HAL
open science

Acibenzolar-S-methyl and resistance quantitative trait loci complement each other to control apple scab and fire blight

Juliette Bénéjam, Elisa Ravon, Matthieu Gaucher, Marie-Noëlle Brisset, Charles-Eric Durel, Laure Perchepied

To cite this version:

Juliette Bénéjam, Elisa Ravon, Matthieu Gaucher, Marie-Noëlle Brisset, Charles-Eric Durel, et al.. Acibenzolar-S-methyl and resistance quantitative trait loci complement each other to control apple scab and fire blight. Plant Disease, 2020, 105 (6), pp.1702-1710. 10.1094/pdis-07-20-1439-re . hal-03034383

HAL Id: hal-03034383

https://hal.inrae.fr/hal-03034383v1

Submitted on 1 Dec 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Copyright

Acibenzolar-S-methyl and resistance quantitative trait loci complement each other to control apple scab and fire blight

Juliette Bénéjam, Elisa Ravon, Matthieu Gaucher, Marie-Noëlle Brisset, Charles-Eric Durel*, Laure Perchepied

UMR 1345 Institut de Recherche en Horticulture et Semences (IRHS), INRAE, Université d'Angers, Institut-Agro Agrocampus-Ouest, SFR 4207 QuaSaV, 49071, Beaucouzé, France

*Corresponding author: Charles-Eric Durel, charles-eric.durel@inrae.fr

Abstract

Diversifying disease control methods is a key strategy to sustainably reduce pesticides. Plant genetic resistance has long been used to create resistant varieties. Plant resistance inducers (PRI) are also considered to promote crop health, but their effectiveness is partial and can vary according to the environment and the plant genotype. We investigated the putative interaction between intrinsic (genetic) and PRI-induced resistance in apple when affected by scab and fire blight diseases. A large F1 mapping population was challenged by each disease after a pre-treatment with acibenzolar-S-methyl (ASM) and compared with the water control. Apple scab and fire blight resistance quantitative trait loci (QTLs) were detected in both conditions and compared. ASM exhibited a strong effectiveness in reducing both diseases. When combined, QTL-controlled and ASM-induced resistance acted complementarily to reduce the symptoms from 85% to 100% depending on the disease. In our conditions, resistance QTLs were only slightly or rarely affected by ASM treatment, despite their

probable implication in various stages of the resistance build-up. Implications of these results are discussed considering already known results, the underlying mechanisms, cross-protection of both types of resistance against pathogen adaptation, and practical application in orchard conditions.

Keywords: Intrinsic resistance, induced defense, *Malus domestica, Venturia inaequalis, Erwinia amylovora*

Introduction

Plant diseases threaten global agricultural production, leading to the extensive use of pesticides. Plant genetic resistance is considered as a major lever, and breeding for new resistant varieties is very active in most crop species. However resistance genes exert selection pressures on pathogens, triggering their evolution (McDonald and Linde, 2002). Diversifying and pyramiding resistance genes, especially when controlling both qualitative and quantitative resistance, is considered as a promising approach for achieving durable resistance (Pilet-Nayel et al., 2017). Such diversification is indeed expected to promote conflicting selection pressures on pathogen populations, which should constrain them to an evolutionary compromise limiting their development.

Reduced reliance on conventional pesticides can be also achieved by biocontrol (Pal and McSpadden Gardener, 2006; Burketova et al., 2015). Plant resistance inducers (PRIs, also called elicitors or plant defense activators) are part of biocontrol methods. They include a range of chemical (Bektas and Eulgem, 2015) or biological (Wiesel et al., 2014) stimulators able to activate plant defenses, without direct toxicity against pathogens (Oostendorp et al., 2001; Oliveira et al., 2016). PRIs provide most often partial resistance only and their performance are greatly influenced by abiotic and biotic factors including the pathogen and the plant genotype (Walters et al., 2013). However,

50 mechanisms underlying these numerous interactions are not clearly understood.
51 Regarding the plant, comprehensive knowledge on genotype-PRI interactions could
52 re-orientate plant breeding programs towards responsive genotypes or assist the
53 choice of varieties to be deployed in practice, especially if PRIs are intended to be used
54 in pest management programs. Combination of genetic resistance with PRIs are
55 expected to multiply selection pressures on pathogen populations and thus limit their
56 evolution, similarly to the combination of genetic resistance.

57 Apple (*Malus domestica*) is a major fruit tree species which requires a tremendous
58 amount of pesticides in temperate climate conditions (MacHardy, 1996). Apple
59 genotypes display a great variability of responses to apple scab, caused by the
60 ascomycete fungus *Venturia inaequalis* and fire blight, caused by the bacterium
61 *Erwinia amylovora*, two major diseases impacting orchards. Genetic mapping studies
62 revealed numerous R genes and QTLs involved in resistance against apple scab
63 (summarized in Khajuria et al., 2018) and fire blight (reviewed in Malnoy et al., 2012;
64 Emeriewen et al., 2019), conferring partial to complete resistance to the diseases.
65 Some of these loci are known to be strain-specific, with breakdown of resistance
66 already demonstrated (Parisi, 1993; Caffier et al., 2010, 2015; Wöhner et al., 2014;
67 Peil et al., 2020; Patocchi et al., 2020). The *Rvi6* gene, also called *Vf* from *Malus*
68 *floribunda*, was one of the genes most widely used in apple breeding programs but
69 was overcome as early as 1981 by *V. inaequalis* race 6 (Parisi, 1993). In apple, as in
70 most plant species, quantitative resistance is considered more durable than qualitative
71 resistance due to the multiple loci controlling selection pressure on pathogen
72 populations (Parlevliet, 2002; Pilet-Nayel et al., 2017). However a slow erosion of some
73 QTLs has already been demonstrated (Caffier et al., 2014, 2016).

Acibenzolar-S-methyl (ASM), a functional salicylic acid analog, is one of the most promising PRIs on several plant species (Gozzo and Faoro, 2013). It promotes systemic acquired resistance (SAR) and consequently the induction of various defense responses including pathogenesis-related proteins, leading to the protection of many species against a broad spectrum of pathogens (Romero et al., 2001; Assis et al., 2015; Matsuo et al., 2019; Youssef et al., 2019; Ishiga et al., 2020). On apple, several studies reported significant control of apple scab (Bengtsson et al., 2006, 2009; Marolleau et al., 2017) and fire blight (Brisset et al., 2000; Maxson-Stein et al., 2002; Hassan and Buchenauer, 2007; Abo-Elyousr et al., 2010; Shahini Sough et al., 2010; Dugé de Bernonville et al., 2014; Aćimović et al., 2015; Johnson et al., 2016; Marolleau et al., 2017), as well as the triggering of molecular defense response (Brisset et al., 2000; Ziadi et al., 2001; Maxson-Stein et al., 2002; Dugé de Bernonville et al., 2014; Warneys et al., 2018). Although significant, performance of ASM exhibits variability that remains to be understood for its practical use in the orchard. Among others, the genetic factor is still poorly investigated.

In this paper, we explored the added value of combining intrinsic (genetic) resistance against apple scab and fire blight with induced resistance conferred by ASM using a genetic mapping approach. QTLs composition in a segregating population was compared between ASM-treated and -untreated plants in order to highlight genetic determinants which could explain or interact with ASM performance.

Materials and Methods

Plant material. All experiments were performed with a F1 population referred as the 'TxF progeny' and previously described in Laloi et al. (2016). The 267 individuals were derived from a controlled cross between TN10-8 and Fiesta, two genotypes partially resistant to apple scab. Fiesta is also partially resistant to fire blight. For each

99 experiment, up to ten replicates per individual were grafted and grown in greenhouse
100 under semi-controlled growing conditions (23°C day/20°C night, humidity 40-80% and
101 artificial light to complement natural light). Graftwood was collected from a
102 conservatory orchard located at INRAE (Angers, France) and grafted on MM106 apple
103 rootstock. The two parents and two susceptible control cultivars (Golden Delicious and
104 Gala) were also included in each experiment in 10 replicates.

105 **Experimental design, treatment application and phenotypic data collection.** For
106 each experiment, out of the ten, four replicates with active growing shoots per individual
107 and treatment condition were chosen and distributed in each treatment group in
108 randomized blocks in the greenhouse. Two days before inoculation, plants were
109 sprayed with a solution of BION® 50 WG (50% ASM; Syngenta, Basel, Switzerland)
110 (called ASM treatment) or with reverse osmosis water as control (called the water
111 control). A water dilution of 0.2 $g.L^{-1}$ for *V. inaequalis*-inoculated plants and 0.4 g.L-1
112 for *E. amylovora*-inoculated ones was applied. The commercial advice (0.4 $g.L^{-1}$) was
113 reduced for scab to maintain enough phenotypic variability across TxF progeny.

114 Two *V. inaequalis* isolates were used: the reference isolate EU-B04 (Origin : Belgium,
115 host : Golden Delicious) previously described in Caffier et al. (2015) and Le Cam et al.
116 (2019) and the isolate 09BCZ014 (Origin : France, host : TN10-8 x Prima progeny
117 (individual E063), referred to as isolate 2557 in Laloi et al. (2016)). Monoconidial
118 suspensions were prepared from diseased dry leaves at a concentration of 2.5 x 10^5
119 $conidia.mL^{-1}$ and, sprayed on grafted trees, incubated thereafter two days at 17°C
120 under plastic sheet to maintain a high humidity, according to the conditions described
121 by Caffier et al. (2010). The percentage of leaf surface exhibiting sporulating lesions
122 was scored at 14, 21 and 28 days post-inoculation using the ordinal scale (0-7)

described in Calenge et al. (2004). Two experiments were performed with isolate EU-B04 (coded Vi-B04_1 et Vi-B04_2) and one with 09BCZ014 (coded Vi-Z14).

The reference strain CFPB1430 of *E. amylovora* from the French collection of phytopathogenic bacteria (Paulin and Samson, 1973) was used for inoculation. The bacterial suspension was prepared as described in Dugé de Bernonville et al. (2014) at 10^8 colony-forming units (CFU).mL^{-1}. Growing shoots (>10cm) were inoculated by cutting the two youngest unrolled leaves with scissors previously soaked in the bacterial suspension. The length of necrosis developing on stem was measured at 7, 14 and 21 days post-inoculation. The ratio between necrosis length and total shoot length was used as a severity score. Two experiments were performed (coded Ea-1430_1 and Ea-1430_2).

