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# Genetic mapping and QTL analysis in European hazelnut (*Corylus avellana* L.)

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## Abstract

The European hazelnut (*Corylus avellana* L.) is the most economically important nut species in the Betulaceae family. Despite the need for new improved hazelnut cultivars, few breeding programs are carried out because of the large plant size, the long life cycle of the plant, and the expense and time required.

To date, there are no reports of maps with Quantitative Trait Loci (QTL) in hazelnut. Our objective in the present study was to identify QTL associated with vegetative traits to allow marker-assisted selection (MAS). A F<sub>1</sub> progeny (275 plants) of 'Tonda Gentile delle Langhe' X 'Merveille de Bollwiller' obtained in 2009 was used to develop a QTL linkage map for vigour, sucker habit and time of bud burst, after three years of observations. A set of 163 plants were analysed with 152 microsatellite markers. A map of 11 linkage groups was obtained, covering 663.1 cM and 15 QTLs were identified and mapped for the examined traits. Among them, 10 were 'major' QTL, including a stably expressed region on LG\_02 for leaf budburst. At least one major QTL for each year underlays the variation in each trait and a clustering of QTL for *tc* and *s/tc* ratio with a high inter-trait correlations was observed on LG\_05, suggesting a single pleiotropic locus.

This research represents an initial step for the future identification of chromosomal regions carrying genes of interest, important for breeding programs and MAS.

### **Key words**

SSR – MAS – vegetative traits – leaf budburst – sucker habit - vigour

### **Introduction**

The genus *Corylus* (Betulaceae) is spread throughout the temperate regions of the Northern Hemisphere, extending from Japan, Korea, China and the Russian Far East to the Caucasus, Turkey, Europe and North America (Kasaplilgil 1972). The European hazelnut (*Corylus avellana* L.) is the most economically important nut species in the Betulaceae family with a worldwide production of about 872,000 t of in-shell nuts and a cultivated area of approximately 604,000 ha (average 2008-2012, FAOstat, 2015), resulting the sixth most important commodity among the tree nuts behind cashew (*Anacardium occidentale* L.), walnut (*Juglans regia* L.), almond (*Prunus dulcis* (Miller) D.A. Webb), chestnut (*Castanea sativa* Miller), and pistachio (*Pistacia vera* L.). The major producers are Turkey (598,158 t) and Italy (104,577 t), followed by USA (32,399 t), Azerbaijan (30,035 t), Georgia (25,020 t), Iran (20,833 t), China (19,700 t) and Spain (16,239 t) (average 2008-2012, FAOstat 2015). It is estimated that over 90% of the hazelnut crop is destined to processing. *C. avellana* is diploid ( $2n = 2x = 22$ ), monoecious, wind-pollinated, dichogamous, and shows sporophytic incompatibility. Because of the large plant size, the long life cycle of the plant, and the expense and time required, very few breeding programs are currently being carried out in the world. The major one is underway at Oregon State University (OSU). On the other hand, there is a strong demand of plant material for new plantings in several countries and interest in new hazelnut cultivars with higher yield and tolerance/adaptation to particular pathogens or environmental conditions is very high.

The construction of genetic linkage maps and identification of molecular markers linked to trait of interest could allow marker-assisted selection (MAS), thereby enriching the population of seedlings planted in the field for those carrying desired traits. Many important agronomic and quality traits, such as time of bud burst, flowering time, yield and fruit quality are controlled by many genes: genomic regions containing these genes are known as Quantitative Trait Loci (QTL) (Collard et al. 2005). In this case, the MAS procedure involves the construction of a genetic map and identifies markers tightly linked to the major genes or QTL of agronomic interest (Francia et al. 2005). This would allow selection at the seedling stage. Application of MAS and QTL mapping in fruit and forestry tree breeding programs has made considerable progress during the last two decades (Rai and Shekhawat 2014). Molecular markers associated with traits of interest have

been identified for a wide variety of traits, including disease resistance genes in apples (Bus et al. 2010), grapevine (Riaz et al. 2011), apricot (Soriano et al. 2008), chestnut (Kubisiak et al. 2013), poplar (Jorge et al. 2005), Norway spruce (Lind et al. 2014), eucalyptus (Zarpelon et al. 2015) and abiotic stress tolerance in apple (Virlet et al. 2015), oak (Parelle et al. 2007), and poplar (Tschaplinski et al. 2006). Various QTL controlling morphological and qualitative fruit traits, maturity, flowering time, bud phenology, have also been identified in different species, including apples (Chagne et al. 2012, Sun et al. 2015, Virlet et al. 2015), apricot (Campoy et al. 2011), cranberry (Schlautman et al. 2015), grapevine (Chen et al. 2015), peach (Martínez-García et al. 2013, Bielenberg et al. 2015), pear (Zhang et al. 2013), pomegranate (Harel-Beja et al. 2015), sweet cherry (Castède et al. 2015), chestnut (Casasoli et al. 2004), oak (Scotti-Saintagne et al. 2004), pine (Yang et al. 2015), and poplar (Rohde et al. 2011, Du et al. 2015).

A high density linkage map of hazelnut was previously constructed using RAPD (Random Amplified Polymorphic DNA) and microsatellite (SSR - Simple Sequence Repeat) markers (Mehlenbacher et al. 2006) by crossing two selections developed at OSU, and was improved by the addition of 150 SSRs by Gürcan and Mehlenbacher (2010a) and Gürcan et al. (2010). The reference map was developed by the OSU hazelnut breeding program aimed to identify molecular markers to be used in MAS for selecting individuals bearing resistance to Eastern Filbert Blight (EFB), a disease caused by *Anisogramma anomala* (Peck) E. Müller (Mehlenbacher et al. 2004); a second objective of the work was to find markers linked to the alleles at the S-locus that controls incompatibility (Mehlenbacher et al. 2006), to aid the identification of S-alleles in cultivars and selections. More recent work carried out at OSU led to the identification of 9 RAPDs, 31 SSRs and 2 AFLPs (Amplified Fragment Length Polymorphisms) markers linked to EFB resistance loci, 4 RAPDs and 4 SSRs markers linked to the S locus, and 1 SSR marker linked to style colour (Chen et al. 2005; Sathuvalli et al. 2011; Sathuvalli and Mehlenbacher 2011; Sathuvalli et al. 2012; Sathuvalli and Mehlenbacher 2013; Ives et al. 2014; Colburn et al. 2015). To date, there are no reports of QTL analysis in hazelnut. Our objective in the present study was to identify QTL associated with three traits. In this paper, we present the results of three years of observations of young seedlings, a new linkage map, and the QTL analysis for vigour, sucker habit and time of bud burst.

## **Materials and Methods**

### *Plant materials*

A progeny of 275 F<sub>1</sub> individuals were obtained by crossing ‘Tonda Gentile delle Langhe’ (syn. ‘Tonda Gentile Trilobata’, female parent, hereafter TGdL) with ‘Merveille de Bollwiller’ (syn. ‘Hall’s Giant’ male parent, MB). In December 2007, a TGdL plant was emasculated and then caged with a nonwoven tissue to avoid uncontrolled pollination. At the same time, pollen was collected from a MB plant and stored at -20°C until TGdL female flowering time. The controlled

pollination was manually made using a paintbrush in February 2008. The cage was removed at the end of female flowering when the stigmas were dry and dark brown.

Nuts were collected from the plant in early August 2008 when the shells were at least halfway brown but before they fell to the ground. They were then stored in a mesh bag at 4°C for about three months. In early November, nuts were removed from storage and soaked for two days in a bucket filled with water, changing the water after 24 h. After the soaking, nuts were stratified using an equal volume of moistened vermiculite in a plastic box. The box was covered with a polyethylene bag not hermetically closed, and stored in a cooler at 4°C for 150 days.

At the end of March 2009, the plastic box was removed from the cooler and left at room temperature (about 20°C) for a week to promote germination. Only seeds that showed root tips were transferred to pots (5cm x 5cm x 25cm) filled with a substrate composed by peat and perlite (3:1 ratio). The pots were kept under a glass greenhouse until plants reached a height of about 20 cm. In summer 2009, the plants were kept in a tunnel, covered with a shading net and with drip irrigation. Nutrients were provided using irrigation lines.

The 275 seedlings and three individuals obtained from rooted suckers of each of the two parent cultivars were planted in November 2010 and evaluated over the years 2011, 2012, 2013 and 2014. The field is located at the campus of University of Torino, Department of Agricultural, Forest and Food Sciences (45°07'N; 7°58'E; 293 m a.s.l.). The plants were trained in an open vase system with a spacing of 4 x 4 m. From 2010, water was supplied using an integral PC drip line (UniRam™ 20010 AS, Netafim) from mid-June to mid-September. Fertilization was supplied by foliar sprays using Hascon 12 (Green, Italia) or through the drip lines every two weeks from mid-June to late July. Soil was maintained covered with grass that was mowed and chopped during the growing season; before harvest, the grass was killed in the area below the tree canopy using broadleaf active contact herbicide (SPOTLIGHT PLUS®, carfentrazone-ethyl 60 g/L EO, Belchim Crop Protection Italia). A copper-based bactericide was applied in autumn, while thiophanate-methyl fungicide was applied at the beginning of leaf drop. No insecticide treatments were applied during the trial.

During the trials, weather data (temperature, relative humidity, rainfall) were recorded using an automatic weather station located near the field (data collected by Regione Piemonte - Rete Agrometeorologica Regionale). The sensors of the weather stations were installed 2 m above the ground, according to World Meteorological Organization (WMO) guidelines.

#### *SSR analyses*

DNA was extracted from young leaves collected in the spring following Doyle and Doyle (1987). Each individual was preliminarily checked to confirm the parentage by genotyping with 7 SSR loci selected from Boccacci et al. (2005) and

Bassil et al. (2005a). A set of 163 individuals, planted in the core of the field, was then used for SSR analysis at this first stage of the study.

The 163 F<sub>1</sub> individuals of the progeny were genotyped with 152 microsatellite markers (including 15 EST-SSRs) identified by Bassil et al. (2005a,b), Boccacci et al. (2005), Gürcan et al. (2010), Gürcan and Mehlenbacher (2010a,b) and Boccacci et al. (2015) (Online Resource 1).

