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New Robinson Creek Cranberry Research Station

by Matthew Lippert
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UW Researchers recently had the opportunity to visit the site of the soon-to-be dedicated cranberry research station in Wisconsin, Robinson Creek Cranberry near Black River Falls. The site is easily accessible to Interstate 94 and is near much of the Central Wisconsin cranberry growing area. Robinson Creek currently has over 32 acres of producing cranberry beds, ranging from 1.5 to just over 6 acres in eleven cranberry beds.

The site has been actively managed for commercial production and is in good condition to be used immediately for research projects. The following photographs will help you visualize the potential of Robinson Creek Research Station.

[Figure A] This is the landscape, not part of the station, just across the county road from the research station. Much of the soil is sandy with mixed jack pine forest. The bluffs of the southwest Wisconsin driftless area are not very far in the distance.

[Figure B] Beautiful nearly-white sand occupies areas above the cranberry beds. The NRCS Soil Survey indicates the primary soil in the area is Tarr Sand with some small areas of various muck soils. Sand continues very deep in the soil profile. Even the muck soils are sand below one foot of soil depth.

[Figure C] Cranberry beds are primarily Stevens variety and have excellent weed control and dense canopy.

[Figure D] Most of the beds were established in the mid 1980's, with some renovation as recently as 2014. Most of the beds utilize above ground irrigation. Some have been renovated with buried irrigation.

[Figure E] Irrigation: Water is diverted from Robinson Creek which borders the north side of the marsh. There is a new hydro unit on the creek that was installed as part of the Farm Conservation Program's alternative energy pilot projects.

[Figure F] The property includes a workshop and storage area. A house and mobile home are also part of the property. The sale was made possible with efforts of the Jim Bible family, previous owners of Robinson Creek Cranberry. Over $600,000 was raised so far to the research foundation through the generous support of sponsors.

Cranberry Genetics and Genomics Lab (CGGL) Update 2017

by Juan Zalapa and the CGGL team members and collaborators
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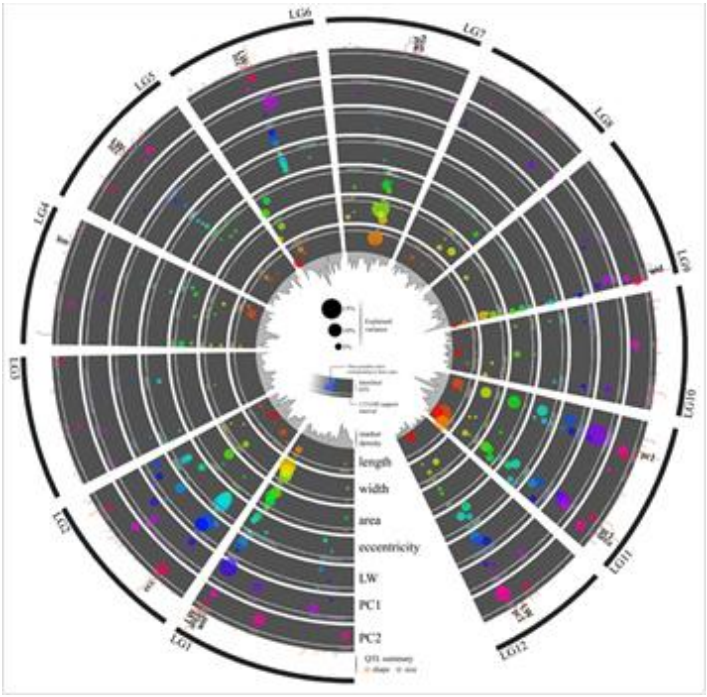
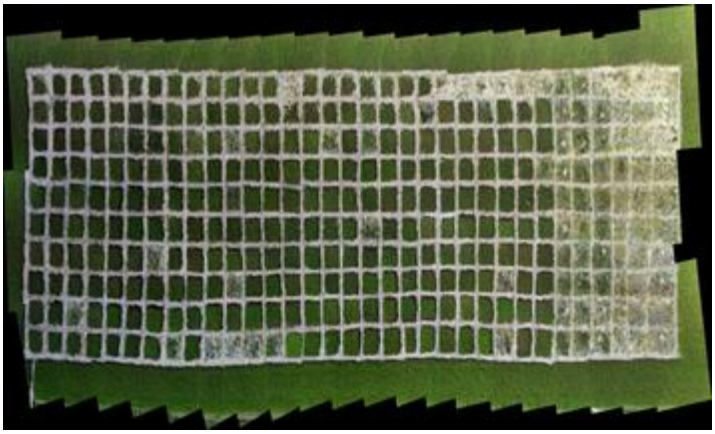
Phenotypic Data Collection: In the last five years, my lab and collaborators have been conducting the most complete study of cranberry traits ever conducted in the ~200 years of cranberry domestication and breeding history. We leveraged on 742 individuals from three current "elite" breeding populations to produce large amounts of phenotypic and field data useful for growers, breeders, and other scientists alike. The three invaluable elite biparental populations studied consisted of 72 ('Stevens' x 'Crimson Queen'), 236 ('Mullica Queen' x 'Crimson Queen'), and 434 (BGBLNL95 x 'GH1') clones. We collected three years of data in Wisconsin (W. Hatch, N. Hansen, E. Grygleski, P. Normington, and W. Normington) and New Jersey (N. Vorsa). We collected per plot data for total yield (g/900 cm2), total sound yield (rot), berry size and weight, total fruit anthocyanin content (mg/100g FW), soluble solids (Brix), titratable acidity, and proanthocyanidin. Additionally, we collected data on 10 individual uprights per plot to determine upright (vertical stem) length of current season's growth, dry weight of leaves, total number of flowers (pedicels with and without fruit), number of berries, number of aborted flowers (pedicels without fruit), berry weight and status of terminal bud (vegetative or reproductive), the biggest berry for each upright measured for length, width, weight, and calyx diameter, seeds counted and weighed for each fruit, and the fruit categorized based on calyx shape, skin, and seed characters. Additionally, we created two high-throughput image phenotyping software packages that greatly increased our ability to efficiently phenotype yield and quality traits. They can process different horticultural traits such as top yield per square area and fruit morphological parameters such as length, width, two-dimensional area, volume, projected skin, surface area, color, among other parameters. The phenotypic data generated was used or is currently being used to identify and localize marker-trait associations for horticulturally important traits in cranberry.