Data analysis of phenotypic data. Phenotypic data were analyzed separately for ASM treatment or the water control. The area under the disease-progress curve (AUDPC) was calculated as a quantitative summary of disease severity over time:

$$\mathrm{AUDPC} = \sum_{i=0}^{2} \frac{y_i + y_{i+1}}{2} x (t_{i+1} - t_i)$$

where y_i is the disease score at the ith day of observation and t_i the number of day post-inoculation at the ith observation.

All statistical analyses were performed using R software (Dalgaard, 2010). AUDPC were fitted for environmental trend effects using SpATS package (Rodríguez-Álvarez et al., 2018) which estimates a Best Linear Unbiased Prediction (BLUP) for each individual. Broad-sense heritability of each trait for each treatment was also estimated with the function 'getHeritability' of the same package.

145 **Genotyping data and genetic maps construction.** DNA was extracted from fresh
146 young leaf samples using oKtopure™ LGC Genomics robot and quantified with
147 Hoechst protocol. The TxF progeny was genotyped with the Illumina Infinium 20K
148 SNPs array (Bianco et al., 2014). Genotyping data were analyzed using
149 GenomeStudio® Genotyping Module (V2.0, Illumina Inc., San Diego, California, USA)
150 software with manual correction whenever necessary to improve dataset quality.
151 Markers were filtered according to their parental segregation profile (ABxAA for the
152 female map and AAxAB for the male map; markers in ABxAB were not considered).
153 Then a linkage map was constructed for each parent with JoinMap 4.1 software using
154 the Kosambi mapping function (Van Ooijen, 2006). Map quality was checked by
155 comparison with the apple reference genetic map of Di Pierro et al. (2016) and an
156 updated version of the map (Howard et al., submitted). The software BiomercatorV4.2
157 (Arcade et al., 2004) was used to curate manually erroneous marker positions.
158 Seventeen microsatellite (SSR) markers located in genomic regions where scab
159 resistance QTLs were expected according to previous publications were added after
160 genotyping of the TxF progeny (Supplementary Table S1).

161 **QTL mapping.** In order to compare the contribution of QTLs in resistance and in the
162 interaction between genotypes and ASM, a mapping of QTLs was performed
163 independently in water-control and ASM-treated populations. QTL analyses were
164 conducted using the R/qtl package (Broman et al., 2003). Simple interval mapping
165 (SIM) and composite interval mapping (CIM) were estimated using multiple imputation
166 method and normal distribution model. Cofactors for CIM were determined from the
167 best prediction model simulated with 'stepwise' function. LOD score threshold were
168 determined using 1000 permutations to identify the statistically significant QTLs (α =
169 0.05 genome-wide). LOD thresholds were about 5 for both scab and fire blight

experiments. Suggestive QTLs with LOD score between 3 and 5 were also considered. LOD score, 2-LOD support confidence interval (CI) and contribution of each QTL to the overall phenotypic variance (individual R^2) were extracted from R/qtl analyses, together with the global QTL contribution (global R^2). Individual and global R^2 were calculated with the 'fitqtl' (for fitting a defined multiple-QTL model) function. Interactions between QTLs were studied by variance analysis using the genotyping data of each SNP closest to the peak of each QTL and were detailed by the 'effectplot' function. These results were used to define the model for the calculation of the global R^2 with 'fitqtl'. To adequately compare QTL effects between treatments by taking into account the overall phenotypic variation in each treatment, relative QTL effect (rEffect) were calculated for each QTL as follows: $rEffect = \frac{1}{\sigma_B} \times \frac{|\mathrm{BLUP(AA)} - \mathrm{BLUP(AB)}|}{2}$, where AA and AB are the allelic versions at the SNP closest to the QTL peak and σ_B is the standard deviation of BLUP (adjusted for all other significative QTLs effects than the QTL considered) for a given treatment condition. The confidence intervals at 5% of rEffects were simulated by bootstrapping with 5000 replicates using 'boot' function: when comparing rEffects of a given QTL between the water control and ASM treatment, the overlap of the confidence intervals was interpreted as if the effects were not significantly different. For simplicity, QTL alleles were then considered equivalent to SNP alleles at QTL peaks. Besides, a QTL detected at almost the same genomic position in various experiments were considered and named as the same QTL.

In Vi-B04 experiments, a clear bimodal distribution was observed (see results below). This distribution fitted with the strong effect of the major QTL (simply called qT1 here) detected on LG1 of TN10-8 after inoculation with this isolate (Calenge et al., 2004) or with a mixture of isolates including EU-B04 (Lê Van et al., 2012). For that reason, the TxF progeny was subdivided into two subsets of individuals according to the

195 presence/absence of the resistance allele at qT1 predicted by SNP data at the QTL
196 peak. QTL analyses were then conducted on both sub-populations (further called qT1+
197 and qT1- sub-populations). Conversely, isolate 09BCZ014 was shown to partially
198 overcome the QTL qT1 by Laloi et al. (2016; isolate '2557'). QTL analysis was thus
199 performed on the whole TxF progeny with the latter isolate.
200

201 **Results**

202 **Phenotypic variability.** Only experiments involving the most replicates per individual,
203 Vi-B04_1, Vi-Z14 and Ea-1430_1 are presented here (the two additional experiments
204 Vi-B04_2 and Ea-1430_2 are available as supplementary data).

205 A significant reduction of AUDPC was observed for both scab and fire blight after ASM
206 treatment compared to the water control (Table 1). For the TxF progeny, AUDPC was
207 reduced by 54% for Vi-B04_1, 73% for Vi-Z14 and 50% for Ea-1430_1. Similar
208 reductions were observed for the two parents and susceptible controls (Figure 1). A
209 large variation was observed among individuals regardless of the conditions, with
210 AUDPC values ranging from 0 to 150 for Vi-B04_1, from 0 to 75 for Vi-Z14 and from 1
211 to 11 for Ea-1430_1 (Figure 1). A higher coefficient of variation was observed for scab
212 (CV=0.75 – 1.27) than for fire blight (CV=0.27 – 0.34; Table 1). The distributions were
213 generally unimodal except for the water control in Vi-B04_1 where a clear bimodal
214 distribution was observed (Figure 1A), fitting with the expected effect of QTL qT1 (see
215 Materials and Methods). Broad-sense heritabilities (h^2) were generally high whatever
216 the conditions, ranging from 0.63 for fire blight after ASM treatment to 0.94 for scab
217 after the water control (Table 1). Adjusting the data for spatial effects resulted in a
218 limited increase of heritability from 0.01 to 0.08 units compared to no adjustment (data
219 not shown). Correlation coefficients (Cor) between the water control and ASM

220 treatment were intermediate to high (0.6 – 0.9) according to the experiments (Figure
221 1). The range of AUDPC values observed in ASM-treated individuals increased as
222 AUDPC values of the corresponding water-treated individuals increased, suggesting
223 interactions between genotypes and treatments especially for the less resistant
224 individuals (Figure 1). AUDPC mean values were lower in Vi-B04_2 and Ea-1430_2
225 experiments but the variation of AUDPC was similar (Supplementary Table S2 and
226 Supplementary Figure S1). The correlation coefficients between both Vi-B04
227 experiments were 0.74 for the water control and 0.73 for ASM-treatment, while they
228 were only 0.19 and 0.16 between both Ea_1430 experiments, respectively.

229 **QTL detection for *V. inaequalis* isolate 'EU-B04'.** A total of 6245 SNPs was found
230 polymorphic in the TxF progeny and one or both parents. After discarding 4433 SNPs
231 polymorphic in both parents and redundant, two parental genetic maps of 17 linkage
232 groups were constructed with 853 and 959 SNPs for TN10-8 and Fiesta, respectively.
233 Both parental maps were merged in a single file for further detections of QTLs
234 (Supplementary Table S3).

235 For the water control condition, a major QTL effect (LOD ~ 77; R^2 = 69.9%) was
236 detected on LG1 together with three other significant QTLs on LG T13, F11 and F17
237 and one suggestive on LG F12 when considering the whole TxF progeny
238 (Supplementary Table S4, Figure 2). The presence of the former QTL (corresponding
239 to qT1) was consistent with the bimodal distribution observed above. In the qT1- sub-
240 population, four significant QTLs and one suggestive QTL were detected on linkage
241 groups T13, F3, F11, F17 and F12, respectively (Table2, Figure 2). They explained
242 from 3.7 to 29.0 % of phenotypic variation and their relative effect (rEffect) varied from
243 0.32 (QTL qF12) to 0.66 (QTL qF17), compared to 0.85 for QTL qT1 in the whole TxF
244 progeny (Figure 2). A significant interaction was found between QTLs qF11 and qF17

245 (Table 3). No AUDPC difference was detectable between both alleles of qF11 when
246 the 'unfavorable' (i.e., susceptible) allele of qF17 (AA) was present (genotypic classes
247 AA:AA and AB:AA with high AUDPC values at 149.6 and 146.2, respectively). With the
248 'favorable' (i.e., resistant) allele of qF17, the 'favorable' allele of qF11 was on the
249 contrary very efficient with AUDPC values decreasing from 131.3 to 99.5 for the
250 combination of QTL alleles AA:AB, indicating a complementary relationship between
251 'favorable' alleles of both QTLs. Altogether, QTLs on LG T1, T13, F11, F12 and F17
252 explained 81.9% of phenotypic variation in the whole progeny, whereas the five QTLs
253 including the QTL interaction explained 65.1% of phenotypic variation in the qT1- sub-
254 population (Table 1). For ASM-treatment condition, QTL qT1 still exhibited a strong
255 effect (LOD ~ 46; R^2 = 60%) in the whole TxF progeny (Supplementary Table S4,
256 Figure 2) together with QTLs qF17 and qF11 as a suggestive QTL (Supplementary
257 Table S4). All three explained 70.2% of the phenotypic variation. In the qT1- sub-
258 population, only three out of the five QTLs detected in the water-control condition were
259 detected (Table 2). QTLs qT13 and qF3 completely disappeared after ASM treatment
260 with a LOD score lower than 0.2 at the SNP near to the peak of the same QTL detected
261 in the water control and a non-significant effect for qF3 (Figure 2). The three other
262 QTLs were detected at roughly the same positions on linkage groups as with the water
263 control and the significant interaction between qF11 and qF17 was also found with the
264 same pattern as above (Table 3). Their relative effects were not significantly different
265 from the water control and were thus not significantly modulated by ASM treatment,
266 despite much stronger LOD score and R^2 for qF17 (21.2 and 39.9% with ASM
267 treatment compared to 12.4 and 29.0% with the water control) and lower LOD score
268 and R^2 for qF11 (7.6 and 10.7% compared to 10.7 and 18.1%, respectively) (Table 2,
269 Figure 2).