PCR reactions were performed in a volume of 15 µl containing 1X PCR buffer, 2.25 mM MgCl<sub>2</sub>, 200 µM of each dNTP, 0.4 µM of reverse primer and 5'-labelled M13 tail, 0.1 µM of forward primer (with complementary M13 tail sequence added to 5'-end), 0.1 U of Taq polymerase (Bioline, USA) and 40 ng of template DNA. The thermal cycler program had two stages: after an initial 3 min at 94°C, the first stage comprised 30 cycles of 30 sec at 94°C, 45 sec at 56/58/60°C, 45 sec at 72°C; the second stage consisted of 10 cycles of 30 sec at 94°C, 45 sec at 54°C, 45 sec at 72°C and a final elongation step of 10 min at 72°C (Schuelke 2000). Amplification products were analysed on a 3130 Genetic Analyzer capillary sequencer (Applied Biosystems, USA). The internal GeneScan™ size standard 500 LIZ® was included in each run. Allele sizes in the output were called using GeneMapper v4.0 software (Applied Biosystems).

#### *Linkage analysis and consensus map construction*

All SSR loci were used for the construction of a consensus linkage map with JoinMap v4.0 (Van Ooijen 2006), applying the Kosambi (1944) mapping function: in particular loci belonging to the segregation classes 1:2:1 (the same pair of alleles segregating in each parent) and 1:1:1:1 (different alleles segregating in each parent) were used as 'bridge markers'. Differences between observed and expected segregation ratios were assessed using a  $\chi^2$  test. Markers associated with a  $\chi^2$  value  $\leq \chi^2_{\alpha=0.1}$  or with only a minor deviation ( $\chi^2_{\alpha=0.1} < \chi^2 \leq \chi^2_{\alpha=0.01}$ ) were used for map construction and for estimation of genetic distance, if their presence did not alter the local marker order in the linkage group (LG). LGs were established based on an initial threshold logarithm of odds (LOD) of 6.0, with the following parameters set to determine locus order and distances between loci: Rec=0.40, LOD=1.0, Jump=5.

Markers with highly significant deviation from Mendelian expectation ( $\chi^2 > \chi^2_{\alpha=0.01}$ ) were subsequently added with a LOD threshold of 4.0: they were checked one by one and placed in their most likely position within LGs without forcing, in order to avoid artefacts.

Markers deviating in their segregation only marginally from the expected Mendelian ratio were identified with one ( $\chi^2_{\alpha=0.1} < \chi^2 \leq \chi^2_{\alpha=0.05}$ ), two ( $\chi^2_{\alpha=0.05} < \chi^2 \leq \chi^2_{\alpha=0.01}$ ), three ( $\chi^2_{\alpha=0.01} < \chi^2 \leq \chi^2_{\alpha=0.005}$ ), four ( $\chi^2_{\alpha=0.005} < \chi^2 \leq \chi^2_{\alpha=0.001}$ ) and five ( $\chi^2 > \chi^2_{\alpha=0.001}$ ) asterisks. LGs were numbered according to Gürcan et al. (2010) map order.

#### *Evaluation of phenotypic traits*

The progeny segregates for several traits, including vigour, number of suckers, time of leaf bud burst.

In years 2011 to 2014 trunk circumference, suckering index and time of bud burst were recorded. Trunk circumference (*tc*) was measured in mm at about 20 cm from the ground to evaluate vigour. Suckers were removed by manual pruning and counted in June of each year; suckering index was calculated as the number of suckers/trunk circumference (*s/tc*). Time of leaf bud burst (*lb*) was recorded at the first leaf appearance out of the bud (“stage C1”, Germain and Sarraquigne 2004). Time of bud burst was expressed using the classification in levels of expression of the trait from very early (1) to very late (9), by UPOV (1979) guidelines.

#### *Trait evaluation and QTL detection*

Population means, standard deviations, ranges, distribution histograms and trait correlations were calculated using R software (R Development Core Team 2006). For analyses of variance, each season was treated as an independent replicate. Broad sense heritability ( $H^2_{BS}$ ) was estimated with the formula  $H^2 = \sigma_g^2 / (\sigma_g^2 + \sigma_e^2 / y)$ , where  $\sigma_g^2$  is the genetic variance,  $\sigma_e^2$  is the error variance, and  $y$  is the number of years. The difference in traits between two parents was compared using a  $t$  test ( $P < 0.05$ ). Correlations between traits were calculated using the Spearman coefficient, while normality, Kurtosis and Skewness measures were assessed with the Shapiro-Wilks test ( $\alpha = 0.05$ ). Segregation was considered as transgressive where at least one  $F_1$  individual recorded a trait value higher or lower than the parental value by at least two standard deviations.

The consensus map was used at first to assign putative QTL locations by performing a Kruskal-Wallis (KW) non-parametric test in conjunction with the simple interval mapping procedure (SIM) (Lander and Botstein 1989), based on the CP (cross-pollination) algorithm implemented within MapQTL v4.0 software (Van Ooijen et al. 2002). Next, one linked marker per putative QTL was identified using interval mapping, after which it was treated as a co-factor in the approximate multiple QTL model (MQM) (Jansen and Stam 1994). For the MQM, a backward elimination procedure was applied to select the appropriate co-factors (e.g. significantly associated with each trait at  $P < 0.02$ ). The LOD thresholds for QTL significance were confirmed using a permutation test comprising 1,000 replications, which implies a genome-wide significance level of 0.05 (Churchill and Doerge 1994). Only those QTL associated with a LOD greater than either the genome-wide threshold or the threshold for that linkage group were considered, and 1-LOD support intervals were determined for each LOD peak (Van Ooijen 1992). The proportion of the overall phenotypic variance (PV) associated with each QTL was estimated from the MQM model. Linkage maps and QTL positions were drawn using MapChart (Voorrips 2002). Each QTL was designated by an abbreviated version of the trait name as a prefix, followed by the relevant linkage group and the suffix indicating the year of its expression. So for example “*s/tc\_01\_14*” indicates

the QTL underlying the ratio suckers/trunk circumference, mapping to the linkage group 01 by analysing data of the year 2014.

## Results

### *Genotyping and linkage analysis*

Of the 152 microsatellite loci, 101 segregated in the F<sub>1</sub> population for both parents: 89 in a 1:1:1:1 ratio, and 12 in a 1:2:1 ratio. The other 51 loci segregated 1:1, 28 from TGdL and 23 from MB (Online Resource 1).

The analysis of genotype frequencies showed that about 7% of the loci produced distorted segregation ratios. Four loci (B788, CaC-A014a, CaC-B108, KG800) showed the presence of null alleles: these loci were not discarded but analysed twice with JoinMap 4, considering them both segregating for one parent (1:1 ratio), and segregating for both parents with a dominant genotype (1:2:1 ratio).

Three loci (B719, Cac-B101 and CaT-B503) showed  $\chi^2$  values slightly deviating from expectation ( $\chi^2_{\alpha=0.1} < \chi^2 \leq \chi^2_{\alpha=0.05}$ ), while three others (KG815, A614 and KG801) showed significant segregation distortion ( $\chi^2_{\alpha=0.01} < \chi^2 \leq \chi^2_{\alpha=0.005}$ ,  $\chi^2_{\alpha=0.005} < \chi^2 \leq \chi^2_{\alpha=0.001}$ ,  $\chi^2 > \chi^2_{\alpha=0.001}$ , respectively), and were initially set aside. The subsequent addition of these six loci did not alter the initial marker order; moreover, they showed linkage only to a single LG and with a LOD score  $\geq 4$  (Online Resource 2): for these reasons they were included in the final map construction.

The 152 SSRs segregating in the F<sub>1</sub> population were used to generate a map of 11 LGs (each with four or more loci), for a total genetic length of 663.1 cM, with a mean inter-marker distance (discounting completely co-segregating ones) of 4.45 cM (Fig. 1 and Table 1). LG length varied from 33.8 cM (LG\_06) to 98.9 cM (LG\_01). The number of markers per chromosome was the highest in LG\_09 (25) and the lowest in LG\_06 (4) (Table 1). The majority (85%) of map intervals were less than 10 cM, but some large gaps remained. In particular 8 gaps >15cM were present (2 in LG\_01, 1 in LG\_02, 1 in LG\_03, 1 in LG\_05, 2 in LG\_07, 1 in LG\_11). For each of the marker pairs involved, the specific LOD in support of the two-point placement was checked, to confirm the robustness of the LGs (Online Resource 3). Only B720 was ungrouped: the strongest linkage for it was with CaC-A014b on LG\_04 with a LOD value of 2.8. Due to this low LOD value, it was not considered for the map construction, nevertheless Gürcan et al. (2010) placed B720 on LG\_05.

Genic and EST-SSRs were distributed in six LGs (Fig. 1). In particular, both LG\_01 and LG\_09 had 4 EST-SSRs (Corav1232, BPT6452, Corav2208, AG4314 and AG4765, AG3754, Corav2564, Corav1859, respectively). The loci created noticeable clustering only on LG\_11 (CD278264 and Corav2560 clustered with 1.4 cM distance). The other EST-SSRs were on LG\_02 (AJ417975b and BP0585), LG\_03 (AG4395), LG\_10 (Corav2241 and Corav6822) and LG\_11 (Corav1576).



The six loci that showed segregation distortion mapped to LGs 05, 06 and 09 (Fig. 1): in particular, B719 and CaC-B101 ( $\alpha=0.1$ ) clustered in a central position on LG\_09 with a distance  $< 4$  cM, while A614 and KG801 ( $\alpha=0.001$  and  $\alpha=0.005$  respectively) grouped at 5.6 cM on LG\_06. We also note that KG815 ( $\alpha=0.01$ ) was placed at the end of LG\_09.

