

Improved and Novel Resources for Blueberry Mapping and Genomics

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Introduction

- Blueberry is one of the few crops that native to North America, and is the 2nd most important small fruit in the United States
- United States is the world largest blueberry producer and North Carolina is one of the largest blueberry producing states
- Potential health benefits include anti-cancer activity, protection against age related cognitive decline, and reducing the incidence of diabetes
- Blueberry contains high antioxidant content, presumably attributed to high anthocyanin concentration
- Blueberry breeding programs are arduous because of:
 - Long juvenile period (3+ years)
 - Inbreeding depression (self-incompatibility)
 - Complex ploidy level, includes diploid, tetraploid, and hexaploid 2015
- North Carolina State University is one of the research institutes/universities that study blueberry genome, aiming to develop advent genomic tools for breeding programs

Other Linkage Map Populations

- Four sources of genetic linkage maps were included:
- Diploid blueberry
 - Dr. Jeannine Rowland, USDA-ARS, Beltsville, MD
- Tetraploid blueberry
 - Dr. Nahla Bassil, USDA-ARS, Corvallis, OR
- Dr. Susan McCallum, The James Hutton Institute, Scotland
- Interspecific hybrid of blueberry x sparkleberry Dr. James Olmstead, University of Florida
- Cranberry (Georgi et al., 2013)



Sparkleberry (V. arboreum)



Draper Jewel Tetraploid blueberry population Fla4B x W85-20 corvmbosun F₁ #10 x W85-23 V. corymbosum

screening population Diploid blueberry population



Cranberry (V. macrocarpon)

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- Overall, SNPs were more powerful in scaffold assignment
- In both tetraploid map (Jewel and Draper), more than 300 scaffolds assigned to each map with the total size of > 100 Mbp
- The total of 686 scaffolds were assigned to at least one linkage map
- The size of these scaffolds (214 Mbp) represented about 44% of the estimate blueberry haploid genome (608 Mbp)

Fig 3. Scaffold assignment results. Using one linkage group from each map as example: Jewel LG 03a, Draper LG 8, interspecific hybrid LG 10, cranberry LG 4, and diploid blueberry LG 01b. Scaffolds assigned to a linkage group repeatedly were marked in the same color.

Objective 4 – Identify genes in anthocyanin biosynthesis

Using scaffolds as anchors to link markers on different linkage maps

- In most cases, linkage map comparisons between different populations are not effective. This might due to:
- SSR markers are less specific (multiple hits when aligning to whole-genome sequences)
- Errors in the linkage maps (linkage maps of both tetraploid blueberry parents and interspecific hybrid were not completed at the time)

Fig. 4. Consensus linkage maps that consisted of Draper linkage group 12 (D12), interspecific hybrid linkage group 10 (FL 10), Jewel linkage group 12a (J12a), and Diploid linkage group 10 (DI10). Each line that linked to two markers indicates that both markers were assigned to the same scaffold. The number following scaffold number is the size (bp) of the scaffold.

Objective 3 – Consensus Map Comparison

Table 1. BLAST results of genes involved in anthocyanin biosynthesis pathway, using grapevine (Vitis vinifera) as reference and align against diploid blueberry genomic sequences of W85-23. With PAL (phenylalanine ammonia lyase), 4 CL (4coumarate:CoA ligase), and CHI (chalcone Isomerase) as examples.

E-value	Length	Annotation	Locus Name	Entry	Organism
anine ammonia lyase)					
6.00E-66	431	71156_t	-	-	-
		model.g25340.t1	-	-	-
0	1748	CUFF.1944.1	Potri.008G038200.1	EC-4.3.1.24	Populus trichocarpa
0	1748	CUFF.51381.1	Potri.010G224100.1	EC-4.3.1.24	Populus trichocarpa
rate:CoA ligase)					
E-141	1004	CUFF.31671.1	Glyma11g01240.1	EC-6.2.1.12	Glycine max
6.00E-65	653	CUFF.16581.1	cassava4.1_027178m	EC-6.2.1.12	Manihot esculenta
1.00E-64	1232	15863_t	-	-	-
		model.g5996.t1	-	-	-
7.00E-48	197	CUFF.4.1	-	gi 297737319	Vitis vinifera
2.00E-44	895	CUFF.46453.1	-	EC-6.2.1 3	Carica papaya
lsomerase)					
2.00E-29	224	CUFF.50629.1	GSVIVT01032619001	EC-5.5.1.6	Vitis vinifera
1.00E-11	164	-	-	-	-
2.00E-05	156	CUFF.37529.1	GSVIVT01032685001	EC-5.5.1.6	Vitis vinifera

After collecting annotation data from IGB, the putative genes of blueberry were named after the scaffold location. The location, gene length, locus name and the reference organism are included in table 1