Molecular Mapping: This project produced the first high-quality genetic map in cranberry. We developed three parental consensus maps, one for each elite cross, and a composite high-resolution cranberry map (Schlautman et al. 2015; Covarrubias-Pazaran et al. 2016; Daverdin et al. 2017; Schlautman et al. 2017a). These maps are essential for any and all future cranberry

breeding or genetic studies to identify and integrate genes into breeding backgrounds and genotypes. The composite cranberry genetic map developed consists of transferrable and universal molecular markers of two types, simple sequence repeat (SSR) and single nucleotide polymorphic (SNP) markers. First, SSR markers were derived from next-generation sequencing (NGS) data available from the New Jersey and Wisconsin. SSR mining of NGS data resulted in the development of SSR markers sets consisting of 697, 54 and 61 useful SSRs. The SNP markers were derived from genotyping by genotyping by sequencing (GBS) experiments. The composite map was anchored with universal SSR markers. Subsequently, the SSR backbone map was augmented using SNP markers, and a composite cranberry map was developed containing 6073 markers (5437 SNPs and 636 SSRs) to represent the 12 cranberry chromosomes (Schlautman et al. 2017a). This high-resolution molecular map is an essential prerequisite for the genetic mapping of important traits and future marker-assisted selection in cranberry. Additionally, we developed two software packages that greatly increase the efficiency of SSR scoring, and facilitate the creation and visualization of genetic data resulting from genetic mapping studies. We also applied the SSR markers in genetic diversity and fingerprinting studies and evaluated genotype purity impacts on productivity and trait performance. Finally, we transferred the SSR markers to blueberry and developed a molecular map for comparative traits mapping and evolution studies in cranberry and blueberry (Schlautman et al. 2017b).



Marker-Trait Associations Discovery: For each mapping cross, we combined the phenotypic data and molecular map to establish the associations between traits and genetic markers. For each trait, we identified and localized map positions of markers-trait association. We also investigated the genetic correlations among traits, and the genetic effect interactions in each cross. Hundreds of marker trait-associations have been identified and localized in the composite high-resolution cranberry molecular map within and among genetic backgrounds for total yield, biennial bearing, fruit weight and size, fruit rot, fruit shape, anthocyanin content (mg/100g FW), soluble solids (Brix), titratable acidity, and proanthocyanidin. All the information is currently being compiled in the composite high-resolution cranberry molecular map. The construction of such composite high-resolution molecular map with trait-makers associations is one of the most important accomplishment in ~200 years of cranberry domestication, breeding, and genetics work.



