Updated Apple Genomics at GDR


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Agricoltura Migliore output con minore input
Fondazione Edmund Mach
Alimentazione
Center of Research & Innovation

‘Golden Delicious’ genome v1.0
- Sequencing and assembly
  - Whole-genome shotgun
    - 16.9x coverage
    - 103,076 contigs included in 1,629 scaffolds
    - Total contig length 603.9 Mb
    - 81.3% apple genome
  - 598.3 Mb (439 scaffolds) anchored to genetic map
- Estimated genome size 742.3 Mb
  - 57,386 predicted genes (93% mapped)

‘Golden Delicious’ genome v3.0
- Re-sequencing (Illumina, SOLID)
  - SOLID 40x coverage (mate pairs 5 Kb)
  - 81,815 contigs included in 10,805 scaffolds
  - Total contig length 806 Mb (two haplotypes)
    - N50: 14.5 Kb; L50: 14.9 Kb
    - Size overestimation due to heterozygosity
  - 595 Mb anchored (65,537 contigs ordered along the chromosomes, >80% of the total contigs)
  - new markers anchored to 21 genetic maps (Di Pierro et al. submitted)
    - 18,019 markers 17 linkage groups
    - unique transcripts mapped on the genome

Revised SNP pipeline towards 487K Affymetrix array
- 63 cultivars, more diversity
- 10-40x Illumina re-seq
- 12.7 Millions quality filtered SNPs
- 487K SNPs evenly distributed along the genome
- GWAS on 1300 accessions (entire EU germplasm collection)

Factorial component analysis (FCA) over ~1800 unique diploid genotypes/accessions

Affimetrix Axiom® array

Comparison between resequenced cultivars

Revision SNP pipeline towards 487K Affymetrix array
Improving assembly of apple genome

- Phasing Golden Delicious with 20K SNP array
- Identifying GD haplotypes in the two di-haploids
- Aligning GD contigs against DHs contigs
- Merging only GD contigs that target same DH

Align GD Contigs
vs DHs Contigs

Merging only 2 contigs

‘Golden Delicious’ Double Haploid

Re-sequencing (Illumina, PacBio, BioNano)
- ~120x Illumina PE, ~60x Illumina MF,
- ~35x PacBio, ~600x BioNano
- Assembled in:
  - 1,081 assembled sequences
  - Contigs N50: ~70kb; scaffolds N50: ~5.6Mb
- 649 Mb anchored [362 scaffolds x 111 single contigs ordered along the chromosomes] using 21 genetic maps and 15,417 markers in 17 linkage groups (Bianco et al. Pl. Journal; Di Pierro et al. submitted)
- 45 Mb unanchored (LG0)
- 44,105 predicted genes

(Di Pierro, et al., submitted)

Application of the Axiom®Apple 487K SNP array for Genome Wide Association Studies

Genome Wide Association components

- Very high density genotyping
  Affymetrix Axiom Apple487K array
- Phenotypic data (e.g., phenology)

Scoring
Detection

Genetic vs physical position

Application of the Axiom® Apple 487K SNP array for Genome Wide Association Studies

Flowering period
Harvest date

Manhattan plots (A-B) and quantile-quantile plots (C-D) of association analysis for flowering period (A, C) and harvest date (B, D) using a model including structure and kinship.

Kindly supplied by Charles-Eric Durel

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Malus Resources in GDR

Riccardo Velasco, Sook Jung, Taein Lee, Chun-Huai Cheng, Ping Zheng, Jodi Humann, Sushan Ru, Kristin Scott, Morgan Frank, Heidi Haugh, Jing Yu, Ksenija Gasic, Jim McFerson, Kate Evans, Cameron Peace, Lisa DeVetter, Mike Kahn, Dorrie Main

**Talk overview**

- Apple Resources in GDR
- New genome Assembly of Malus x domestica