LG numbers were those assigned by Gürcan et al. (2010), based on a cross between genotypes from a maternal parent (OSU 252.146) susceptible and a male parent (OSU 414.062) resistant to eastern filbert blight. The two maps have 111 SSR loci in common, but 5 loci were assigned to a different LG compared to the map by Gürcan et al. (2010): B640 (LG\_04 instead of LG\_08), CaT-B504 (LG\_02 instead of LG\_07), CaC-B005 (LG\_02 instead of LG\_07), B660 (LG\_02 instead of LG\_07), CaC-B101 (LG\_09 instead of LG\_07). The others 106 SSR loci were distributed across all of the 11 LGs (3 to 15 present on each LG) allowing to identify each LG (Table 1). Marker order and genetic separation are comparable between the two maps, except for LG\_09 and LG\_10. Initially by JoinMap analysis, a single linkage group was found for markers belonging to LG\_09 and LG\_10; in particular, a set of 25 markers was grouped together by the first two rounds of attempts for comparing the goodness-of-fit of the calculated map for each tested position, while another 14 markers were added to the LG only after the third round without the constraints of maximum allowed reduction in goodness-of-fit and no negative distances. It was noticed that the first two rounds grouped together all the markers belonging to the Gürcan et al. (2010) LG\_09, while during the third one, all LG\_10 markers were added. For this reason, we chose to maintain the two groups separated, creating a linkage map of 11 LGs, corresponding to the haploid chromosome number for hazelnut ( $n = x = 11$ ) (Fig. 1).

Of the 152 SSRs used for mapping, 40 were here placed for the first time on a hazelnut genetic map.

#### *Phenotypic variation and inter-trait correlations*

A summary of the phenotypic and statistical values are listed in Table 2. There were significant ( $P < 0.1$ ) phenotypic differences between TGdL and MB for each trait, except for the suckering index ( $s/tc$ ) in 2012 and 2013 (Table 2). TGdL was less vigorous ( $tc$ ) and had a lower suckering index and earlier leaf bud burst ( $lb$ ) than MB, which confers the higher value for each trait. The  $F_1$  progeny phenotype distribution was intermediate between the two parents for  $lb$  (Fig. 2c) and  $s/tc$  (considering for  $s/tc$  the year 2014, when parents showed significant differences; Fig. 2b) while for  $tc$  the mean of the population was below the mid-parent value in 2013 and 2014 (Fig. 2a). Significant inter-trait correlations ( $P < 0.05$ ) were detected both within and between years (Online Resource 4): in particular  $tc$  and  $s/tc$  showed positive correlations between them in 2012 (0.346) and 2013 (0.175). The correlation of a trait between years were significant and ranged from 0.540 to 0.962. Transgressive segregations (Fig. 2) were observed for  $s/tc$  (positive transgression for two plants) and for  $tc$  (positive transgression for seven plant) in 2012; for  $lb$  (negative transgression for one plant and positive transgression for four plants) and  $tc$  (negative transgression for 85 plants and positive transgression for six plants) in 2013; for  $lb$  (positive

transgression for one plant), *s/tc* (negative transgression for five plants and positive transgression for six plants) and *tc* (negative transgression for 106 plants and positive transgression for one plant) in 2014.  $H^2_{BS}$  was relatively high ranging from 0.60 (*tc*) to 0.85 (*s/tc*) (Table 2).

### *QTL identification*

A separate QTL analysis was performed in each year. Overall, 15 QTL were identified and mapped onto seven genomic regions dispersed on six of the 11 LGs: 1, 2, 5, 8, 10 and 11. Ten of these QTL explained more than 10% of the phenotypic variance (PV) and are hereafter referred to as “major” QTL. Table 3 documents the properties of each of the QTL: maximum LOD value, location on the genetic map and proportion of phenotypic variance explained. In year 2012, five QTL (3 major) were identified; in 2013 four QTL (3 major) were found, while in 2014 six were detected (4 major). Among the QTL detected, three were expressed in all years, one in both 2013 and 2014, while four were only detected in one year. The genomic locations of these QTL are shown in Fig. 1. At least one major QTL for each year underlays the variation in each trait. Clustering of QTL associated with different traits was observed on LG\_05, harbouring QTL for *tc* and *s/tc* ratio. The high inter-trait correlations between the traits controlled by this cluster (Online Resource 4) suggests either a set of closely linked loci or, more likely, a single pleiotropic locus.

*Trunk circumference.* Two regions harboured *tc* loci (Table 3), one of which was expressed in all three years and the other was detected only in 2012. The former was located on LG\_05 (linked closely to three SSR loci) and over the three years explained 11.4 to 13.6% of the PV. The latter was a minor one, located on LG\_08 and accounted for 8.5% of the PV in 2012 only.

*Suckers/trunk circumference.* QTL associated with *s/tc* were detected in five genomic regions, of which one was detected in all three years, one in two years, and three were detected in only a single year.

The SSR locus A602 mapped on LG\_10 and was stably associated with *s/tc* trait across the three years and explained from 8.7% to 14.9% of the PV. The QTL mapped on LG\_01 were expressed in both 2013 and 2014 explained from 8.1 to 10.9% of the PV. The other QTL were expressed in one season only, the most interesting of them was a major one, accounting for 17.1% of the PV, that mapped to the LG\_05 region where *tc* QTL were also located, with overlapping LOD confidence intervals.

*Leaf bud burst.* One major *lb* QTL was detected in all three years. It explained 45-53% of the PV and mapped in the vicinity of the SSR locus AJ417975b on LG\_02.

## **Discussion**

### *Genetic map construction*

A genetic map was constructed on a F<sub>1</sub> progeny using a two-way pseudotestcross approach. The parent cultivars showed several phenotypic differences. Previous studies showed a very high level of genetic variation and heterozygosity in hazelnut, attributable in part to the sporophytic incompatibility that enforces cross pollination (Mehlenbacher 1991; Mehlenbacher et al. 2006), and the clonal propagation of superior genotypes.

SSR markers were analysed as they are ideal for linkage mapping for their robustness, polymorphism, co-dominance and conservation (Wu et al. 2004), even if they are based on relatively low-throughput technologies, which tend to limit marker density across the genome (Bowers et al. 2012). The development of new high-throughput sequencing technologies enable to achieve high-density linkage maps by direct analyses of sequence variations, including single nucleotide polymorphisms (SNPs) (Huang et al. 2014). Markers such SNPs are more abundant and genome wide distributed and can be analysed multiplexing hundreds of markers (Salazar et al. 2015). Nevertheless, SSRs are found to be more polymorphic and are considered as the best marker system for construction of framework linkage map (Jones et al. 2007).

The map consisted of 151 markers distributed across 11 LG (Fig. 1); length and average density (663.1 and 4.45 cM respectively) were lower than those found by Gürcan et al. (2010). The presence of an unlinked marker and 8 gaps >15 cM (Online Resource 3) suggested that there are parts of the genome not covered yet, remaining under-represented (Sargent et al. 2004; Portis et al. 2009).

Only 7% of the markers showed segregation distortion (Online Resource 2), consistent with observations (Lorieux et al. 1995a; Lorieux et al. 1995b; Portis et al. 2012) that distortion at co-dominant marker loci such as SSRs occurs at a lower frequency than at dominant marker loci. Segregation distortion has been reviewed by Lyttle (1991) to indicate the excessive transmission of one allele at a heterozygous locus to the progeny without following Mendelian proportion. Segregation distortion has been associated with statistical bias or errors in genotyping, but also with biological factors (such as chromosome/locus loss, zygotic survival, self-incompatibility alleles) that can affect meiosis, fertilization and embryogenesis (Bradshaw et al. 1994; Jenczewski et al. 1997) or with the presence of null alleles (Pekkinen et al. 2005). Markers were included even when their segregation distortion was significant, as their presence did not alter marker order. Cervera et al. (2001) and Doucleff et al. (2004) reported that it was appropriate to include markers with <1% distortion, as their exclusion can lead to a failure of analysis in significant parts of a linkage group. Moreover, some mapping studies

demonstrated a positive effect of inclusion of highly distorted markers in linkage analyses (Kuang et al. 1999; Fishman et al. 2001).

Four markers showed null alleles and were analysed as dominant markers. Null alleles at SSR loci are not uncommon, in hazelnut (Gürcan et al. 2010). They are probably due to amplification failure for one allele in heterozygotes, resulting in a loss of data and a higher apparent number of homozygotes (Pekkinen et al. 2005, Gürcan et al. 2010). Apart from biological factors such as inbreeding, reasons for the occurrence of null alleles can be sequence mismatch or deletion that affected primer annealing, the competition which often favours amplification of the smaller allele, or poor quality/quantity of the DNA template (Dakin and Avise 2004). In this situation possible solutions are to disregard the affected loci, to score segregation in the same way as for a dominant marker (Rodzen and May, 2002), to redesign primers (Shaw et al. 1999; Van Oosterhout et al. 2004), or to adjust allele frequencies relating to a global estimate of the frequency of null alleles (Portis et al. 2012).

A total of sixteen genic/EST-SSR markers were mapped on six linkage groups. Boccacci et al. (2015) developed fourteen of them from sequences of alder, birch and hazelnut. BLASTx analyses and functional annotation by Blast2Go programme suggested their involvement in biological processes associated with stress response, signal transduction and processes regulation. AJ417975b and CD278264, derived from *Corylus* and *Betula* expressed sequences, respectively, were developed by Gürcan and Mehlenbacher (2010b) but were not previously mapped. In particular, AJ417975b from the *Lox* gene, coding for a lipoxygenase (LOXs) and was mapped on the LG\_02, the same as AJ417975c, a marker designed from the same sequence and mapped by Gürcan and Mehlenbacher (2010a). CD278264 was a sequence from a root tissue cDNA library (Johansson et al. 2004).

The use of 111 markers in common with the map developed at OSU (Mehlenbacher et al. 2006; Gürcan et al. 2010; Gürcan and Mehlenbacher 2010a) allowed the comparison between corresponding linkage groups and the assignment of the same LG numbers (Fig. 1). Marker order was similar, with some exceptions. These discrepancies could reflect genetic differences between the pairs of mapping parents and/or be statistical artefacts resulting from the use of different mapping parameters (Barchi et al. 2012). In fact, re-ordering of closely linked markers is relatively commonplace (Cervera et al. 2001; Jeuken et al. 2001; Lespinasse et al. 2000; Sebastian et al. 2000). For this reason, variation in stringency (LOD threshold), marker choice, genotyping errors, excess of missing values and the mapping of distorted markers can cause mapping inconsistency (Portis et al. 2009; Hackett and Broadfoot 2003).

