## Marker validation for *Rpf*1 red stele resistance in strawberry

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Red stele is a devastating root rot disease in strawberries. Several sources for genetic resistance are exploited in breeding, and several race-specific R-genes were distinguished. Recently, a tightly linked SSR marker was found for the Rpf1 gene at Wageningen-UR, The Netherlands. One hundred and forty nine individuals with known and unknown response to this pathogen, Phytophthora fragariae, were tested in bench tests for response to two races of this disease: Canadian race 4 (A-3) isolate ONT-3, and Cdn-5 (A-5) isolates BC-23 and NOV-77 where Rpf1 confers resistance to race 4 and is ineffective against race Cdn-5. Twenty-nine individuals consisting mostly of wild accessions or recent derivatives of crosses with wild relatives were identified as having other, potentially new factors of resistance by exhibiting resistance to race A-5 and may be valuable for widening the genetic base of resistance in commercial cultivars. To avoid epistatic effects, these individuals were e xcluded from validation of the Rpf1 marker. For the120 individuals that showed high disease scores for Cnd-5, 41 showed and 79 lacked the marker allele. Preliminary analysis for correlations between marker and disease scores revealed 30 deviations, 17 individuals being susceptible despite having the marker and 13 individuals having low disease scores despite lacking the marker. Causes for the lower (75%) than previously observed (99%) marker to disease correlations are being investigated.

## Towards high throughput phenotyping of the multisensory space of apple quality

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The perceivable quality of apple is one of the most important aspects to be considered in breeding, for the selection as well as the commercialization of new accessions. Sensory science allows the definition and control of the multidimensional space behind the perceived quality of apple, but it is usually expensive and time consuming. For this reason the implementation of sensory attributes as phenotypic descriptors for genomic investigation is, in general, difficult.
In 2010 we started a large sensory/instrumental phenotyping activity on several apple based on innovative technology and multidisciplinary know how to define models that,

on the basis of rapid instrumental characterization, can provide reliable quantification of key sensory traits on large data sets to be used in genome wide association analysis, particularly elucidating the genetic basis of fruit texture and flavor related traits. Here we describe the general frame of our project and the results obtained as follows: i) the set up of a comprehensive sensory methodology to provide reliable, unified and competitive sensory characterization, ii) the setting and validation of models to estimate sensory attributes based on instrumental data, iii) the study of the complexity of the interaction between product and consumer during apple fruits consumption by nose space analysis and psycho-physical experiments and iv) the investigation of the link with genomic information.

**Use of genotyping-by-sequencing for quantitative trait loci mapping of chilling requirement and bloom date in peach**

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Bloom date (BD) and chilling requirement (CR) are economically important traits for breeding fruit and nut tree species adapted to local climate conditions. We have developed a peach F2 mapping population with 57 genotypes from a selfed F1 progeny of a cross between 'Hakuho' (high CR) and 'UFGold' (low CR). We scored BD in seven years; CR was evaluated over two winter seasons by scoring bud break of forced cuttings. Initial marker screening identified 37 polymorphic simple sequence repeat (SSR) markers distributed across all linkage groups (G). In order to saturate our genetic map with markers, we tested a genotyping-by-sequencing (GBS) approach to discover single nucleotide polymorphisms (SNP) present in the population. Genomic DNA was ApeKI restricted, ligated to barcoded adaptors, and pooled and amplified for multiplex sequencing on the Illumina HiSeq 2000 platform. Approximately 160 million sequence reads were processed using TASSEL 3.0. SNPs were filtered to retain only loci homozygous within each parent, but polymorphic between parents. This conservative genetic linkage map consisting of 37 SSRs and >380 SNPs in eight linkage groups was constructed using JoinMap v4.1. Several quantitative trait loci (QTL) were detected for BD and CR on G4 and G7. GBS provided a rapid and relatively low cost method to produce a SNP-based map in a novel progeny.