270 For experiment Vi-B04_2, the same QTLs were detected despite at lower LOD scores
271 than in the first experimentation (Supplementary Table S5). In the whole TxF progeny,
272 qT1 was still detected as the strongest QTL for both treatment conditions (LOD ~ 35;
273 R^2 ~40-48%) together with qF11 and qF12 as suggestive QTL (water control) and qF17
274 (both conditions) and still a significant interaction between qF11 and qF17
275 (Supplementary Table S6, water control). In the qT1- sub-population, qF17 was the
276 single significant QTL detected, while qT13, qF3, qF11 and qF12 were detected as
277 suggestive QTLs with mostly similar R^2 compared to the Vi-B04_1 experiment. Three
278 significant interactions between QTLs were detected, two of them involving qT13 with
279 qF11 and qF17 respectively (Supplementary Table S6). In this experiment, ASM
280 treatment did not significantly modulate the QTL effect on any of the QTLs detected
281 (Supplementary Figure S2).

282 **QTL detection for *V. inaequalis* isolate '09BCZ14'.** For the water control condition,
283 all the QTLs detected in Vi-B04_1 were also detected in Vi-Z14, except on LG F12,
284 and a new suggestive QTL was detected on LG T10. The phenotypic variation
285 explained by these QTLs ranged from 3.5 to 10.7% and the relative effects from 0.25
286 (QTL qT10) to 0.42 (QTLs qT13 and qF17) (Table 2, Figure 2). Interaction between
287 QTLs qF11 and qF17 was still significant whereas new interactions were found
288 significant between qT1 and qF3, between qT13 and qF3 and between qT10 and qF11
289 (Table 3). Altogether, these QTLs and interactions explained 47.5% of the phenotypic
290 variation (Table 1). For ASM-treatment condition, three out of the six QTLs identified
291 in the water control were still detected but only as suggestive QTLs (qT13, qF11, qF17;
292 Table 2). Altogether, they explained only 15.0% of the phenotypic variation without any
293 interactions. The relative effects of these QTLs were not significantly different when

294 compared with the water control (Figure 2). Conversely, the relative effect of qT1 was
295 significantly lower for ASM treatment than for the water control (Figure 2).

296 **QTL mapping for fire blight resistance.** For the water control condition, four QTLs
297 (two significant and two suggestive) were detected on LG T3, T5, F7 and F15
298 explaining from 3.1 to 20.1% of total phenotypic variation (Table 2, Figure 3).
299 Altogether, these QTLs explained 35.0 % of the phenotypic variation. The same QTLs
300 except LG F15 were found for ASM-treatment condition, together with a new significant
301 QTL on LG F5 (Table 2). These QTLs explained from 4.6 to 13.2% of the phenotypic
302 variation (33.1% altogether). On LG T5, the peak of the QTLs was offset by ~20cM
303 between the water control and ASM treatment, which suggests two different QTLs. The
304 relative effects of these QTLs were not significantly different when compared with the
305 water control (Figure 3). No significant interaction could be identified between the QTLs
306 in both conditions.

307 In the Ea-1430_2 experiment for water-control condition, three QTLs previously
308 identified were maintained (qT3, qT5, qF15), two new QTLs were detected (qT15, qF5)
309 and one was no longer detected (qF7) (Supplementary Table S5). Surprisingly, qF7
310 was the QTL with the strongest effect in the first experiment; only a weak peak was
311 detected here with a LOD of 1.8. For ASM treatment condition, three new QTLs qT1,
312 qT7 and qF1 were identified while three others disappeared (qT3, qT15, qF15). The
313 QTL interactions in the two conditions are totally different (Supplementary Table S6).
314 Among the nine QTLs identified, qT3 and qF15 relative effect were significantly
315 modulated by ASM (Supplementary Figure S3).

316 **Discussion**

317 A first result of our study has been to confirm already known scab and fire blight
318 resistance QTLs and to detect new ones under the water control condition. For scab

319 resistance, QTLs located on LG1 of TN10-8 (qT1) and on LG11 and LG17 of Fiesta
320 (qF11 and qF17, respectively) were previously detected and confirmed in various
321 studies (Durel et al., 2003; Liebhard et al., 2003; Calenge et al., 2004; Soufflet-Freslon
322 et al., 2008; Lê Van et al., 2012). The added value of the present study is the refinement
323 of their genetic position with reduced confidence intervals compared to previous
324 studies. As stated above, qT1 is precisely colocalized with the *Rvi6* (*Vf*) gene at
325 position 43.03 cM of the genetic map corresponding to the CH-Vf1 SSR marker, tightly
326 associated to that R-gene (Vinatzer et al., 2004). qT1 is thus a potential allele or
327 paralog of *Rvi6* and can thus be postulated as an extracellular leucine-rich repeat
328 receptor-like gene (Belfanti et al., 2004; Calenge et al., 2004). Another key aspect is
329 the confirmation of the strong complementary (synergistic) interaction between qF11
330 and qF17 as already highlighted by Caffier et al. (2014). Such an interaction can be
331 interpreted as the complementary action of two genes successively involved in a
332 metabolic pathway (McMullen et al., 1998). The dependency of the qF11 allelic
333 contrast upon the unfavorable or favorable allele of qF17 could be tentatively
334 interpreted as an upstream position of the gene underlying qF17 and a downstream
335 position of the gene underlying qF11. Thus, qF11 and qF17 could rather be involved
336 in a signaling or defense pathway, unlike qT1 more probably involved in pathogen
337 effector or PAMP recognition. Although reduced, the confidence intervals of these
338 QTLs were still too wide to search for sufficiently plausible candidate genes. An attempt
339 was made for qF17 and yielded over 160 positional candidates (data not shown). New
340 scab resistance QTLs were detected on LGs 10 and 13 of TN10-8 and LGs 3 and 12
341 of Fiesta. The most significant were qT13 and qF3 detected at genomic positions not
342 yet identified in other scab resistance studies. They will therefore be considered as a
343 priority for further marker-assisted breeding.

344 For fire blight resistance, the QTL qF7 was consistently detected on LG7 of Fiesta in
345 the first experiment as already published (Calenge et al., 2005; Khan et al., 2007). The
346 refinement of its genetic position was allowed with reduced confidence intervals
347 compared to previous studies. This QTL was shown to interact with two other ones on
348 LG8 and LG13 (van de Weg et al., 2018), but these genomic regions were not detected
349 in our study. Implication in a metabolic pathway could nevertheless be postulated for
350 qF7 due to such interactions. We also identified resistance QTLs on LGs 3, 5 and 15
351 which may coincide with those published by Calenge et al. (2005), Durel et al. (2009)
352 and Le Roux et al. (2010) respectively, despite their genomic position was not very
353 accurate. In our second experiment, qF7 was no more detected which calls into
354 question the relevance of this experiment, especially in view of the low AUDPC and
355 heritability values obtained and the weak correlation between both Ea-1430
356 experiments. This second experiment was performed very early in the season (early
357 February) at an unusual time for fire blight experiment which could explain this
358 surprising result.

359 In the present study, we propose for the first time a QTL mapping approach to search
360 for genetic factors influenced by a PRI. A few studies highlighted the influence of
361 genotypes on the effectiveness of PRIs but without any link with intrinsic genetic
362 resistance of varieties (Vallad and Goodman, 2004; Sharma et al., 2010; Maisonneuve
363 et al., 2013). Pawlowski et al. (2016) underlined the specific interaction between the
364 genetic and PRI-induced resistance but did not characterize the genetic resistance
365 factors. A mapping approach has the advantage of exploring in detail the putative
366 modulation of genetic resistance factors by PRIs. In our study, the results show that
367 genetic resistance controlled by QTLs is only slightly or rarely affected by ASM
368 treatment. Out of the seven scab resistance QTLs detected, only two QTLs (qF3 for

369 Vi-B04_1, and qT1 for Vi-Z14) almost disappeared after treatment with ASM. We also
370 detected two fire blight resistance QTLs (qT3, qF15) which effects significantly
371 decreased after ASM treatment in the second Ea-1430 experiment, but the
372 experimental conditions were questionable. Despite a large mapping population, the
373 confidence intervals surrounding relative effects of QTLs were large and therefore
374 precluded the detection of low modulation of QTL effects by ASM. More individuals
375 and replicates per individual would have been necessary to detect such modulations.
376 Furthermore, no QTL specific to the ASM treatment condition was detected: all QTLs
377 detected with ASM were already identified as resistance QTLs under the water control.
378 The general trend was either a maintenance or a reduction in the relative effect of
379 QTLs. Some of them fully disappeared (significantly) but this observation was hard to
380 repeat for both diseases. To some extent, this QTL effect disappearance could also be
381 explained by a scale effect. Indeed, the application of ASM strongly reduces the global
382 variability in disease severity and the weakest QTLs under the water control can
383 become insignificant under ASM treatment due to a consequent lack of statistical
384 power. However, a general trend of maintenance or small reduction of most QTLs is
385 surprising: considering the overall effectiveness of ASM on reducing disease
386 symptoms and the interactions observed between less resistant genotypes and
387 treatment, it would have been expected to found more interactions between pathways
388 leading to this resistance.

389 To go further, according to the diverse nature of the QTLs present in our population,
390 we expected to observe some QTLs responding to ASM and others remaining
391 unchanged. ASM is known to act on salicylic acid signaling pathway. In tobacco, it is
392 perceived by the SABP2 protein (Salicylic acid-binding protein 2) which transforms it
393 into acibenzolar which then interacts with NPR1 to activate the transcription of a set of

394 genes in the SAR pathway (Tripathi et al., 2010; Warneys et al., 2018; De Jong et al.,
395 2019; Ishiga et al., 2020; Li et al., 2020). If we consider the three stages of resistance
396 build-up, namely recognition, signaling and defense, we could postulate that QTLs
397 involved in signaling and defense could be more affected by ASM than QTLs involved
398 in effectors or PAMPs recognition. However, the qT1 previously described as most
399 probably involved in pathogen recognition disappeared with 09BCZ014 isolate but not
400 with EU-B04, whereas the QTLs qF11, qF17 and qF7, potentially rather involved in
401 signaling or defense pathways were not significantly affected by ASM. Various
402 hypotheses can be formulated for interpreting our results. In Arabidopsis, Tsuda et al.
403 (2009) showed that each of the salicylic acid (SA), jasmonic acid (JA) and ethylene
404 (ET) signaling sectors can positively contribute to immunity against both biotrophic and
405 necrotrophic pathogens. The authors schematized various situations of compensation
406 or synergy between different sectors of a complex signaling network where the effector
407 or PAMP recognition (input) can generate equivalent restriction of pathogen growth
408 (output) while mobilizing very different sectors interacting or not. In our situation, ASM
409 treatment would reinforce one of the signaling sectors with possible consequences on
410 other sectors given SA *versus* JA/ET compensation, while resistance QTLs positioned
411 at various locations of the network would impact the flow along some of these
412 pathways. Some of the detected QTLs could therefore be located on metabolic
413 pathways independent of the SA pathway while others could be implied in the SA
414 pathway and thus be affected by the strong initial supply of ASM. In-depth exploration
415 of the metabolic mechanisms involved in genotypes carrying or not resistance QTL
416 alleles, with or without ASM treatment, is needed to precise the interactions between
417 pathways.