The choice of these markers was done to enable the future merging of the two maps, developed with the same mapping strategy. Integration of mapping data from several crosses on a single integrated map would be useful to determine the relative positions of transferable markers, independent of the heterozygous stated in either parents of the cross (Doligez

et al. 2006). In this way, it would be possible to integrate 40 SSRs not mapped by Gürcan et al. (2010) as well as the genes/QTL responsible for the phenotypic variation in the different progenies (Aranzana et al. 2003; Doligez et al. 2006). Preliminary results in linkage map construction showed only 10 LGs rather than the expected 11 (the haploid chromosome number for hazelnut), for merging of markers located on LG\_09 and LG\_10 at the third round of JoinMap analyses. It is possible to speculate about the presence of a reciprocal translocation event during meiosis: in fact using standard linkage analysis, translocations usually lead to “pseudo-linkage” with the creation of a single linkage group showing a mix of markers from the chromosomes involved in the phenomenon (Livingstone et al. 2000; Farré et al. 2011). Recombination is severely suppressed near the translocation breakpoints, so reordering markers in those regions is not feasible (Farré et al. 2011). This type of event has been described in different hazelnut cultivars, including TGdL, by Salesses (1973) and Salesses and Bonnet (1988).

#### *Phenotyping, QTL mapping and clustering of agronomic traits*

The QTL approach allows analysis of the genetic basis of variation in quantitative traits and identification of genomic regions on a linkage map (Paterson et al. 1988), not yet been published for hazelnut. Agronomic traits are often quantitative in nature and are under polygenic control. This type of study has not been published yet for hazelnut, so this is the first report identifying QTL for agronomic traits in the species.

Concerning the parental characteristics for the examined traits, according to the literature, they differ for trunk circumference and leaf bud burst (IPGRI, FAO and CIHEAM 2008), while the suckering habit (and suckers/trunk circumference ratio, consequently) was more evident in MB than TGdL, although no significant differences were highlighted during the first two years of study (Fig. 2 and Table 2). It is noteworthy that the presence of suckers is undoubtedly a genetic character linked to the cultivar. Nevertheless their amount is also influenced by climatic and soil factors, and by propagation and cultural systems. For instance sucker production increases for plants growing in sandy soil (Germaine and Serraigne 2004) or those originating as rooted suckers (as the parents in our study) (Radicati et al. 1994).

Phenotypic trait distributions were not normal and changed over the years, especially between 2012 and 2013 (Fig. 2). This could be due to the development of plants in the progeny during growth: in fact characters such suckering habit become stable only after some years after plantation (Germaine and Sarraquigne 2004). Distribution of traits in 2013 and 2014 were more similar, suggesting a stabilization of the characters. Leaf bud burst data was similar over the three years (Fig. 2c). Only in 2014 the distribution was less uniform than the previous years. A temperature decrease recorded after stage 3 suggested a possible effect on leaf bud burst. Indeed, temperature influence on timing of bud burst is evident in forest trees and fruit trees (Howe et al. 2003; Cooke et al. 2012).

The  $H^2_{BS}$  was 0.74 for *lb* and 0.85 for *s/tc*, while it was 0.60 for *tc* (Table 2). High heritability estimates have been reported for phenological traits in many other crops, even though the populations growing conditions and measurement methods are different (Dicenta et al. 1993; Tancred et al. 1995). Heritability studies of phenological traits such as leaf bud burst and vigour have been reported for several forest trees, including poplar (Bradshaw and Stettler 1995; Frewen et al. 2000, Rohde et al. 2011), chestnut (Casasoli et al. 2004; Casasoli et al. 2006), oak (Scotti-Saintagne et al. 2004), Douglas-fir (Jermstad et al. 2001; Jermstad et al. 2003), and eucalyptus (Bundock et al. 2008). Only a preliminary work on QTL analyses was published for *Betula platyphylla* Suk, with the identification of two QTL for stem circumference (Zhang et al. 2012).

Bradshaw and Stettler (1995) reported  $H^2_{BS}$  estimates of 0.67 for vigour and 0.98 for spring bud flush. Several studies in forest trees have shown that bud phenology is highly heritable, with values ranging from 0.50 to 0.80, (Bradshaw and Stettler 1995; Jermstad et al. 2001; Scotti-Saintagne et al. 2004; Billington and Pelham 1991). Heritability estimates for growth range from low to high (0.20 to 0.80). (Bradshaw and Stettler 1995; Byrne et al. 1997, Scotti-Saintagne et al. 2004). These values indicate strong genetic control of bud phenology (Li and Adams 1993; Bradshaw and Stettler 1995). For *s/tc* it is not possible to compare  $H^2_{BS}$  of hazelnut with other species since suckering is not a commonly studied trait. Work on tobacco (*Nicotiana tabacum* L., Julio et al. 2006) and sugarcane (*Saccharum officinarum* L., Jordan et al. 2004) attempted to identify QTL for suckering. In both cases, high sucker production was negatively correlated with yield. The estimate in tobacco. ( $H^2_{BS}=0.69$ ) was high, as in our work.

Transgression, both positive and negative, was present for all the three traits studied during the three years (Fig. 2). Transgressive genotypes derived from the combination of alleles from both parents with effect on the same direction (De Vicente and Tanksley 1993). Transgression was evident for the examined traits also in other studies (Bradshaw and Stettler 1995; Julio et al. 2006). The effect of these allele combinations will be investigated, keeping in mind that traits such as sucker habit and tree vigour in hazelnut can be considerably influenced by environment (Valentini et al. 2004). These considerations will be accounted also for the suggesting semi-dominance for poor vigour, highlighted by the mean value of *tc* in the progeny minor of the mid-parent value in 2013 and 2014. In fact, it is well accepted that traits such as growth can be considered as developmental traits, and show a temporal shift for what concern their action (Kremer 1992). This work identified 15 QTL, of which 10 are major and stably expressed over years (Collard et al. 2005; Li et al. 2001; Pilet-Nayel et al. 2002). At least one major QTL was identified for each of the three traits studied in hazelnut: *tc\_05*, *s/tc\_10* and *lb\_02* which were detected in all three years with LOD values of 3.3 and 5.3. Particularly striking was *lb\_02* which explained around 50% of the PV with a LOD score > 20. This QTL is associated to the SSR locus AJ417975b, an EST-SSR derived from a *Betula* sequence of the Lox gene: it coded for lipoxygenases (LOXs), a class of widespread dioxygenases that catalyse the addition of oxygen to polyunsaturated fatty acids containing a cis,cis-1,4-pentadiene

structure. This reaction produces hydroperoxides that are the starting point for a series of other enzymatic reactions for the synthesis of a group of biologically active compounds named oxylipins, playing diverse functions in several physiological processes such as growth, development, and response to biotic and abiotic stresses (Santino et al. 2003).

The other QTL were identified for *tc* and *s/tc*, of which four were year-specific. The presence of year-specific QTL for *tc* and *s/tc* agrees with observation on other forest trees. The higher proportion of year-specific QTL for growth, compared to phenology, was explained by Wu et al. (2002) who considered growth as a trait determined by loci expressed at a specific stage of development. Previous work detected QTL for growth varying from one developmental stage to another (Plomion et al. 1996; Emebiri et al. 1998; Tsarouhas et al. 2002).

The number of QTL identified in other forest trees varied among the different species studied. In poplar Bradshaw and Stettler (1995) identified 2 QTL for growth and 5 QTL for leaf bud burst; in chestnut Casasoli et al. (2004) found 11 QTL for bud phenology and 4 for growth; 32 and 33 QTL were identified for leaf bud burst in oak and Douglas-fir, respectively (Scotti-Saintagne et al. 2004; Jermstad et al. 2001), and 3 QTL were found for growth in eucalyptus (Bundock et al. 2008). For sucker production, the number of QTL varied in two species: 3 QTL were found in tobacco and 14 in sugarcane (Julio et al. 2006; Jordan et al. 2004). The power to detect the QTL controlling a trait and to accurately estimate the magnitude of their effects is strongly influenced by the size of the mapping populations, the marker information and the accuracy of trait measures (Jermstad et al. 2001). In particular, simulation studies have shown that with a decrease in sample size there is a reduction in QTL detection power and an overestimation of their magnitude (Beavis 1995).

The clustering of QTL associated with different traits was observed on LG\_05, which harboured QTL for *tc* and *s/tc* ratio (Fig. 1 and Table 3). Co-localization of QTL is very important for practical applications in breeding programs (Portis et al. 2012). If the traits are highly correlated, plant breeders can select for both traits with the same markers. This leads to maximum genetic gain for both traits in segregating populations (Carter et al. 2011). Our data showed a positive correlation between *tc* and *s/tc* in 2012 and 2013, while leaf bud burst showed no correlation with other traits (Online Resource 4). Valentini et al. (2004) studied progenies obtained from the same female parent used in this work, but from different male parents. In their work, early time of bud burst showed a positive correlation with tree vigour, and a negative correlation with the amount of suckers; in addition, the amount of suckers showed negative correlation with tree vigour. In our research, correlation data (Online Resource 4) showed that vigour and *s/tc* ratio had a positive correlation only during the first two years, and values decreased over time. In particular, *s/tc* in 2014 showed a negative correlation with vigour in 2012 and 2014, although these values were not significant. It could be speculated that *tc* and *s/tc* traits require time for stabilization of the character and thus further observations of these traits during the next years will show if this trend is confirmed.

## Conclusion

This work presents the first QTL analyses for hazelnut. Fifteen QTLs were identified, including at least one major QTL for each of the three traits. A major QTL on LG\_02 for time of leaf bud burst explained about 50% of the PV. This is an initial step in the identification of chromosomal regions carrying genes of interest, which will be important for breeding programs and allow marker-assisted selection.

## Conflict of interest

The authors declare that they have no conflict of interest.