Future Work: We have been working to provide growers and breeders phenotypic and molecular data to increase breeding efficiency. We have collaborated with Valley Corporation (E. Grygleski), Cranberry Creek Cranberries (W. Hatch, N. Hansen), Rutgers (N. Vorsa), and Saddle Mound Cranberries (P. Normington and W. Normington) to establish plantings, collect trait data, and generate molecular resources for trait mapping. Currently, available trait and molecular data on the three breeding populations studied is being used to determine superior individuals to be released to growers. For the next 5 years, we plan to keep collecting trait information to continue trait-mapping, conduct fine mapping to identify candidate genes, and develop molecular breeding methods based on the markers and genes identified. Traits such as anthocyanin content and color imaging resulted in excellent correlations with the available data collected, thus the identified genetic effects were very strong and will be easily usable for molecular breeding applications in the short-term. For complex traits such as yield that is affected by biennial bearing, our initial analyses indicate that more data is needed to refine the statistical prediction models, thus we will continue to collect productivity data and test methodologies to facilitate data collection, e.g., digital imaging, hyperspectral, microwave, etc.

Additionally, we plan to map new traits such as fruit firmness and other fruit quality traits, particularly those related to the health properties of cranberries. In the future, the accumulated information in cranberry regarding phenotypic and genetic associations will make it possible to build invaluable statistical and genetic models for selection that will significantly reduce the time and effort to breed superior cranberry cultivars.

We are currently moving forward with next-generation breeding at USDA-ARS and UW using molecular tools at the new Cranberry Research Station (Figure 1). The study of horticultural and commercially important traits and the identification of marker-trait associations will allow us to use molecular information in conjunction with traditional plant breeding to develop a molecular-assisted selection breeding program. We have already began using molecular markers to test the available Stevens beds Wisconsin Cranberry Station for genetic purity (Figure 1). Based on the genetic results and available yield data, best decisions will be made about renovation priorities for the 10 productions beds at the station. For our breeding plots, and based on our genetic research, our goal is to create new breeding stocks and genetically interesting populations to be planted in statistically augmented designs at the new Wisconsin Cranberry Station. Interesting segregating bi-parental populations and accessions will also be replicated throughout Wisconsin to test performance for our different growers. We have also been accumulating hundreds of cultivated cranberry accessions and seeds from elite crosses that we will plant at the station in statistically augmented and replicated designs. We also have hundreds of wild cranberry accessions preserved as potted plants in our UW-Madison greenhouses that we will plant in statistically augmented designs at the station. In this regard, we recently completed an exhaustive search and genetic analysis of wild cranberry populations in the U.S. We have detailed information about different habitats and genetic parameter information of many populations around the country, particularly about locations never explored before in Wisconsin and Minnesota. We plan to use these wild collections for breeding to preserve genetic diversity and bring new traits into cultivated varieties, particularly cold tolerance and other stress and pest related traits.

Figure 1. Google earth aerial photograph of the new Cranberry Research Station DNA purity testing.

In order to increase the number of breeding materials in our collection, in 2017, we gathered 8-12 fruit bearing uprights for most of the almost 100 varieties planted at the Dubay breeding collection. Our goal is to assess the Dubay collection in terms of genetic purity and integrity and preserve the unique genotypes identified as a part of our collection at the new Wisconsin Cranberry Station. Also, in 2017, we established a high-density planting consisting of 846 plants at Saddle Mound Cranberries. The planting consist of 132 Pilgrim selfs, 166 Stevens selfs, 80 HyRed selfs, 127 Sundance selfs, 95 BenLear selfs, 81 PilgrimxLeMunyon selfs, 82 Stevens controls, 73 unique wild cranberries, and 10 BL x LeMunyon crosses. This planting was established using molecular information derived from our previous studies. Our goal is to leverage all available and future genetic information to conduct a molecular-assisted, inbred/hybrid cranberry breeding program. The high-density planting at Saddle Mound will serve as a model to provide information to plan the establishment of our breeding plantings at new the Wisconsin Cranberry Station.

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GROWER UPDATE

SARATOGA CRANBERRY COMPANY

Harvest began later than usual waiting for our 'Stevens" to color up. When we finally received the okay to begin the second week of October, we lucked out and had a beautiful week of weather. The crop was down from our average; the biggest culprits being early hail, a cold growing season, and heavy sanding from this past spring. Now post-harvest, we are in the process of putting equipment and implements away, winterizing the property and pre-stacking the splash boards for winter flooding. In our down time within the coming months, we have all sorts of projects planned with the biggest one being the construction of a new pump house.

Russell Sawyer

The workman pulls the tines,
the vines yield their red fruit.
On the marsh all is right,
and life is good.
Another year of blessing,
a future bright with hope.
-Anonymous

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