

A High Quality Draft Assembly of the Diploid 'Regina' Sweet Cherry Genome

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SUMMARY

Sweet cherry (*Prunus avium* L.) is a diploid species with an estimated genome size of 338 MB (Arumuganathan et al. 1991). It is mostly self-incompatible, and therefore has a heterozygous genetic background. We have sequenced and assembled the genome of the 'Regina' sweet cherry variety, which is a late blooming cultivar. Here we present a draft phased sweet cherry genome assembly using a combination of sequencing strategies (long reads sequencing with PacBio RSII and optical mapping with BioNano whole-genome maps).

PacBio Sequencing
RSII P6-C4 chemistry
30 SMRT cells

PacBio Assembly
Falcon and FalconUnzip

Optical Mapping
Bionano

Total (30SMRT Cells)	
Number of bases	27,9 billions
N50	17,5kb
Depth	82,5 x

	PacBio assembly Falcon (draft)	PacBio assembly FalconUnzip (polished primary contigs)	PacBio assembly FalconUnzip (polished haplotigs)
# contigs	2019	1078	1289
N50 (Mb)	1,2	1,23	0,35
L50	77	68	150
Max Size (Mb)	10,7	10,5	1,83
total Size (Mb)	339	323	177
% genome coverage (338 Mb)	100 %	95 %	52 %

Nicking enzyme	BssS1
Theoretical nb labels/100kb	13,6
Real nb labels/100kb	11
Filtered data >100kb (Gb)	156(459X)
Molecules N50 (kb)	178

Bionano Assembly	
# contigs	433
Median length (Mb)	0,809
N50 (Mb)	1,7
Max Size (Mb)	9,9
total Size (Mb)	535
% genome coverage (338 Mb)	158

Hybrid Assembly: Scaffolding

Assessment of genome assembly : BUSCO (V2.0)

Contig set	PacBio FalconUnzip Primary + Haplotigs	Hybrid Assembly scaffolds	Hybrid Assembly scaffolds + not scaffolded PacBio Contigs	Hybrid Assembly scaffolds + not scaffolded PacBio Contigs + FalconUnzip haplotigs
Complete	95,6%	90,9%	93,6%	95,9%
Duplicated	48,5%	2,9%	5%	46,5%
Fragmented	1,3%	2,1%	1,7%	1,1%
Missing	3,1%	7%	4,7%	3%

PacBio polished primary contigs + bionano assembly

# scaffolds	92
Median length (Mb)	1,9
N50 (Mb)	5,96
Max Size (Mb)	16,3
total Size (Mb)	279
% genome coverage (338 Mb)	83%

Hybrid scaffolds + not scaffolded PacBio contigs : 338Mb

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CONCLUSION

PacBio long reads were de novo assembled using FALCON assembler and phased using FALCON UNZIP. BioNano optical whole genome maps were used for further scaffolding. Our de novo genome assembly resulted in a genome of 279 Mb (83 % of estimated genome size), 92 scaffolds and a largest scaffold of 16,3 Mb. The assembly has high contiguity (contig N50 1,23Mb, scaffold N50 ~6Mb) and good completeness with 95,9% BUSCO genes complete (scaffolds+ unscaffolded contigs). We are now in the process of reconstructing the pseudo molecules using high density genetic linkage maps and GBS data. Structural annotation is on the way using the integrative EuGene platform with different sources of evidence available for gene prediction including transcriptomic data from Regina obtained previously in the lab (Unigene set and RNASeq).