## References

- Aranzana MJ, Pineda A, Cosson P, Dirlewanger E, Ascasibar J, Cipriani G, Ryder CD, Testolin R, Abbott A, King GJ, Iezzoni AF, Arús P (2003) A set of simple-sequence repeat (SSR) markers covering the *Prunus* genome. *Theor Appl Genet* 106:819-825
- Barchi L, Lanteri S, Portis E, Valè G, Volante A, Pulcini L, Ciriaci T, Acciarri N, Barbierato V, Toppino L, Rotino GL (2012) A RAD tag derived marker based eggplant linkage map and the location of QTLs determining anthocyanin pigmentation. *PLoS ONE* 7(8):e43740
- Bassil NV, Botta R, Mehlenbacher SA (2005a) Microsatellite markers in hazelnut: isolation, characterization, and cross-species amplification. *J Am Soc Hortic Sci* 130:543-549
- Bassil NV, Botta R, Mehlenbacher SA (2005b) Additional microsatellite markers of the European hazelnut. *Acta Hort* 686:105-110
- Beavis WD (1995) The power and deceit of QTL experiments: lessons from comparative QTL studies. In: Wilkinson DB (ed) *Proceedings of the 49th Annual Corn and Sorghum Industry Research Conference*, ASTA, Washington DC, pp 250-266
- Bielenberg DG, Rauh B, Fan S, Gasic K, Abbott AG, Reighard GL, Okie WR, Wells CE (2015) Genotyping by sequencing for SNP-based linkage map construction and QTL analysis of chilling requirement and bloom date in peach [*Prunus persica* (L.) Batsch]. *PLoS ONE* 10(10):e0139406
- Billington HL, Pelham J (1991) Genetic variation in the date of budburst in Scottish birch populations: implications for climate change. *Funct Ecol* 5:403-409
- Boccacci P, Akkac A, Bassil NV, Mehlenbacher SA, Botta R (2005) Characterization and evaluation of microsatellite loci in European hazelnut (*Corylus avellana* L.) and their transferability to other *Corylus* species. *Mol Ecol Notes* 5:934-937
- Boccacci P, Beltramo C, Sandoval Prando MA, Lembo A, Sartor C, Mehlenbacher SA, Botta R, Torello Marinoni D (2015) In silico mining, characterization and cross-species transferability of EST-SSR markers for European hazelnut (*Corylus avellana* L.). *Mol Breeding* 35:21, DOI 10.1007/s11032-015-0195-7
- Bowers JE, Bachlava E, Brunick RL, Rieseberg LH, Knapp SJ, Burke JM (2012) Development of a 10,000 locus genetic map of the sunflower genome based on multiple crosses. *G3 (Bethesda)* 2(7):721-729



- Bradshaw H, Villar M, Watson B, Otto K, Stewart S, Stettler R (1994) Molecular genetics of growth and development in *Populus*. 3. A genetic-linkage map of a hybrid poplar composed of RFLP, STS and RAPD markers. *Theor Appl Genet* 89(2-3):167-178
- Bradshaw HD, Stettler RF (1995) Molecular genetics of growth and development in *Populus*. IV. Mapping QTLs with large effects on growth, form, and phenology traits in a forest tree. *Genetics* 139:963-973
- Bundock PC, Potts BM, Vaillancourt RE (2008) Detection and stability of quantitative trait loci (QTL) in *Eucalyptus globulus*. *Tree Genet Genomes* 4:85-95
- Bus VGM, Bassett HCM, Bowatte D, Chagné D, Ranatunga C, Ulluwishewa D, Wiedow C, Gardiner S (2010) Genome mapping of an apple scab, a powdery mildew and a woolly apple aphid resistance gene from open-pollinated mildew immune selection. *Tree Genet Genomes* 6:477-487
- Byrne M, Murrell LC, Owen JV, Kriedemann P, Williams ER, Moran GF (1997) Identification and mode of action of quantitative trait affecting seedling height and leaf area in *Eucalyptus nitens*. *Theor Appl Genet* 94:674-681
- Campoy JA, Ruiz D, Egea J, Reesw DJG, Celton JM, Martínez-Gómez P (2011) Inheritance of flowering time in apricot (*Prunus armeniaca* L.) and analysis of linked quantitative trait loci (QTLs) using simple sequence repeat (SSR) markers. *Plant Mol Biol Rep* 29:404-410
- Carter AH, Garland-Campbell K, Kidwell KK (2011) Genetic mapping of quantitative trait loci associated with important agronomic traits in the spring wheat (*Triticum aestivum* L.) cross 'Louise' x 'Penawawa'. *Crop Sci* 51:84-95
- Casasoli M, Pot D, Plomion C, Monteverdi MC, Barreneche T, Lauteri M, Villani F (2004) Identification of QTLs affecting adaptive traits in *Castanea sativa* Mill. *Plant Cell Environ* 27:1088-1101
- Casasoli M, Derory J, Morera-Dutrey C, Brendel O, Porth I, Guehl JM, Villani F, Kremer A (2006) Comparison of Quantitative Trait Loci for adaptive traits between oak and chestnut based on an Expressed Sequence Tag consensus map. *Genetics* 172:533-546
- Castède S, Campoy JA, Le Dantec L, Quero-García J, Barreneche T, Wenden B, Dirlwanger E (2015) Mapping of candidate genes involved in bud dormancy and flowering time in sweet cherry (*Prunus avium*). *PLoS ONE* 10(11): e0143250
- Cervera MT, Storme V, Ivens B, Gusmao J, Liu BH, Hostyn V, Slycken JV, Montagu MV, Boerjan W (2001) Dense genetic linkage maps of three *Populus* species (*Populus deltoides*, *P. nigra* and *P. trichocarpa*) based on AFLP and microsatellite markers. *Genetics* 158:787-809
- Chagne D, Krieger C, Rassam M, Sullivan M, Fraser J, André C, Pindo M, Troggo M, Gardiner SE, Henry RA, Allan AC, McGhie TK, Laing WA (2012) QTL and candidate gene mapping for polyphenolic composition in apple fruit. *BMC Plant Biol* 12:12
- Chen H, Mehlenbacher SA, Smith DC (2005) AFLP markers linked to Eastern Filbert Blight resistance from OSU 408.040 hazelnut. *J Amer Soc Hort Sci* 130(3):412-417
- Chen J, Wang N, Fang LC, Liang ZC, Li SH, Wu BH (2015) Construction of a high-density genetic map and QTLs mapping for sugars and acids in grape berries. *BMC Plant Biol* 15:28
- Churchill GA, Doerge RW (1994) Empirical threshold values for quantitative trait mapping. *Genetics* 138: 963-971
- Colburn BC, Mehlenbacher SA, Sathuvalli VR, Smith DC (2015) Eastern filbert blight resistance in hazelnut accessions 'Culplá', 'Crvenje', and OSU 495.072. *J Amer Soc Hort Sci* 140(2):191-200
- Collard BCY, Jahufer MZZ, Brouwer JB, Pang ECK (2005) An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: the basic concepts. *Euphytica* 142:169-196

- Cooke JK, Eriksson ME, Junttila O (2012) The dynamic nature of bud dormancy in trees: environmental control and molecular mechanisms. *Plant Cell Environ* 35:1707-1728
- Dakin EE, Avise JC (2004) Microsatellite null alleles in parentage analysis. *Heredity* 93:504-509
- De Vicente MC, Tanksley SD (1993) QTL analysis of transgressive segregation in an interspecific tomato cross. *Genetics* 134:585-596
- Dicenta FJ, Garcia E, Carbonell EA (1993) Heritability of flowering, productivity and maturity in almond. *J Hort Sci* 68:113-120
- Doligez A, Adam-Blondon AF, Cipriani G, Di Gaspero G, Laucou V, Merdinoglu D, Meredith CP, Riaz S, Roux C, This P (2006) An integrated map of grapevine based on five mapping populations. *Theor Appl Genet* 113:369-382
- Doucleff M, Jin Y, Gao F, Riaz S, Krivanek AF, Walker MA (2004) A genetic linkage map of grape, utilizing *Vitis rupestris* and *Vitis arizonica*. *Theor Appl Genet* 109:1178-1187
- Doyle JJ, Doyle JL (1987) A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochem Bull* 19:11-15
- Du Q, Gong C, Wang Q, Zhou D, Yang H, Pan W, Li B, Zhang D (2015) Genetic architecture of growth traits in *Populus* revealed by integrated quantitative trait locus (QTL) analysis and association studies. *New Phytol*. doi:10.1111/nph.13695
- Emebiri LC, Devey ME, Matheson AC, Slee MU (1998) Age-related changes in the expression of QTLs for growth in radiata pine seedlings. *Theor Appl Genet* 97:1053-1061
- Farré A, Lacasa Benito I, Cistué L, de Jong JH, Romagosa I, Jansen J (2011) Linkage map construction involving a reciprocal translocation. *Theor Appl Genet* 122:1029-1037
- FAOSTAT, 2015. Agriculture data. Available from: <http://faostat3.fao.org/home/index.html>. Accessed 25 November 2015.
- Fishman L, Kelly AJ, Morgan E, Willis JH (2001) A genetic map in the *Mimulus guttatus* species complex reveals transmission ratio distortion due to heterospecific interactions. *Genetics* 159:1701-1716
- Francia E, Tacconi G, Crosatti C, Barabaschi D, Bulgarelli D, Dall'Aglio E, Valè G (2005) Marker-assisted selection in crop plants. *Plant Cell Tissue Organ Cult* 82:317-342
- Frewen BE, Chen THH, Howe GT, Davis J, Rohde A, Boerjan W, Bradshaw HD (2000) Quantitative trait loci and candidate gene mapping of bud set and bud flush in *Populus*. *Genetics* 154:837-845
- Germain E, Sarraquigne JP (2004) Le noisetier. Ctifl INRA, pp 299
- Gürçan K, Mehlenbacher SA, Botta R, Boccacci P (2010) Development, characterization, segregation, and mapping of microsatellite markers for European hazelnut (*Corylus avellana* L.) from enriched genomic libraries and usefulness in genetic diversity studies. *Tree Genet Genomes* 6:513-531
- Gürçan K, Mehlenbacher SA (2010a) Development of microsatellite loci for European hazelnut (*Corylus avellana* L.) from ISSR fragments. *Mol Breeding* 26:551-559
- Gürçan K, Mehlenbacher SA (2010b) Transferability of microsatellite markers in the Betulaceae. *J Am Soc Hortic Sci* 135(2):159-173
- Hackett CA, Broadfoot LB (2003) Effects of genotyping errors, missing values and segregation distortion in molecular marker data on the construction of linkage maps. *Heredity* 90:33-38
- Harel-Beja R, Sherman A, Rubinstein M, Eshed R, Bar-Ya'akov I, Trainin T, Ophir R, Holland D (2015) A novel genetic map of pomegranate based on transcript markers enriched with QTLs for fruit quality traits. *Tree Genet Genomes* 11:109