418 Our study revealed that the intrinsic resistance controlled by QTLs and the resistance
419 induced by ASM have a complementary effect for the control of apple scab and fire
420 blight. In our study, the average effectiveness of ASM in reducing the disease ranged
421 from 50% for Ea-1430_1 to 78% for V1-B04_2. Under the water control, the individuals
422 cumulating favorable alleles at all detected QTLs exhibited a disease reduction of 91%
423 for Vi-B04_1 and 98% for Vi-Z14 compared to individuals carrying only unfavorable
424 QTL alleles for scab, and 78% for fire blight. When intrinsic and ASM-induced
425 resistance was combined, the disease reduction was close to 100% for scab and 85%
426 for fire blight. These results confirm that there is no incompatibility between intrinsic
427 and ASM-induced resistance for apple as reported for cucumber (da Rocha and
428 Hammerschmidt, 2005). The present results were obtained under controlled conditions
429 but arguments suggest that the same trends could be observed in orchards. On the
430 one hand, Caffier et al. (2014, 2016) showed that quantitative resistance related to
431 QTLs qT1, qF11 and qF17 significantly reduced scab severity in orchards. On the other
432 hand, Marolleau et al. (2017) confirmed that ASM could be integrated into orchard
433 protection practices to control apple scab. Combining both types of resistance in the
434 orchard should allow a better control of apple scab and similarly for fire blight.

435 In addition to improve protection effectiveness, the interest in combining intrinsic and
436 PRI-induced resistance could rely in a cross-protection of both types of resistance
437 through a diversification of selection pressures on pathogen populations which would
438 reduce or slow down their adaptation (Lê Van et al., 2013; Caffier et al., 2014). The
439 use of ASM in combination with genotypes cumulating several QTLs involved in
440 different defense pathways could be a promising sustainable protection for the control
441 of apple scab and fire blight. A thorough analysis of the mechanisms activated by this

resistance will confirm these hypotheses and all of these results must be confirmed in the orchards for possible integration into the protection practices.

Acknowledgements

The authors greatly thank the PHENOTIC platform, especially M. Boucourt, C. Cattanéo, C. Colas and R. Gardet, for carefully taking care of the plant material in the greenhouse. They thank the Horticole Experimental Unit (UE Horti) for maintaining the trees over many years in a conservatory orchard belonging to the BRC RosePom. X. Cazenave, E. Chevreau, R. Cournol, A. Degrave, C. Denancé, N. Dousset, C. Heintz, A. Juillard, L. Lejus, J. Malabarba, K. Menacer, H. Muranty, A. Petiteau, C. Pubert, P. Robert, E. Vergne helped in preparing the experiments and in scoring apple scab and fire blight disease in the greenhouse: they are all warmly thanked. The genetic map was carefully checked thanks to an updated version of the reference genetic map kindly furnished by N. Howard. They thank E. Millet, D. Lopez-Arias and S. Adamowicz for sharing R scripts for analysis of field trial experiments, QTLs detection and bootstrapping, respectively.

Literature Cited

Abo-Elyousr, A.M.K., Sallam, M.A.A., Hassan, M.H.A. and Zeller, W. 2010. Effect of Acibenzolar-S-methyl and *Rahnella aquatilis* (Ra39) on chitinase and β -1 , 3-glucanase activities and disease resistance of apple plants. *Plant Pathol. J.* 26: 63–69.

Aćimović, S.G., Zeng, Q., McGhee, G.C., Sundin, G.W. and Wise, J.C. 2015. Control of fire blight (*Erwinia amylovora*) on apple trees with trunk-injected plant resistance inducers and antibiotics and assessment of induction of pathogenesis-related protein genes. *Frontiers in Plant Science* 6: 1–10.

Arcade, A., Labourdette, A., Falque, M., Mangin, B., Chardon, F., Charcosset, A. and Joets, J. 2004. BioMercator: integrating genetic maps and QTL towards discovery of candidate genes. *Bioinformatics* 20: 2324–2326.

Assis, F.A., Moraes, J.C., Assis, G.A. and Parolin, F.J.T. 2015. Induction of caterpillar resistance in sunflower using silicon and acibenzolar-S-methyl. *J. Agr. Sci. Tech.* 17: 543–550.

Bektas, Y. and Eulgem, T. 2015. Synthetic plant defense elicitors. *Frontiers in Plant*

Science 5: 1–9.

Belfanti, E., Silfverberg-Dilworth, E., Tartarini, S., Patocchi, A., Barbieri, M., Zhu, J., Vinatzer, B.A., Gianfranceschi, L., Gessler, C. and Sansavini, S. 2004. The *HcrVf2* gene from a wild apple confers scab resistance to a transgenic cultivated variety. *Proceedings of the National Academy of Sciences of the United States of America* 101: 886–890.

Bengtsson, M., Lyngs Jørgensen, H.J., Pham, A., Wulff, E. and Hockenhull, J. 2006. Screening of organically based fungicides for apple scab (*Venturia inaequalis*) control and a histopathological study of the mode of action of a resistance inducer. *Pome Fruit Diseases IOBC/wprs Bull* 29: 123–127.

Bengtsson, M., Wulff, E., Lyngs Jørgensen, H.J., Pham, A., Lübeck, M. and Hockenhull, J. 2009. Comparative studies on the effects of a yucca extract and acibenzolar-S-methyl (ASM) on inhibition of *Venturia inaequalis* in apple leaves. *European Journal of Plant Pathology* 124: 187–198.

Bianco, L., Cestaro, A., Sargent, D.J., Banchi, E., Derdak, S., Di Guardo, M., Salvi, S., Jansen, J., Viola, R., Gut, I., Laurens, F., Chagné, D., Velasco, R., van de Weg, E. and Troggio, M. 2014. Development and validation of a 20K single nucleotide polymorphism (SNP) whole genome genotyping array for Apple (*Malus* × *domestica* Borkh). *PLoS ONE* 9: e110377.

Boudichevskaia, A., Flachowsky, H. and Dunemann, F. 2009. Identification and molecular analysis of candidate genes homologous to *HcrVf* genes for scab resistance in apple. *Plant Breeding* 128: 84–91.

Brisset, M.-N., Cesbron, S., Thomson, S. V. and Paulin, J. 2000. Acibenzolar-S-methyl induces the accumulation of defense-related enzymes in apple and protects from fire blight. *European Journal ofPlant Pathology* 106: 529–536.

Broggini, G.A.L., Galli, P., Parravicini, G., Gianfranceschi, L., Gessler, C. and Patocchi, A. 2009. *HcrVf* paralogs are present on linkage groups 1 and 6 of *Malus*. *Genome* 52: 129–138.

Broman, K.W., Wu, H., Sen, Ś. and Churchill, G.A. 2003. R/qtl: QTL mapping in experimental crosses. *Bioinformatics* 19: 889–890.

Burketova, L., Trda, L., Ott, P.G. and Valentova, O. 2015. Bio-based resistance inducers for sustainable plant protection against pathogens. *Biotechnology Advances* 33: 994–1004.

Caffier, V., Le Cam, B., Al Rifaï, M., Bellanger, M.-N., Comby, M., Denancé, C., Didelot, F., Expert, P., Kerdraon, T., Lemarquand, A., Ravon, E. and Durel, C.-E. 2016. Slow erosion of a quantitative apple resistance to *Venturia inaequalis* based on an isolate-specific quantitative trait locus. *Infection, Genetics and Evolution* 44: 541–548.

Caffier, V., Didelot, F., Pumo, B., Causeur, D., Durel, C.E. and Parisi, L. 2010. Aggressiveness of eight *Venturia inaequalis* isolates virulent or avirulent to the major resistance gene *Rvi6* on a non-*Rvi6* apple cultivar. *Plant Pathology* 59: 1072–1080.

Caffier, V., Lasserre-Zuber, P., Giraud, M., Lascostes, M., Stievenard, R.,

Lemarquand, A., van de Weg, E., Expert, P., Denancé, C., Didelot, F., Le Cam, B. and Durel, C.-E. 2014. Erosion of quantitative host resistance in the apple ×*Venturia inaequalis* pathosystem. *Infection, Genetics and Evolution* 27: 481–489.

Caffier, V., Patocchi, A., Expert, P., Bellanger, M.-N., Durel, C.-E., Hilber-Bodmer, M., Broggini, G.A.L., Groenwold, R. and Bus, V.G.M. 2015. Virulence characterization of *Venturia inaequalis* reference isolates on the differential set of *Malus* hosts. *Plant Disease* 99: 370–375.

Calenge, F., Drouet, D., Denancé, C., van de Weg, W.E., Brisset, M.-N., Paulin, J.-P. and Durel, C.-E. 2005. Identification of a major QTL together with several minor additive or epistatic QTLs for resistance to fire blight in apple in two related progenies. *Theoretical and Applied Genetics* 111: 128–135.

Calenge, F., Faure, A., Goerre, M., Gebhardt, C., van de Weg, W.E., Parisi, L. and Durel, C.-E. 2004. Quantitative trait loci (QTL) analysis reveals both broad-spectrum and isolate-specific QTL for scab resistance in an apple progeny challenged with eight isolates of *Venturia inaequalis*. *Phytopathology* 94(4): 370–379.

Howard, N.P., Troggio, M., Durel, C.-E., Muranty, H., Denancé, C., Bianco, L.; Tillman, J. and van de Weg, E. 2020. Integration of Infinium and Axiom SNP array data in the outcrossing species *Malus* × *domestica* and causes for seemingly incompatible calls. BioRxiv 2020.09.01.276758.

Le Cam, B., Sargent, D., Gouzy, J., Amselem, J., Bellanger, M.-N., Bouchez, O., Brown, S., Caffier, V., De Gracia, M., Debuchy, R., Duvaux, L., Payen, T., Sannier, M., Shiller, J., Collemare, J. and Lemaire, C. 2019. Population genome sequencing of the scab fungal species *Venturia inaequalis*, *Venturia pirina*, *Venturia aucupariae* and *Venturia asperata*. *G3: Genes, Genomes, Genetics* 9: 2405–2414.

