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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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The PacBio sequencing was done by the GeT-PlaGe INRA platform (<http://get.genotoul.fr/>) and the optical map was performed by INRA CNRGV (<http://cnrgv.toulouse.inra.fr/>). We are grateful to the genotoul bioinformatics platform Toulouse Midi-Pyrenees (Bioinfo Genotoul) for providing computing and storage resources.

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).