- Howe GT, Aitken SN, Neale DB, Jermstad KD, Wheeler NC, Chen TH (2003) From genotype to phenotype: unraveling the complexities of cold adaptation in forest trees. *Can J Bot* 81:1247-1266
- Huang YF, Poland JA, Wight CP, Jackson EW, Tinker NA (2014) Using genotyping-by-sequencing (GBS) for genomic discovery in cultivated oat. *PLoS ONE* 9:e102448
- IPGRI (Bioversity International), FAO and CIHEAM (2008) Descriptors for hazelnut (*Corylus avellana* L.). Bioversity International, Rome, Italy; Food and Agriculture Organization of the United Nations, Rome, Italy; International Centre for Advanced Mediterranean Agronomic Studies, Zaragoza, Spain. Available at: <http://www.bioversityinternational.org>
- Ives C, Sathuvalli VR, Colburn BC and Mehlenbacher SA (2014) Mapping the incompatibility and style color loci in two hazelnut progenies. *HortSci* 49(3):250-253
- Jansen RC, Stam P (1994) High-resolution of quantitative traits into multiple loci via interval mapping. *Genetics* 136:1447-1455
- Jenczewski E, Gherardi M, Bonnin I, Prosperi JM, Olivieri I, Huguet T (1997) Insight on segregation distortions in two intraspecific crosses between annual species of *Medicago* (Leguminosae). *Theor Appl Genet* 94:682-691
- Jermstad KD, Bassoni DL, Jech KS, Wheeler NC, Neale DB (2001) Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. I. Timing of vegetative bud flush. *Theor Appl Genet* 102:1142-1151
- Jermstad KD, Bassoni DL, Jech KS, Ritchie GA, Wheeler NC, Neale DB (2003) Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas fir. III. Quantitative trait loci-by-environment interactions. *Genetics* 165:1489-1506
- Jeuken M, van Wijk R, Peleman J, Lindhout P (2001) An integrated interspecific AFLP map of lettuce (*Lactuca*) based on two *L-sativa* x *L-saligna* F-2 populations. *Theor Appl Genet* 103:638-647
- Johansson T, Le Quéré A, Ahren D, Söderström B, Erlandsson R, Lundeberg J, Uhlén M, Tunlid A (2004) Transcriptional responses of *Paxillus involutus* and *Betula pendula* during formation of ectomycorrhizal root tissue. *Mol Plant Microbe Interact* 17(2):202-215
- Jones ES, Sullivan H, Bhattaramakki D, Smith JS (2007) A comparison of simple sequence repeat and single nucleotide polymorphism marker technologies for the genotypic analysis of maize (*Zea mays* L.). *Theor Appl Genet* 115:361–371
- Jordan DR, Casu RE, Besse P, Carroll BC, Berding N, McIntyre CL (2004) Markers associated with stalk number and suckering in sugarcane colocate with tillering and rhizomatousness QTLs in sorghum. *Genome* 47:988-993
- Jorge V, Dowkiw A, Faivre-Rampant P, Bastien C (2005) Genetic architecture of qualitative and quantitative *Melampsora larici-populina* leaf rust resistance in hybrid poplar: genetic mapping and QTL detection. *New Phytol* 167:113-127
- Julio E, Denoyes-Rothan B, Verrier JL, Dorlhac de Borne F (2006) Detection of QTLs linked to leaf and smoke properties in *Nicotiana tabacum* based on a study of 114 recombinant inbred lines. *Mol Breeding* 18:69-91
- Kasapligil B (1972) A bibliography on *Corylus* (Betulaceae) with annotations. *Annual Report of the Northern Nut Growers Association* 63:107-162
- Kosambi D (1944) The estimation of map distances from recombination values. *Ann Eugen* 12:172–175
- Kremer A (1992) Prediction of age-age correlations of total height based on serial correlations between height increments in maritime pine (*Pinus pinaster* Ait.). *Theor Appl Genet* 85:152-158
- Kuang H, Richardson T, Carson S, Wilcox P, Bongarten B (1999) Genetic analysis of inbreeding depression in plus tree 850.55 of *Pinus radiata* D. Don I. Genetic map with distorted markers. *Theor Appl Genet* 98:697-703

- Kubisiak TL, Nelson CD, Staton ME, Zhebentyayeva T, Smith C, Olukolu BA, Fang GC, Hebard FV, Anagnostakis S, Wheeler N, Sisco PH, Abbott AG, Sederoff RR (2013) A transcriptome-based genetic map of Chinese chestnut (*Castanea mollissima*) and identification of regions of segmental homology with peach (*Prunus persica*). *Tree Genet Genomes* 9(2):557-571
- Lander ES, Botstein D (1989) Mapping mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics* 121:185-199
- Lespinasse D, Rodier-Goud M, Grivet L, Leconte A, Legnate H, Seguin M (2000) A saturated genetic linkage map of rubber tree (*Hevea* spp.) based on RFLP, AFLP, microsatellite, and isozyme markers. *Theor Appl Genet* 100:127-138
- Li P, Adams WT (1993) Genetic control of bud phenology in polesize trees and seedlings of coastal Douglas-fir. *Can J For Res* 23:1043-105
- Li Z, Jakkula L, Hussey RS, Tamulonis JP, Boerma HR (2001) SSR mapping and confirmation of the QTL from PI96354 conditioning soybean resistance to southern root-knot nematode. *Theor Appl Genet* 103:1167-1173
- Lind M, Källman T, Chen J, Ma X-F, Bousquet J, Morgante M, Zaina G, Karlsson B, Elfstrand M, Lascoux M, Stenlid J (2014) A *Picea abies* linkage map based on SNP markers identifies QTLs for four aspects of resistance to *Heterobasidion parviporum* infection. *PLoS ONE* 9(7):e101049
- Livingstone KD, Churchill G, Jahn MK (2000) Linkage mapping in populations with karyotypic rearrangements. *J Hered* 91:423-428
- Lorieux M, Goffinet B, Perrier X, Deleon D, Lanaud C (1995a) Maximum-likelihood models for mapping genetic markers showing segregation distortion. 1. Backcross populations. *Theor Appl Genet* 90:73-80
- Lorieux M, Perrier X, Goffinet B, Lanaud C, Deleon D (1995b) Maximum-likelihood models for mapping genetic markers showing segregation distortion. 2. F2 populations. *Theor Appl Genet* 90:81-89
- Lyttle TW (1991) Segregation distorters. *Annu Rev Genet* 25:511-557
- Martínez-García PJ, Parfitt DE, Ogundiwin EA, Fass J, Chan HM, Ahmad R, Lurie S, Dandekar A, Gradziel TM, Crisosto CH (2013) High density SNP mapping and QTL analysis for fruit quality characteristics in peach (*Prunus persica* L.). *Tree Genet Genomes* 9:19-36
- Mehlenbacher SA (1991) Hazelnut (*Corylus*). Genetic resources of temperate fruit and nut crops. *Acta Hort* 290:791-863
- Mehlenbacher SA, Brown RN, Davis JW, Chen H, Bassil NV, Smith DC, Kubisiak TL (2004) RAPD markers linked to eastern filbert blight resistance in *Corylus avellana*. *Theor Appl Genet* 108(4):651-656
- Mehlenbacher SA, Brown RN, Nouhra ER, Gökirmak T, Bassil NV, Kubisiak TL (2006) A genetic linkage map for hazelnut (*Corylus avellana* L.) based on RAPD and SSR markers. *Genome* 49:122-133
- Parelle J, Zapater M, Scotti-Saintagne C, Kremer A, Jolivet Y, Dreyer E, Brendel O (2007) Quantitative trait loci of tolerance to waterlogging in a European oak (*Quercus robur* L.): physiological relevance and temporal effect patterns. *Plant Cell Environ* 30:422-434
- Paterson AH, Lander ES, Hewitt JD, Peterson S, Lincoln SE, Tanksley SD (1988) Resolution of quantitative traits into mendelian factors by using a complete linkage map of restriction fragment length polymorphisms. *Nature* 335:721-72
- Pekkinen M, Varvio S, Kulju K, Karkkainen H, Smolander S, Vihera-Aarnio A, Koski V, Sillanpää M (2005) Linkage map of birch, *Betula pendula* Roth, based on microsatellites and amplified fragment length polymorphisms. *Genome* 48(4):619-625
- Pilet-Nayel ML, Muehlbauer FJ, McGee RM, Kraft JK, Baranger AB, Coyne CJ (2002) Quantitative trait loci for partial resistance to *Aphanomyces* root rot in pea. *Theor Appl Genet* 106:28-39