Celton, J.M., Tustin, D.S., Chagné, D. and Gardiner, S.E. 2009. Construction of a dense genetic linkage map for apple rootstocks using SSRs developed from *Malus* ESTs and *Pyrus* genomic sequences. *Tree Genetics and Genomes* 5: 93–107.

Costa, F., van de Weg, W.E., Stella, S., Dondini, L., Pratesi, D., Musacchi, S. and Sansavini, S. 2008. Map position and functional allelic diversity of *Md-Exp7*, a new putative expansin gene associated with fruit softening in apple (*Malus x domestica* Borkh.) and pear (*Pyrus communis*). *Tree Genetics and Genomes* 4: 575–586.

Dalgaard, P. 2010. R development core team (2010): R: A language and environment for statistical computing. Computer p, http://www.r-project.org/.

Dugé de Bernonville, T., Marolleau, B., Staub, J., Gaucher, M. and Brisset, M.-N. 2014. Using molecular tools to decipher the complex world of plant resistance inducers: an apple case study. *Journal of Agricultural and Food Chemistry* 62: 11403–11411.

Durel, C.-E., Denancé, C. and Brisset, M.-N. 2009. Two distinct major QTL for resistance to fire blight co-localize on linkage group 12 in apple genotypes 'Evereste' and *Malus floribunda* clone. *NRC Research Press* 147: 139–147.

Durel, C.E., Parisi, L., Laurens, F., van de Weg, W.E., Liebhard, R. and Jourjon, M.F. 2003. Genetic dissection of partial resistance to race 6 of *Venturia inaequalis* in

560 apple. *Genome* 46: 224–234.

561 Emeriewen, O.F., Wöhner, T., Flachowsky, H. and Peil, A. 2019. *Malus* hosts–*Erwinia*
562 *amylovora* interactions: strain pathogenicity and resistance mechanisms.
563 *Frontiers in Plant Science* 10: 1–7.

564 Gozzo, F. and Faoro, F. 2013. Systemic acquired resistance (50 years after discovery):
565 moving from the lab to the field. *Journal of Agricultural and Food Chemistry* 61:
566 12473–12491.

567 Hassan, M.A.E. and Buchenauer, H. 2007. Induction of resistance to fire blight in apple
568 by acibenzolar-S-methyl and DL-3-aminobutyric acid. *Journal of Plant Diseases*
569 *and Protection* 114: 151–158.

570 Hokanson, S.C., Szewc-McFadden, A.K., Lamboy, W.F. and McFerson, J.R. 1998.
571 Microsatellite (SSR) markers reveal genetic identities, genetic diversity and
572 relationships in a *Malus x domestica* borkh. core subset collection. *Theoretical and*
573 *Applied Genetics* 97: 671–683.

574 Ishiga, T., Iida, Y., Sakata, N., Ugajin, T., Hirata, T., Taniguchi, S., Hayashi, K. and
575 Ishiga, Y. 2020. Acibenzolar-S-methyl activates stomatal-based defense against
576 *Pseudomonas cannabina pv. alisalensis* in cabbage. *Journal of General Plant*
577 *Pathology* 86: 48–54.

578 Johnson, K.B., Smith, T.J., Temple, T.N., Gutierrez, E., Elkins, R.B. and Castagnoli,
579 S.P. 2016. Integration of acibenzolar-S-methyl with antibiotics for protection of
580 pear and apple from fire blight caused by *Erwinia amylovora*. *Crop Protection* 88:
581 149–154.

582 De Jong, H., Reglinski, T., Elmer, P.A.G., Wurms, K., Vanneste, J.L., Guo, L.F. and
583 Alavi, M. 2019. Integrated use of *Aureobasidium pullulans* strain CG163 and
584 acibenzolar-S-methyl for management of bacterial canker in kiwifruit. *Plants* 8:
585 287.

586 Khajuria, Y.P., Kaul, S., Wani, A.A. and Dhar, M.K. 2018. Genetics of resistance in
587 apple against *Venturia inaequalis* (Wint.) Cke. *Tree Genetics & Genomes* 14: 16.

588 Khan, M.A., Durel, C.E., Duffy, B., Drouet, D., Kellerhals, M., Gessler, C. and Patocchi,
589 A. 2007. Development of molecular markers linked to the “Fiesta” linkage group 7
590 major QTL for fire blight resistance and their application for marker-assisted
591 selection. *Genome* 50: 568–577.

592 Laloi, G., Vergne, E., Durel, C.E., Le Cam, B. and Caffier, V. 2016. Efficiency of
593 pyramiding of three quantitative resistance loci to apple scab. *Plant Pathology* 66:
594 412–422.

595 Lê Van, A., Caffier, V., Lasserre-Zuber, P., Chauveau, A., Brunel, D., Le Cam, B. and
596 Durel, C.-E. 2013. Differential selection pressures exerted by host resistance
597 quantitative trait loci on a pathogen population: a case study in an apple × *Venturia*
598 *inaequalis* pathosystem. *New Phytologist* 197: 899–908.

599 Lê Van, A., Gladieux, P., Lemaire, C., Cornille, A., Giraud, T., Durel, C., Caffier, V. and
600 Le Cam, B. 2012. Evolution of pathogenicity traits in the apple scab fungal
601 pathogen in response to the domestication of its host. *Evolutionary Applications*
602 7: 694–704.

603 Li, C., Wei, M., Ge, Y., Zhao, J., Chen, Y., Hou, J., Cheng, Y., Chen, J. and Li, J. 2020.
604 The role of *glucose-6-phosphate dehydrogenase* in reactive oxygen species
605 metabolism in apple exocarp induced by acibenzolar-S-methyl. *Food Chemistry*
606 308: 125663.

607 Liebhard, R., Gianfranceschi, L., Koller, B., Ryder, C.D., Tarchini, R., van de Weg, E.
608 and Gessler, C. 2002. Development and characterisation of 140 new
609 microsatellites in apple (*Malus x domestica* Borkh.). *Molecular Breeding* 10: 217–
610 241.

611 Liebhard, R., Koller, B., Patocchi, A., Kellerhals, M., Pfammatter, W., Jermini, M. and
612 Gessler, C. 2003. Mapping quantitative field resistance against apple scab in a
613 "Fiesta" x "Discovery" progeny. *Phytopathology* 93: 493–501.

614 MacHardy, W.E. 1996. Apple scab biology, epidemiology and management. *APS*
615 *Press*, St. Paul, Minnesota, USA.

616 Maisonneuve, B., Allen-aubouard, C. and Pitrat, M. 2013. Effect of plant genotype on
617 the efficacy of stimulators of plant defences in two horticultural pathosystems.
618 *IOBC-WPRE Bulletin* 89: 327–331.

619 Malnoy, M., Martens, S., Norelli, J.L., Barny, M.-A., Sundin, G.W., Smits, T.H.M. and
620 Duffy, B. 2012. Fire Blight: applied genomic insights of the pathogen and host.
621 *Annual Review of Phytopathology* 50: 475–494.

622 Marolleau, B., Gaucher, M., Heintz, C., Degrave, A., Warneys, R., Orain, G.,
623 Lemarquand, A. and Brisset, M. 2017. When a plant resistance inducer leaves the
624 lab for the field: integrating ASM into routine apple protection practices. *Frontiers*
625 *in Plant Science* 8: 1–11.

626 Matsuo, Y., Novianti, F., Takehara, M., Fukuhara, T., Arie, T. and Komatsu, K. 2019.
627 Acibenzolar-S-methyl restricts infection of *Nicotiana benthamiana* by *Plantago*
628 *Asiatica* mosaic virus at two distinct stages. *Molecular Plant-Microbe Interactions*
629 32: 1475–1486.

630 Maxson-Stein, K., He, S., Hammerschmidt, R. and Jones, A.L. 2002. Effect of treating
631 apple trees with acibenzolar-S-methyl on fire blight and expression of
632 pathogenesis-related protein genes. *Plant Disease* 86: 785–790.

633 McDonald, B.A. and Linde, C. 2002. Pathogen Population Genetics, Evolutionary
634 potential, and durable resistance. *Annual Review of Phytopathology* 40: 349–379.

635 McMullen, M.D., Byrne, P.F., Snook, M.E., Wiseman, B.R., Lee, E.A., Widstrom, N.W.
636 and Coe, E.H. 1998. Quantitative trait loci and metabolic pathways. *Proceedings*
637 *of the National Academy of Sciences of the United States of America* 95: 1996–
638 2000.

639 Oliveira, M.D.M., Varanda, C.M.R. and Félix, M.R.F. 2016. Induced resistance during
640 the interaction pathogen x plant and the use of resistance inducers.
641 *Phytochemistry Letters* 15: 152–158.

642 Van Ooijen, J. 2006. JoinMap® 4, software for the calculation of genetic linkage maps
643 in experimental populations. *Wageningen, the Netherlands: Kyazma BV*.

644 Oostendorp, M., Kunz, W., Dietrich, B. and Staub, T. 2001. Induced disease resistance
645 in plants by chemicals. *European Journal of Plant Pathology* 107: 19–28.

646 Pal, K.K. and McSpadden Gardener, B. 2006. Biological control of plant pathogens.
647 *The Plant Health Instructor* 1–25.

648 Parisi, L. 1993. A new race of *Venturia inaequalis* virulent to apples with resistance
649 due to the *Vf* gene. *Phytopathology* 83: 533.

650 Parlevliet, J.E. 2002. Durability of resistance against fungal, bacterial and viral
651 pathogens, present situation. *Euphytica* 124: 147–156.

652 Patocchi, A., Wehrli, A., Dubuis, P.-H., Auwerkerken, A., Leida, C., Cipriani, G.,
653 Passey, T., Staples, M., Didelot, F., Philion, V., Peil, A., Laszakovits, H., Rühmer,
654 T., Boeck, K., Baniulis, D., Strasser, K., Vávra, R., Guerra, W., Masny, S., Ruess,
655 F., Le Berre, F., Nybom, H., Tartarini, S., Spornberger, A., Pikunova, A., Bus,
656 V.G.M. 2020. Ten years of vinquest: first insight for breeding new apple cultivars
657 with durable apple scab resistance. *Plant Disease* 104: 2074 – 2081

658 Paulin, J.P. and Samson, R. 1973. Fire blight in France. II. Characters of the strains of
659 *Erwinia amylovora* (Burril) Winslow et al., 1920, isolated from a Franco-Belgian
660 focus. *Ann. Phytopathol.* 5: 389–397.

661 Pawlowski, M.L., Bowen, C.R., Hill, C.B. and Hartman, G.L. 2016. Responses of
662 soybean genotypes to pathogen infection after the application of elicitors. *Crop*
663 *Protection* 87: 78–84.

