

Development and Validation of a 20K Single Nucleotide Polymorphism (SNP) Whole Genome Genotyping Array for Apple (*Malus × domestica* Borkh)

Submitted by Emmanuel Lemoine on Thu, 02/12/2015 - 13:18

Titre Development and Validation of a 20K Single Nucleotide Polymorphism (SNP) Whole Genome Genotyping Array for Apple (*Malus × domestica* Borkh)

Type de publication Article de revue

Auteur Bianco, Luca [1], Cestaro, Alessandro [2], Sargent, Daniel James [3], Banchi, Elisa [4], Derdak, Sophia [5], Di Guardo, Mario [6], Salvi, Silvio [7], Jansen, Johannes [8], Viola, Roberto [9], Gut, Ivo [10], Laurens, Franois [11], Chagn , David [12], Velasco, Riccardo [13], Van de Weg, Eric [14], Troggio, Michela [15]

Editeur Public Library of Science

Type Article scientifique dans une revue   comit  de lecture

Ann e 2014

Langue Anglais

Date 2014/10/10

Num ro 10

Volume 9

Titre de la revue PLoS ONE

R sum  en anglais

High-density SNP arrays for genome-wide assessment of allelic variation have made high resolution genetic characterization of crop germplasm feasible. A medium density array for apple, the IRSC 8 K SNP array, has been successfully developed and used for screens of bi-parental populations. However, the number of robust and well-distributed markers contained on this array was not sufficient to perform genome-wide association analyses in wider germplasm sets, or Pedigree-Based Analysis at high precision, because of rapid decay of linkage disequilibrium. We describe the development of an Illumina Infinium array targeting 20 K SNPs. The SNPs were predicted from re-sequencing data derived from the genomes of 13 *Malus × domestica* apple cultivars and one accession belonging to a crab apple species (*M. micromalus*). A pipeline for SNP selection was devised that avoided the pitfalls associated with the inclusion of paralogous sequence variants, supported the construction of robust multi-allelic SNP haploblocks and selected up to 11 entries within narrow genomic regions of ± 5 kb, termed focal points (FPs). Broad genome coverage was attained by placing FPs at 1 cM intervals on a consensus genetic map, complementing them with FPs to enrich the ends of each of the chromosomes, and by bridging physical intervals greater than 400 Kbps. The selection also included ~ 3.7 K validated SNPs from the IRSC 8 K array. The array has already been used in other studies where ~ 15.8 K SNP markers were mapped with an average of ~ 6.8 K SNPs per full-sib family. The newly developed array with its high density of polymorphic validated SNPs is expected to be of great utility for Pedigree-Based Analysis and Genomic Selection. It will also be a valuable tool to help dissect the genetic mechanisms controlling important fruit quality traits, and to aid the identification of marker-trait associations suitable for the application of Marker Assisted Selection in apple breeding programs.

URL de la notice <http://okina.univ-angers.fr/publications/ua7918> [16]
DOI [10.1371/journal.pone.0110377](https://doi.org/10.1371/journal.pone.0110377) [17]
Lien vers le document <http://dx.doi.org/10.1371/journal.pone.0110377> [17]

Liens

- [1] [http://okina.univ-angers.fr/publications?f\[author\]=12923](http://okina.univ-angers.fr/publications?f[author]=12923)
- [2] [http://okina.univ-angers.fr/publications?f\[author\]=12416](http://okina.univ-angers.fr/publications?f[author]=12416)
- [3] [http://okina.univ-angers.fr/publications?f\[author\]=12924](http://okina.univ-angers.fr/publications?f[author]=12924)
- [4] [http://okina.univ-angers.fr/publications?f\[author\]=12925](http://okina.univ-angers.fr/publications?f[author]=12925)
- [5] [http://okina.univ-angers.fr/publications?f\[author\]=12926](http://okina.univ-angers.fr/publications?f[author]=12926)
- [6] [http://okina.univ-angers.fr/publications?f\[author\]=12927](http://okina.univ-angers.fr/publications?f[author]=12927)
- [7] [http://okina.univ-angers.fr/publications?f\[author\]=12928](http://okina.univ-angers.fr/publications?f[author]=12928)
- [8] [http://okina.univ-angers.fr/publications?f\[author\]=12929](http://okina.univ-angers.fr/publications?f[author]=12929)
- [9] [http://okina.univ-angers.fr/publications?f\[author\]=12930](http://okina.univ-angers.fr/publications?f[author]=12930)
- [10] [http://okina.univ-angers.fr/publications?f\[author\]=12931](http://okina.univ-angers.fr/publications?f[author]=12931)
- [11] [http://okina.univ-angers.fr/publications?f\[author\]=91](http://okina.univ-angers.fr/publications?f[author]=91)
- [12] [http://okina.univ-angers.fr/publications?f\[author\]=12803](http://okina.univ-angers.fr/publications?f[author]=12803)
- [13] [http://okina.univ-angers.fr/publications?f\[author\]=12429](http://okina.univ-angers.fr/publications?f[author]=12429)
- [14] [http://okina.univ-angers.fr/publications?f\[author\]=12932](http://okina.univ-angers.fr/publications?f[author]=12932)
- [15] [http://okina.univ-angers.fr/publications?f\[author\]=12417](http://okina.univ-angers.fr/publications?f[author]=12417)
- [16] <http://okina.univ-angers.fr/publications/ua7918>
- [17] <http://dx.doi.org/10.1371/journal.pone.0110377>

Publié sur *Okina* (<http://okina.univ-angers.fr>)