- Plomion C, Durel CE, O'Malley DM (1996) Genetic dissection of height in maritime pine seedlings raised under accelerated growth conditions. *Theor Appl Genet* 93:849-858
- Portis E, Mauromicale G, Mauro R, Acquadro A, Scaglione D, Lanteri S (2009) Construction of a reference molecular linkage map of globe artichoke (*Cynara cardunculus* var. *scolymus*). *Theor Appl Genet* 120:59-70
- Portis E, Scaglione D, Acquadro A, Mauromicale G, Mauro R, Knapp SJ, Lanteri S (2012) Genetic mapping and identification of QTL for earliness in the globe artichoke/cultivated cardoon complex. *BMC Res Notes* 5:252
- Radicati L, Martino I, Vergano G (1994) Factors affecting sucker production in hazelnut. *Acta Hort* 351:489-494
- Rai MK, Shekhawat NS (2014) Genomic resources in fruit plants: an assessment of current status. *Crit Rev Biotechnol* Early Online: 1-10, DOI: 10.3109/07388551.2014.898127
- Riaz S, Tenscher AC, Ramming DW, Walker MA (2011) Using a limited mapping strategy to identify major QTLs for resistance to grapevine powdery mildew (*Erysiphe necator*) and their use in marker-assisted breeding. *Theor Appl Genet* 122:1059-1073
- Rodzen J, May B (2002) Inheritance of microsatellite loci in the white sturgeon (*Acipenser transmontanus*). *Genome* 45:1064-1107
- Rohde A, Storme V, Jorge V, Gaudet M, Vitacolonna N, Fabbrini F, Ruttink T, Zaina G, Marron N, Dillen S, Steenackers M, Sabatti M, Morgante M, Boerjan W, Bastien C (2011) Bud set in poplar-genetic dissection of a complex trait in natural and hybrid populations. *New Phytol* 189:106-121
- Salazar JA, Rubio M, Ruiz D, Tartarini S, Martínez-Gómez P, Dondini L (2015) SNP development for genetic diversity analysis in apricot. *Tree Genet Genomes* 11:15 DOI 10.1007/s11295-015-0845-2
- Salesses G (1973) Etude cytologique du genre *Corylus* mise en évidence d'une translocation hétérozygote chez quelques variétés de noisetier cultivé (*C. avellana*), a fertilité pollinique réduite. *Ann Amélior Plantes* 23:59-66
- Salesses G, Bonnet A. (1988) Etude cytogénétique d'hybrides entre variétés de noisetier (*Corylus avellana*) porteuses d'une translocation à l'état hétérozygote. *Cytologia* 53:407-413
- Santino A, De Paolis A, Gallo A, Quarta A, Casey R, Mita G (2003) Biochemical and molecular characterization of hazelnut (*Corylus avellana*) seed lipoxygenases. *Eur J Biochem* 270:4365-4375
- Sargent DJ, Davis TM, Tobutt KR, Wilkinson MJ, Battey NH, Simpson DW (2004). A genetic linkage map of microsatellite, gene-specific and morphological markers in diploid *Fragaria*. *Theor Appl Genet* 109:1385-1391
- Sathuvalli VR, Chen H, Mehlenbacher SA, Smith DC (2011) DNA markers linked to eastern filbert blight resistance in "Ratoli" hazelnut (*Corylus avellana* L.). *Tree Genet Genomes* 7(2):337-345
- Sathuvalli VR, Mehlenbacher SA (2011) A bacterial artificial chromosome library for 'Jefferson' hazelnut and identification of clones associated with eastern filbert blight resistance and pollen-stigma incompatibility. *Genome* 54: 862-867
- Sathuvalli VR, Mehlenbacher SA, Smith DC (2012) Identification and mapping of DNA markers linked to eastern filbert blight resistance from OSU 408.040 hazelnut. *HortSci* 47:570-573
- Sathuvalli VR, Mehlenbacher SA (2013) De novo sequencing of hazelnut bacterial artificial chromosomes (BACs) using multiplex Illumina sequencing and targeted marker development for eastern filbert blight resistance. *Tree Genet Genomes* 9(4):1109-1118
- Schlautman B, Covarrubias-Pazarán G, Diaz-García LA, Johnson-Cicalese J, Iorizzo M, Rodríguez-Bonilla L, Bougie T, Bougie T, Wiesman E, Steffan S, Polashock J, Vorsa N, Zalapa J (2015) Development of a high-density cranberry SSR linkage map for comparative genetic analysis and trait detection. *Mol Breed* 35:177
- Schuelke M (2000) An economic method for the fluorescent labeling of PCR fragments. *Nat Biotechnol* 18:223-224

- Scotti-Saintagne C, Bodénès C, Barreneche T, Bertocchi E, Plomion C, Kremer A (2004) Detection of quantitative trait loci controlling bud burst and height growth in *Quercus robur* L. *Theor Appl Genet* 109:1648-1659
- Sebastian RL, Howell EC, King GJ, Marshall DF, Kearsey MJ (2000) An integrated AFLP and RFLP *Brassica oleracea* linkage map from two morphologically distinct doubled-haploid mapping populations. *Theor Appl Genet* 100:75-81
- Shaw P, Turan C, Wright J, O'Connell M, Carvalho G (1999) Microsatellite DNA analysis of population structure in Atlantic herring (*Clupea harengus*), with direct comparison to allozyme and mtDNA RFLP analyses. *Heredity* 83:490-499
- Soriano JM, Vera-Ruiz EM, Vilanova S, Martínez-Calvo J, Llácer A, Badenes ML, Romero C (2008) Identification and mapping of a locus conferring plum pox virus resistance in two apricot-improved linkage maps. *Tree Genet Genomes* 4:391-402
- Sun R, Chang Y, Yang F, Wang Y, Li H, Zhao Y, Chen D, Wu T, Zhang X, Han Z (2015) A dense SNP genetic map constructed using restriction site-associated DNA sequencing enables detection of QTLs controlling apple fruit quality. *Genomics* 16:747
- Tancred SJ, Zeppa AG, Cooper M, Stringer JK (1995) Heritability and patterns of inheritance of the ripening date of apples. *Hort Sci* 30:325-328
- Tsarouhas V, Gullberg U, Lagercrantz U (2002) An AFLP and RFLP linkage map and quantitative trait locus (QTL) analysis of growth traits in *Salix*. *Theor Appl Genet* 105:277-288
- Tschaplinski TJ, Tuskan GA, Sewell MM, Gebre GM, Todd DE, Pendley CD (2006) Phenotypic variation and quantitative trait locus identification for osmotic potential in an interspecific hybrid inbred F2 poplar pedigree grown in contrasting environments. *Tree Physiol* 26:595-604
- UPOV [International Union for the Protection of New Varieties of Plants] (1979) Hazelnut (*Corylus avellana* L. & *Corylus maxima* Mill.): Guidelines for the conduct of tests for distinctness, uniformity and stability. Hazelnut/Noisetier/Haselnuss, 79-03-28. Doc. No. TG/71/3. UPOV, Geneva, Switzerland. Available at: [http://www.upov.int/en/publications/tgrom/tg071/tg\\_71\\_3.pdf](http://www.upov.int/en/publications/tgrom/tg071/tg_71_3.pdf)
- Valentini N, Ghirardello D, Me G (2004) Heritability of morphological and vegetative traits in *Corylus* spp. *Acta Hort* 663:317-320
- Van Ooijen JW (1992) Accuracy of mapping quantitative trait loci in autogamous species. *Theor Appl Genet* 84(7-8):803-811
- Van Ooijen JW, Boer MP, Jansen RC, Maliepaard C (2002) MapQTL 4.0: software for the calculation of QTL positions on genetic maps. Plant Research International, Wageningen, The Netherlands
- Van Ooijen J (2006) JoinMap® 4: software for the calculation of genetic linkage maps in experimental populations. Kyazma BV, Wageningen, The Netherlands
- Van Oosterhout C, Hutchinson W, Wills D, Shipley P (2004) MICRO-CHEKER: software for identifying and correcting genotyping errors in microsatellite data. *Mol Ecol Notes* 4:535-538
- Virlet N, Costes E, Martinez S, Kelner JJ, Regnard JL (2015) Multispectral airborne imagery in the field reveals genetic determinisms of morphological and transpiration traits of an apple tree hybrid population in response to water deficit. *J Exp Bot* 66(18):5385-5387
- Voorrips R (2002) MapChart: Software for the graphical presentation of linkage maps and QTLs. *J Hered* 93(1):77-78
- Wu SB, Collins G, Sedgley M (2004) A molecular linkage map of olive (*Olea europaea* L.) based on RAPD, microsatellite, and SCAR markers. *Genome* 47:26-35

- Yang H, Liu T, Xu B, Liu C, Zhao F, Huang S (2015) QTL detection for growth and form traits in three full-sib pedigrees of *Pinus elliottii* var. *elliottii* × *P. caribaea* var. *hondurensis* hybrids. *Tree Genet Genomes* 11:130
- Zarpelon TG, da Silva Guimarães LM, Assis Faria D, Magalhães Coutinho M, Cápua Neto B, Ubirajara Teixeira R., Grattapaglia D, Couto Alfenas A (2015) Genetic mapping and validation of QTLs associated with resistance to *Calonectria* leaf blight caused by *Calonectria pteridis* in Eucalyptus. *Tree Genet Genomes* 11(1):803
- Zhang K, Wang D, Yang C, Liu G, Liu G, Zhang H, Lian L, Wei Z (2012) Linkage map construction and QTL analysis for *Betula platyphylla* Suk using RAPD, AFLP, ISSR and SSR. *Silvae Genet* 61:1-9
- Zhang RP, Wu J, Li XG, Awais Khan M, Chen H, Korban SS, Zhang SL (2013) An AFLP, SRAP, and SSR genetic linkage map and identification of QTLs for fruit traits in pear (*Pyrus* L.). *Plant Mol Biol Rep* 31:678-

## List of Tables

**Table 1** Characteristics and alignment of the TGdL x MB consensus linkage map

Linkage group name	Size (cM)	Total markers	Marker density (cM/No. markers)	Gaps (> 15 cM)	Alignment with OSU 252.146 x OSU 414.062 map <sup>1</sup>	
					Aligned LGs	Shared markers
LG_01	98.9	14	7.06	2	LG1S + LG1R	8
LG_02	58.4	17	3.44	1	LG2S + LG2R	8
LG_03	48.8	11	4.88	1	LG3S + LG3R	7
LG_04	71.7	15	4.78	0	LG4S + LG4R	13
LG_05	52.3	14	3.74	1	LG5S + LG5R	9
LG_06	33.8	4	8.45	0	LG6S + LG6R	3
LG_07	51.8	11	4.71	2	LG7S + LG7R	10
LG_08	47.0	15	3.36	0	LG8S + LG8R	15
LG_09	74.8	25	3.25	0	LG9S + LG9R	14
LG_10	66.6	15	4.76	0	LG10S + LG10R	12
LG_11	59.0	14	4.54	1	LG11S + LG11R	7
<b>Total</b>	<b>663.1</b>	<b>155</b>		<b>8</b>		<b>106</b>
<b>Average</b>	<b>60.28</b>	<b>13.55</b>	<b>4.45</b>	<b>0.73</b>		<b>9.64</b>