664 Peil, A., Emeriewen, O.F., Khan, A., Kostick, S. and Malnoy, M. 2020. Status of fire
665 blight resistance breeding in *Malus*. *Journal of Plant Pathology*.

666 Di Pierro, E.A., Gianfranceschi, L., Di Guardo, M., Koehorst-van Putten, H.J.,
667 Kruisselbrink, J.W., Longhi, S., Troggio, M., Bianco, L., Muranty, H., Pagliarani,
668 G., Tartarini, S., Letschka, T., Lozano Luis, L., Garkava-Gustavsson, L.,
669 Micheletti, D., Bink, M.C., Voorrips, R.E., Aziz, E., Velasco, R., Laurens, F. and
670 van de Weg, W.E. 2016. A high-density, multi-parental SNP genetic map on apple
671 validates a new mapping approach for outcrossing species. *Horticulture Research*
672 3: 16057.

673 Pilet-Nayel, M.-L., Moury, B., Caffier, V., Montarry, J., Kerlan, M.-C., Fournet, S., Durel,
674 C.-E. and Delourme, R. 2017. Quantitative resistance to plant pathogens in
675 pyramiding strategies for durable crop protection. *Frontiers in Plant Science* 8: 1–
676 9.

677 da Rocha, A.B. and Hammerschmidt, R. 2005. History and perspectives on the use of
678 disease resistance inducers in horticultural crops. *HortTechnology* 15: 518–529.

679 Rodríguez-Álvarez, M.X., Boer, M.P., van Eeuwijk, F.A. and Eilers, P.H.C. 2018.
680 Correcting for spatial heterogeneity in plant breeding experiments with P-splines.
681 *Spatial Statistics* 23: 52–71.

682 Romero, A.M., Kousik, C.S. and Ritchie, D.F. 2001. Resistance to bacterial spot in bell
683 pepper induced by acibenzolar-S-methyl. *Plant Disease* 77: 189–194.

684 Le Roux, P.M.F., Khan, M.A., Broggini, G.A.L., Duffy, B., Gessler, C. and Patocchi, A.
685 2010. Mapping of quantitative trait loci for fire blight resistance in the apple
686 cultivars “Florina” and “Nova Easygro.” *Genome* 53: 710–722.

687 Shahini Sough, F., Keshavarzi, M., Hassanzade, N., Hashemi, M., Abdollahi, H. and
688 Tawosi, M. 2010. *In vitro* evaluation of acibenzolar-S-methyl on inhibition of fire

689 blight in apple cv. Golden Delicious. *Iran. J. Plant Path.* 46: 77–78.

690 Sharma, K., Butz, A.F. and Finckh, M.R. 2010. Effects of host and pathogen genotypes
691 on inducibility of resistance in tomato (*Solanum lycopersicum*) to *Phytophthora*
692 *infestans*. *Plant Pathology* 59: 1062–1071.

693 Silfverberg-Dilworth, E., Matasci, C.L., van de Weg, W.E., van Kaauwen, M.P.W.,
694 Walser, M., Kodde, L.P., Soglio, V., Gianfranceschi, L., Durel, C.E., Costa, F.,
695 Yamamoto, T., Koller, B., Gessler, C. and Patocchi, A. 2006. Microsatellite
696 markers spanning the apple (*Malus x domestica* Borkh.) genome. *Tree Genetics*
697 *and Genomes* 2: 202–224.

698 Soriano, J.M., Madduri, M., Schaart, J.G., van der Burgh, A., van Kaauwen, M.P.W.,
699 Tomic, L., Groenwold, R., Velasco, R., van de Weg, E. and Schouten, H.J. 2014.
700 Fine mapping of the gene *Rvi18* (*V25*) for broad-spectrum resistance to apple
701 scab, and development of a linked SSR marker suitable for marker-assisted
702 breeding. *Molecular Breeding* 34: 2021–2032.

703 Soufflet-Freslon, V., Gianfranceschi, L., Patocchi, A. and Durel, C.-E. 2008.
704 Inheritance studies of apple scab resistance and identification of *Rvi14* , a new
705 major gene that acts together with other broad-spectrum QTL. *Genome* 51: 657–
706 667.

707 Tripathi, D., Jiang, Y. and Kumar, D. 2010. SABP2, a *methyl salicylate esterase* is
708 required for the systemic acquired resistance induced by acibenzolar-S-methyl in
709 plants. *FEBS Letters* 584: 3458–3463.

710 Tsuda, K., Sato, M., Stoddard, T., Glazebrook, J. and Katagiri, F. 2009. Network
711 properties of robust immunity in plants. *PLoS Genetics* 5: e1000772.

712 Vallad, G.E. and Goodman, R.M. 2004. Review & interpretation in conventional
713 agriculture. *Crop Sci.* 44: 1920–1934.

714 Vinatzer, B.A., Patocchi, A., Tartarini, S., Gianfranceschi, L., Sansavini, S. and
715 Gessler, C. 2004. Isolation of two microsatellite markers from BAC clones of the
716 *Vf* scab resistance region and molecular characterization of scab-resistant
717 accessions in *Malus* germplasm. *Plant Breeding* 123: 321–326.

718 Walters, D.R., Ratsep, J. and Havis, N.D. 2013. Controlling crop diseases using
719 induced resistance: challenges for the future. *Journal of Experimental Botany* 64:
720 1263–1280.

721 Warneys, R., Gaucher, M., Robert, P., Aligon, S., Anton, S., Aubourg, S., Barthes, N.,
722 Braud, F., Cournol, R., Gadenne, C., Heintz, C., Brisset, M. and Degrave, A. 2018.
723 Acibenzolar-S-methyl reprograms apple transcriptome toward resistance to rosy
724 apple aphid. *Frontiers in Plant Science* 9: 1–16.

725 van de Weg, E., Di Guardo, M., Jänsch, M., Socquet-Juglard, D., Costa, F.,
726 Baumgartner, I., Broggini, G.A.L., Kellerhals, M., Troggio, M., Laurens, F., Durel,
727 C.E. and Patocchi, A. 2018. Epistatic fire blight resistance QTL alleles in the apple
728 cultivar 'Enterprise' and selection X-6398 discovered and characterized through
729 pedigree-informed analysis. *Molecular Breeding* 38: 5.

730 Wiesel, L., Newton, A.C., Elliott, I., Booty, D., Gilroy, E.M., Birch, P.R.J. and Hein, I.
731 2014. Molecular effects of resistance elicitors from biological origin and their

potential for crop protection. *Frontiers in Plant Science* 5: 1–13.

Wöhner, T.W., Flachowsky, H., Richter, K., Garcia-Libreros, T., Trognitz, F., Hanke, M. V. and Peil, A. 2014. QTL mapping of fire blight resistance in *Malus ×robusta* 5 after inoculation with different strains of *Erwinia amylovora*. *Molecular Breeding* 34: 217–230.

Yamamoto, T., Kimura, T., Saito, T., Kotobuki, K., Matsuta, N., Liebhard, R., Gessler, C., van de Weg, W.E. and Hayashi, T. 2004. Genetic linkage maps of japanese and european pears aligned to the apple consensus map. *Acta Horticulturae* 663: 51–56.

Youssef, K., Roberto, S., Colombo, R., Canteri, M. and Elsalam, K. 2019. Acibenzolar-S-methyl against *Botrytis* mold on table grapes *in vitro* and *in vivo*. *Agronomy Science and Biotechnology* 5: 52.

Ziadi, S., Poupard, P., Brisset, M., Paulin, J.-P. and Simoneau, P. 2001. Characterization in apple leaves of two subclasses of PR-10 transcripts inducible by acibenzolar-S-methyl, a functional analogue of salicylic acid. *Physiological and Molecular Plant Pathology* 59: 33–43.

751 **Tables**

752 **Table 1**. Mean values (± standard-deviation) of AUDPC, relative effectiveness of ASM, coefficient of variation of individual BLUPs
753 (CV), broad-sense heritability (h^2) and phenotypic variation explained by all detected resistance QTLs (global R^2) against scab (*V.*
754 *inaequalis* isolates EU-B04 and 09BCZ14; experiments Vi-B04_1 and Vi-Z14, respectively) and fire blight (*E. amylovora* isolate
755 CFPB1430; experiment Ea-1430_1) in the TxF progeny. Values for the sub-population qT1- are indicated within brackets.
756 Effectiveness of ASM is computed as: (Mean-water – Mean-PRI)/Mean-water.

757

Experiment	Treatment	Mean	Effectiveness ASM (%)	CV	h^2	Global R^2
Vi-B04_1	water	41.2 ± 36.8		0.84 $[0.29]_{qT1-}$	0.94	81.9 $[65.1]_{qT1-}$
	ASM	18.9 ± 26.4	54	1.27 $[0.48]_{qT1-}$	0.91	70.2 $[53.8]_{qT1-}$
Vi-Z14	water	24.1 ± 21.4		0.75	0.84	47.5
	ASM	6.6 ± 8.4	73	0.88	0.71	15.0
Ea-1430_1	water	6.2 ± 2.4		0.27	0.70	35.0
	ASM	3.1 ± 1.8	50	0.34	0.63	33.1

758

759

760 **Table 2**. Parameters associated with the quantitative trait loci (QTLs) identified for disease resistance against scab (experiments Vi-
761 B04_1, sub-population qT1-, and Vi-Z14) and fire blight (experiment Ea-1430_1) in the TxF progeny after water- or ASM-treatment.

762

763 [a] LOD thresholds were obtained after permutations (n=1000): 5.1 (Vi-B04$_{qT1-}$_water), 4.6 (Vi-B04$_{qT1-}$_ASM), 5.0 (Vi-Z14_water and
764 Vi-Z14_ASM), 4.7 (Ea-1430_water) and 4.6 (Ea-1430_ASM). Significant QTLs are shown in bold. Suggestive QTLs with LOD score
765 between 3.0 and the LOD threshold are shown in italics. QTLs being insignificant in a condition but significant in another are shown
766 in grey.

