUTURE FUNDING POSSIBILITIES:

- To be determined

REFERENCES

Elshire RJ, Glaubitz JC, Sun Q, Poland JA, Kawamoto K, Buckler ES, Mitchell SE (2011) A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PLoS ONE 6: e19379

Van Ooijen JW (2006) JoinMap® 4, Software for the calculation of genetic linkage maps in experimental populations. *In*. Kyazma B.V., Wageningen, Netherlands

Figure 1. Consensus map of Rubus Linkage Group 6 (RLG 6) combining information from the three full-sib populations showing the relationship of the three aphid resistance loci (in blue font).