<sup>1</sup> Alignment with the maps published by Gürcan et al. 2010 and Gürcan and Mehlenbacher 2010a and based on a cross between genotypes from a maternal parent (OSU 252.146) susceptible and a male parent (OSU 414.062) resistant to eastern filbert blight

**Table 2** Parent means ( $\pm$ SD) and population mean ( $\pm$ SD) and range for the traits. Skewness and Kurtosis ( $\pm$ SE) and values of broad sense heritability for the traits are also listed

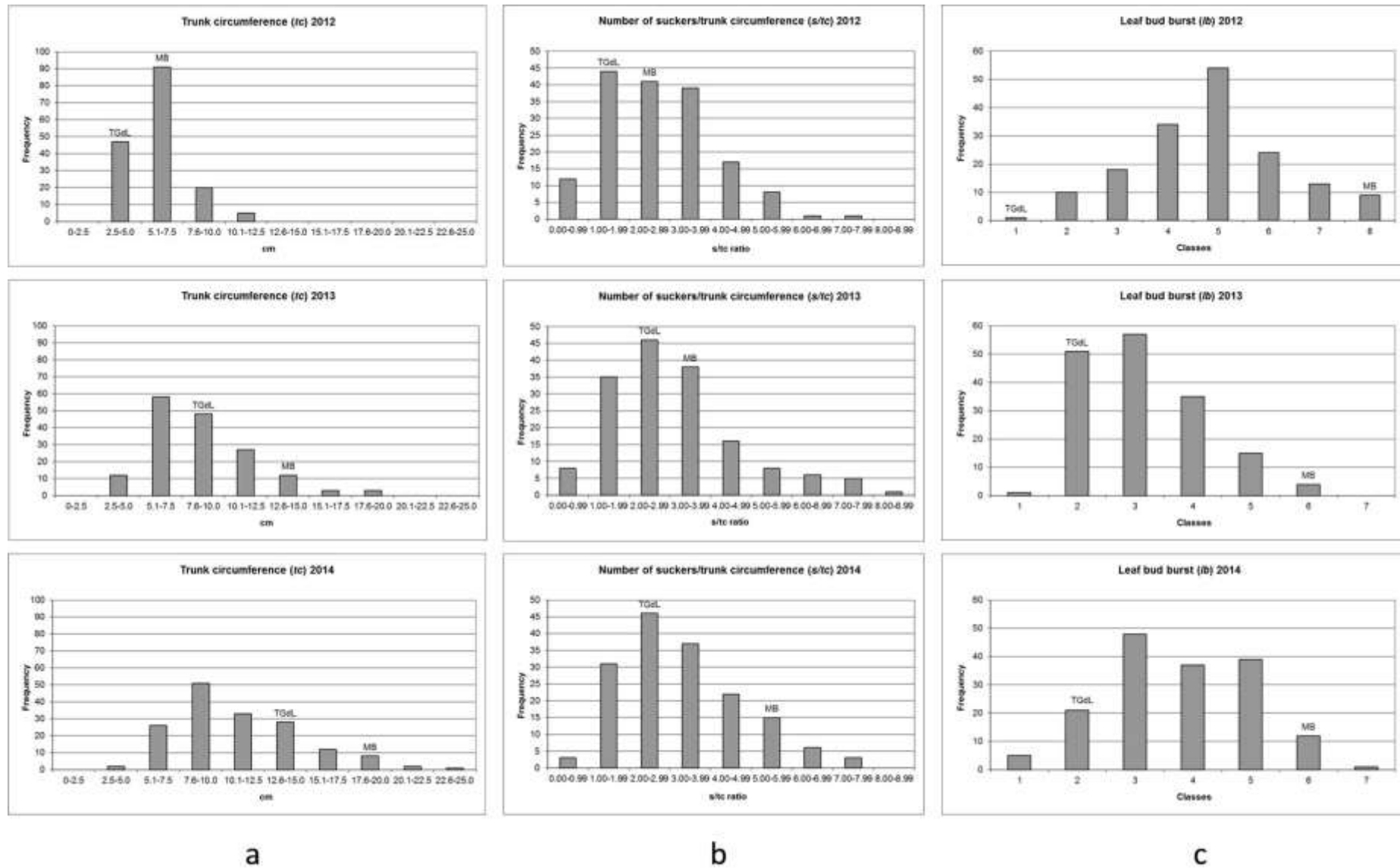
Trait	Trait code	Year	Parent means $\pm$ SD		Significant mean difference among parental values (wilcoxon test)	F <sub>1</sub> population mean $\pm$ SD	Range	SE	Skewness	SE	Kurtosis	SE	Heritability H <sup>2</sup> <sub>BS</sub>
			TGdL	MB									
Trunk circumference (cm)	<i>tc</i>	2012	4.55 $\pm$ 0.7	7.07 $\pm$ 1.1	Yes: p<0.1	5.90 $\pm$ 1.57	3.14 – 10.99	0.12	0.85	0.19	0.89	0.38	0.60
		2013	9.50 $\pm$ 0.7	13.25 $\pm$ 1.0	Yes: p<0.05	8.84 $\pm$ 2.99	4.00 – 18.00	0.23	0.92	0.19	0.53	0.38	
		2014	13.25 $\pm$ 0.4	18.50 $\pm$ 2.8	Yes: p<0.1	11.25 $\pm$ 3.79	4.50 – 25.00	0.30	0.83	0.19	0.54	0.38	
No. of suckers/trunk circumference (No./cm)	<i>s/tc</i>	2012	1.67 $\pm$ 1.8	2.79 $\pm$ 1.5	ns	2.71 $\pm$ 1.30	0.00 – 7.35	0.10	0.56	0.19	0.16	0.38	0.85
		2013	2.79 $\pm$ 2.8	3.77 $\pm$ 2.8	ns	3.03 $\pm$ 1.62	0.00 – 8.67	0.13	0.96	0.19	0.98	0.38	
		2014	2.20 $\pm$ 0.5	5.28 $\pm$ 0.4	Yes: p<0.05	3.26 $\pm$ 1.47	0.25 – 7.37	0.15	0.62	0.19	-0.09	0.38	
Leaf bud burst (rating: 1 to 9)	<i>lb</i>	2012	1.0 $\pm$ 0.0	8.0 $\pm$ 0.0	Yes: p<0.01	4.83 $\pm$ 1.50	1.0 – 8.0	0.12	0.08	0.19	-0.13	0.38	0.74
		2013	2.0 $\pm$ 0.0	5.5 $\pm$ 0.7	Yes: p<0.01	3.15 $\pm$ 1.60	1.0 – 6.0	0.08	0.64	0.19	-0.18	0.38	
		2014	1.5 $\pm$ 0.7	6.0 $\pm$ 0.0	Yes: p<0.01	3.76 $\pm$ 1.28	1.0 – 7.0	0.10	0.01	0.19	-0.61	0.38	

**Table 3** QTL detected in the mapping population for trunk circumference (*tc*), number of suckers/trunk circumference ratio (*s/tc*) and leaf bud burst (*lb*). Each QTL name is formed by the abbreviated form of the trait followed by the relevant LG. The table indicates genome-wide LOD thresholds (GW) as determined by a permutation test at  $P \leq 0.05$ , the closest linked markers (Locus) and their map position in cM, the estimated LODs at the QTL peak (LOD), and the proportions (%) of the total phenotypic variance (PV) explained

Trait code	LG	QTL	2012					2013					2014				
			GW	Position	Locus	LOD	PV	GW	Position	Locus	LOD	PV	GW	Position	Locus	LOD	PV
<i>tc</i>	05	tc_05	3.1	16.4	B625	4.0	11.4	3.3	25.2	KG800b	3.8	12.7	3.2	26.3	KG800a	3.3	13.6
	08	tc_08		26.9	B773	3.1	8.5		-	-	-	-		-	-	-	-
<i>s/tc</i>	01	s/tc_01	3.6	-	-	-	-	3.3	77.8	KG857	3.4	8.1	3.5	77.8	KG857	4.5	10.9
	05	s/tc_05		-	-	-	-		-	-	-	-	17.9	CaT-B503	6.5	17.1	
	08	s/tc_08		-	-	-	-		-	-	-	-	0.0	B726	4.0	9.8	
	10	s/tc_10		11.4	A602	5.3	14.9		11.4	A602	3.5	10.1		11.4	A602	3.5	8.7
	11	s/tc_11		59.0	B652	3.8	9.3		-	-	-	-		-	-	-	-
<i>lb</i>	02	lb_02	4.2	12.1	AJ417975b	21.4	45.4	4.8	12.1	AJ417975b	26.0	52.0	4.7	12.1	AJ417975b	26.9	53.2



**Fig. 2** Frequency distributions of trunk circumference (a), number of suckers/trunk circumference ratio (b), leaf budburst (c) for the progeny derived from TGdL x MB in 2012, 2013 and 2014. Data are grouped in classes. Means for the parents TGdL and MB are shown for each histogram



**Fig. 1** Consensus genetic linkage map of TGdL x MB progeny and locations of QTLs for trunk circumference (*tc*), number of suckers/trunk circumference ratio (*s/tc*) and leaf budburst (*lb*) in 2012, 2013 and 2014 using the multiple QTL mapping method. Marker names are shown to the right of each LG, with map distance (in cM) to the left. Markers showing significant levels of segregation distortion are indicated by asterisks (0.1>\*P>0.05; 0.05>\*\*P>0.01; 0.01>\*\*\*P>0.005; 0.005>\*\*\*\*P>0.001; \*\*\*\*\*P>0.001). Black bars represent QTLs: each is indicated by trait code\_LG number\_year. 1-LOD support intervals of each QTL are marked by thin bars