767 [b] position of 2-LOD support QTL confidence interval borders

768

Juliette Bénéjam
Plant Disease

Trait	Treatment	Linkage group	Position	LOD [a]	R^2	CI [b]
Vi-B04_1$_{qT1-}$	water	**T13**	**3.58**	**8.6**	**9.3**	**0 .00 – 6.80**
		F3	**13.36**	**5.7**	**5.5**	**8.25 – 18.54**
		F11	**5.00**	**10.7**	**18.1**	**0.00 – 20.98**
		F12	*25.99*	*3.0*	*3.7*	*20.46 – 31.56*
		F17	**18.92**	**12.4**	**29.0**	**16.52 – 27.35**
	ASM	T13	3.58	0.3	-	-
		F3	44.80	0.8	-	-
		F11	**0.00**	**7.6**	**10.7**	**0.00 – 7.91**
		F12	*19.28*	*4.0*	*5.1*	*10.83 – 24.43*
		F17	**18.00**	**21.2**	**39.9**	**16.52 – 20.90**
Vi-Z14	water	**T1**	**45.03**	**9.4**	**10.7**	**39.01 – 52.89**
		T10	*62.09*	*3.6*	*3.5*	54.88 – 65.69
		T13	**3.18**	**10.9**	**10.1**	**0.00 – 6.80**
		F3	**3.92**	**5.1**	**5.3**	**0.00 – 9.03**
		F11	**5.53**	**7.8**	**7.9**	**0.00 – 20.98**
		F17	**18.92**	**9.1**	**10.7**	**14.18 – 27.35**
	ASM	T1	36.61	1.7	-	-
		T10	62.09	2.2	-	-
		T13	*0.00*	*4.1*	*6.3*	*0.00 – 6.80*
		F3	5.50	1.1	-	-
		F11	*3.17*	*3.9*	*5.0*	*0.00 – 8.69*
		F17	*18.92*	*4.2*	*5.0*	*13.79 – 27.35*
Ea-1430_1	water	*T3*	*23.57*	*4.1*	*3.1*	*11.81 – 26.76*
		T5	**54.33**	**5.8**	**5.2**	**43.24 – 62.05**
		F5	39.73	2.5	-	-
		F7	**69.46**	**18.4**	**20.1**	**67.10 – 71.42**
		F15	*76.05*	*3.7*	*3.9*	*70.94 – 81.15*
	ASM	*T3*	*20.38*	*3.7*	*4.6*	*17.13 – 29.18*
		T5	**35.22**	**4.9**	**4.6**	**28.37 – 40.84**
		F5	**38.56**	**6.3**	**8.4**	**32.18 – 42.08**
		F7	**69.07**	**12.2**	**13.2**	**67.10 – 71.42**
		F15	86.70	2.9	-	-

769

Juliette Bénéjam
Plant Disease

770 **Table 3**. Interactions between significant and suggestive QTLs identified in Vi-B04_1$_{qT1-}$ and Vi-Z14 experiments.

771

		water					ASM				
Trait	**QTLs combination**	**AA:AA**	**AB:AA**	**AA:AB**	**AB:AB**	**F-value [a]**	**AA:AA**	**AB:AA**	**AA:AB**	**AB:AB**	**F-value [a]**
Vi-B04_1$_{qT1-}$	qF11:qF17	149.6	146.2	99.5	131.3	12.1 ***	94.7	93.2	49.0	70.0	8.9 **
Vi-Z14	qT1:qF3	34.2	19.2	24.7	16.6	6.6 *	-	-	-	-	-
	qT13:qF3	19.9	35.5	15.8	25.4	6.6 *	-	-	-	-	-
	qT10:qF11	15.7	24.3	23.1	31.2	4.9 *	-	-	-	-	-
	qF11:qF17	31.3	32.3	12.8	24.9	4.2 *	-	-	-	-	-

772

773 [a] F-value of the variance analysis Fisher-test where stars represent the significance of the test at the risk of 0.05 (*), 0.01 (**) or
774 0.005 (***).

775 **Figures Captions**

776 **Figure 1.** Relationship between disease severity (BLUP estimates) for water- and
777 ASM-treated individuals of the TxF progeny in (A) Vi-B04_1, (B) Vi-Z14 and (C) Ea-
778 1430 experiments. Distributions of BLUPs are shown in the upper (water control) and
779 right (ASM treatment) part of each graph where the complete population is represented
780 in grey and the sub-population qT1- (i.e., individuals selected as not-carrying the
781 resistance allele of the major QTL qT1) in green. The same color code is used in the
782 graph where the green dots are superimposed on the grey dots. Control and parental
783 genotypes are shown with triangles in orange (TN10-8), red (Fiesta) and black (Gala
784 and Golden Delicious). Cor is the Pearson coefficient of correlation between water and
785 ASM BLUPs. Values for the sub-population qT1- are indicated within brackets.

786 **Figure 2.** LOD score curves of QTLs involved in resistance against scab (Vi-B04_1
787 and Vi-Z14) for each treatment identified in the TxF progeny (upper part) and relative
788 effects (rEffects) of these QTLs (lower part). Blue and orange colors represent
789 respectively the water control and ASM treatment. LOD score thresholds are drawn as
790 horizontal lines with the respective colors. In each rEffect plot, mean and standard
791 deviation of each rEffect, calculated with bootstrapping, are represented by a point and
792 a vertical bar respectively, with the respective blue and orange color for water-control
793 and ASM-treatment respectively.

794 **Figure 3.** LOD score curves of QTLs involved in resistance against fire blight (Ea-
795 1430_1) for each treatment identified in the TxF progeny (upper part) and relative
796 effects (rEffects) of these QTLs (lower part). Blue and orange colors represent
797 respectively the water control and ASM treatment. LOD score thresholds are drawn as
798 horizontal lines with the respective colors. In each rEffect plot, mean and standard
799 deviation of each rEffect, calculated with bootstrapping, are represented by a point and

a vertical bar respectively, with the respective blue and orange color for water-control and ASM-treatment respectively.

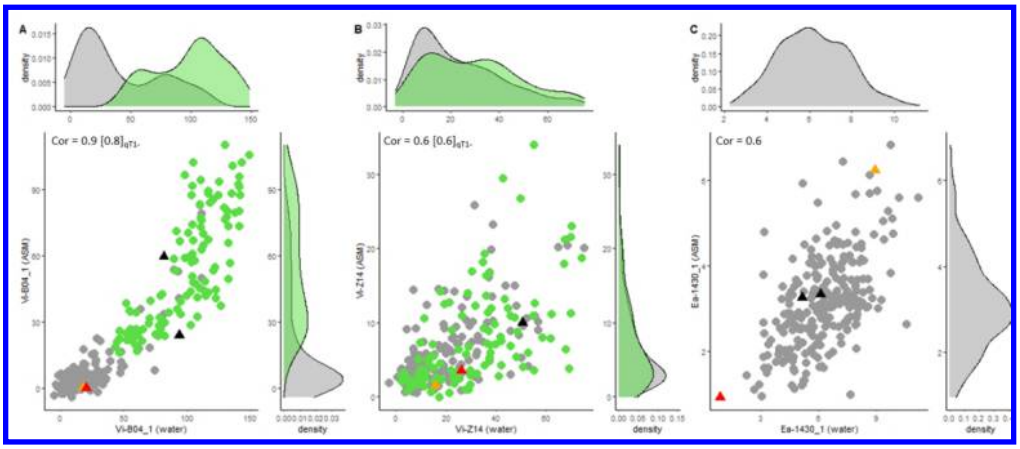


Figure 1. Relationship between disease severity (BLUP estimates) for water- and ASM-treated individuals of the TxF progeny in (A) Vi-B04_1, (B) Vi-Z14 and (C) Ea-1430 experiments. Distributions of BLUPs are shown in the upper (water control) and right (ASM treatment) part of each graph where the complete population is represented in grey and the sub-population qT1- (i.e., individuals selected as not-carrying the resistance allele of the major QTL qT1) in green. The same color code is used in the graph where the green dots are superimposed on the grey dots. Control and parental genotypes are shown with triangles in orange (TN10-8), red (Fiesta) and black (Gala and Golden Delicious). Cor is the Pearson coefficient of correlation between water and ASM BLUPs. Values for the sub-population qT1- are indicated within brackets.

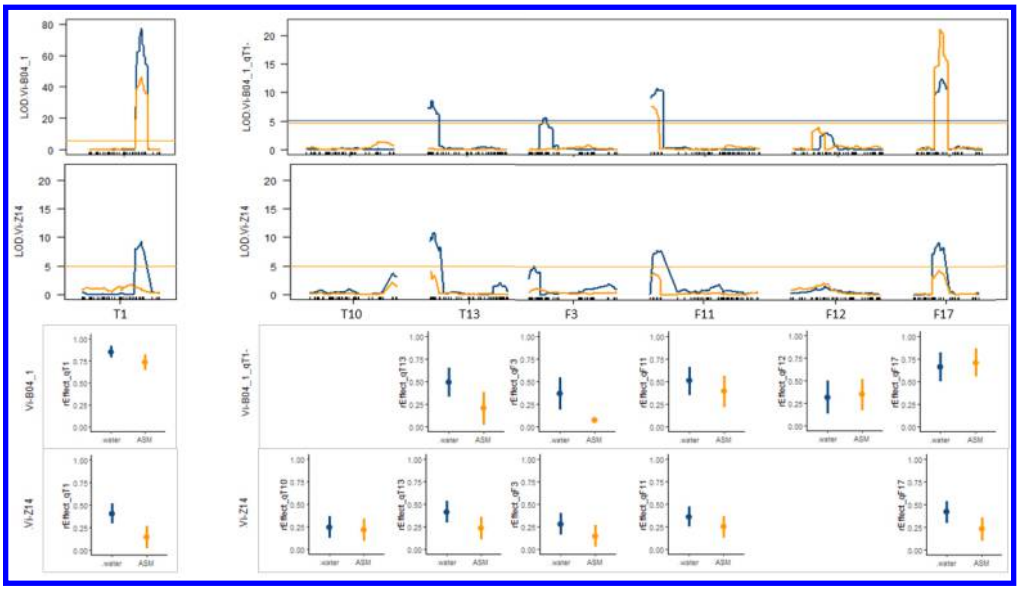


Figure 2. LOD score curves of QTLs involved in resistance against scab (Vi-B04_1 and Vi-Z14) for each treatment identified in the TxF progeny (upper part) and relative effects (rEffects) of these QTLs (lower part). Blue and orange colors represent respectively water control and ASM treatment. LOD score thresholds are drawn as horizontal lines with the respective colors. In each rEffect plot, mean and standard deviation of each rEffect, calculated with bootstrapping, are represented by a point and a vertical bar respectively, with the respective blue and orange color for water-control and ASM-treatment respectively.

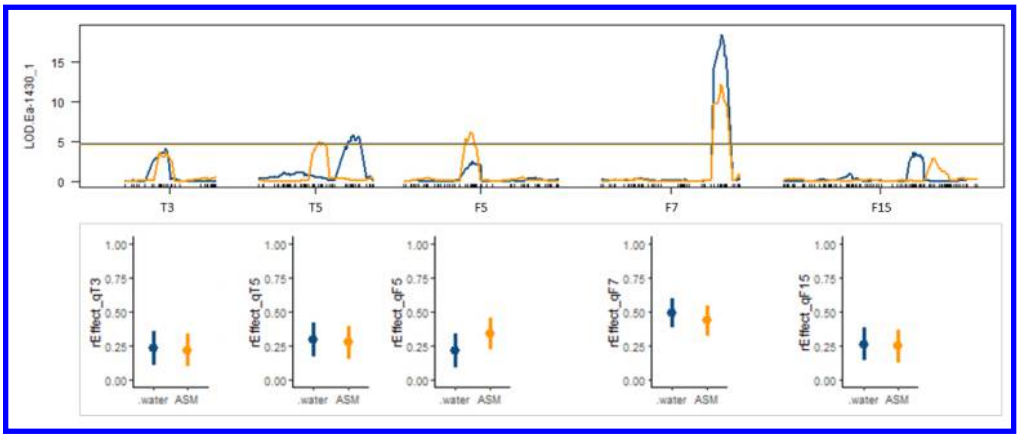


Figure 3. LOD score curves of QTLs involved in resistance against fire blight (Ea-1430_1) for each treatment identified in the TxF progeny (upper part) and relative effects (rEffects) of these QTLs (lower part). Blue and orange colors represent respectively water control and ASM treatment. LOD score thresholds are drawn as horizontal lines with the respective colors. In each rEffect plot, mean and standard deviation of each rEffect, calculated with bootstrapping, are represented by a point and a vertical bar respectively, with the respective blue and orange color for water-control and ASM-treatment respectively.

Supplementary Table S1. List of microsatellite markers added to the genetic map

Marker Name	Marker type	Linkage group	Reference
CH05g08	SSR	T1	(Liebhard et al., 2002)
CH-Vf1	SSR	T1	(Vinatzer et al., 2004)
HB04p	SSR	T1	(Broggini et al., 2009)
Hi02c07	SSR	T1	(Silfverberg-Dilworth et al., 2006)
KA4b	SSR	T1	(Yamamoto et al., 2004)
Md-Exp7	SSR	T1	(Costa et al., 2008)
NZmsCN879773	SSR	T1	(Celton et al., 2009)
Vf2ARD	SCAR	T1	(Boudichevskaia et al., 2009)
CH02d08	SSR	F11	(Liebhard et al., 2002)
CH04h02	SSR	F11	(Liebhard et al., 2002)
Rvi18SSR	SSR	F11	(Soriano et al., 2014)
CH01h01	SSR	F17	(Liebhard et al., 2002)
CH04f08	SSR	F17	(Liebhard et al., 2002)
CH05g03	SSR	F17	(Liebhard et al., 2002)
GD96	SSR	F17	(Hokanson et al., 1998)
Hi02f12	SSR	F17	(Silfverberg-Dilworth et al., 2006)
Hi03c05	SSR	F17	(Silfverberg-Dilworth et al., 2006)

Supplementary Table S2. Mean values (± standard-deviation) of AUDPC, relative effectiveness of ASM, coefficient of variation of individual BLUPs (CV), broad-sense heritability (h^2) and phenotypic variation explained by all detected resistance QTLs (global R^2) against scab (*V. inaequalis* isolate EU-B04; experiment Vi-B04_2) and fire blight (*E. amylovora* isolate CFPB1430; experiment Ea-1430_2) in the TxF progeny. Values for the sub-population qT1- are indicated within brackets. Effectiveness of ASM is computed as: (Mean-water – Mean-PRI)/Mean-water.

Experiment	Treatment	Mean	Effectiveness ASM (%)	CV	h^2	Global R^2
Vi-B04_2	water	22.9 ± 26.2		1.03 [0.47]$_{qT1-}$	0.89	56.1 [68.8]$_{qT1-}$
	ASM	5.1 ± 8.9	78	1.62 [0.59]$_{qT1-}$	0.85	56.3 [56.7]$_{qT1-}$
Ea-1430_2	water	4.2 ± 2.5		0.30	0.51	30.2
	ASM	2 ± 1.5	52	0.43	0.56	26.1

Supplementary Table S4. Parameters associated with the quantitative trait loci (QTLs) identified for disease resistance against scab (experiment Vi-B04_1, whole population) in the TxF progeny after water- or ASM-treatment.

Trait	Treatment	Linkage group	Position	LOD [a]	R^2	CI [b]
Vi-B04_1	water	**T1**	**43.00**	**77.1**	**69.9**	**41.01 – 44.23**
		T13	**3.58**	**6.3**	**2.8**	**0.00 – 6.80**
		F3	12.19	1.6	-	-
		F11	**6.00**	**8.9**	**7.7**	**0.00 – 20.98**
		F12	*4.00*	*3.3*	*0.6*	*0.00 – 6.87*
		F17	**18.92**	**16.7**	**12.8**	**16.52 – 20.90**
	ASM	**T1**	**43.03**	**46.1**	**60.0**	**41.01 – 44.23**
		T13	3.58	0.8	-	-
		F3	1.96	0.3	-	-
		F11	*4.75*	*4.3*	*6.9*	*0.00 – 20.98*
		F12	19.28	2.3	-	-
		F17	**18.92**	**15.9**	**24.9**	**16.52 – 20.90**

[a] LOD thresholds were obtained after permutations (n=1000): 5.5 (Vi-B04_water) and 5.4 (Vi-B04_ASM). Significant QTLs are shown in bold. Suggestive QTLs with LOD score between 3.0 and the LOD threshold are shown in italics. QTLs being insignificant in a condition but significant in another are shown in grey.

[b] position of 2-LOD support QTL confidence interval borders

Supplementary Table S5. Parameters associated with the quantitative trait loci (QTLs) identified for disease resistance against scab (experiment Vi-B04_2) and fire blight (experiment Ea-1430_2) in the TxF progeny after water- or ASM-treatment.

[a] LOD thresholds were obtained after permutations (n=1000): 4.70 (Vi-B04_water); 4.50 (Vi-B04_ASM); 5.82 (Vi-B04$_{qT1-}$_water); 7.33 (Vi-B04$_{qT1-}$_ASM); 4.77 (Ea-1430_water); 5.27 (Ea_1430_ASM). Significant QTLs are shown in bold. Suggestive QTLs with LOD score between 3.0 and the LOD threshold are shown in italics. QTLs being insignificant in a condition but significant in another are shown in grey.

[b] position of 2-LOD support QTL confidence interval borders

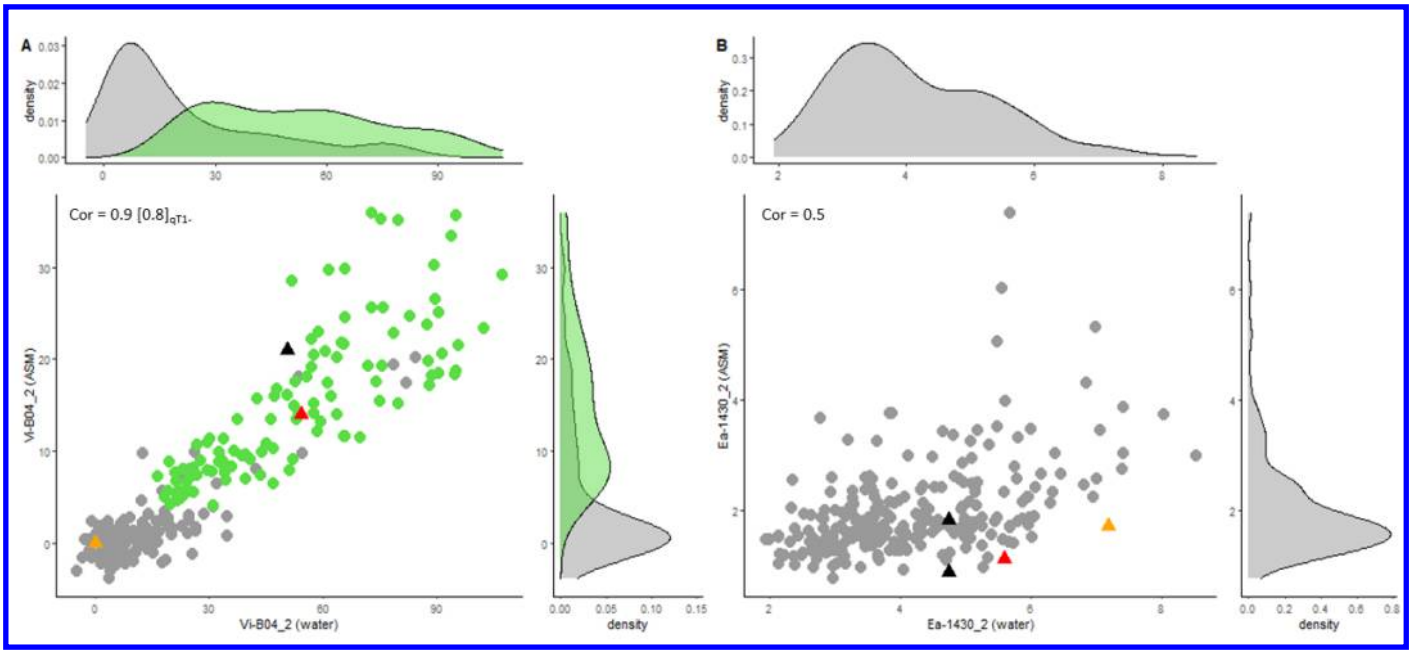
Trait	Treatment	Linkage group	Position	LOD [a]	R^2	CI [b]
Vi-B04_2	water	**T1**	**43.03**	**35.2**	**40.42**	**41.01 – 44.23**
		T13	44.94	2.1	-	-
		F3	13.36	1.6	-	-
		F11	**5.53**	**5.3**	**4.99**	**0.00 – 7.91**
		F12	*25.99*	*3.9*	*3.54*	*0.00 – 46.60*
		F17	**18.92**	**14.4**	**13.30**	**16.52 – 20.90**
	ASM	**T1**	**43.03**	**34.5**	**48.1**	**41.01 – 45.43**
		T13	0.40	1.1	-	-
		F3	22.88	2.1	-	-
		F11	5.53	2.9	-	-
		F12	25.99	2.2	-	-
		F17	**18.92**	**12.5**	**21.8**	**16.52 – 20.90**
Vi-B04_2_qT1-	water	*T13*	*0.40*	*5.4*	*12.7*	*0.00 – 6.80*
		F3	*13.36*	*4.3*	*4.9*	*9.81 – 18.54*
		F11	*20.98*	*5.2*	*13.8*	*8.69 – 26.31*
		F12	*25.99*	*4.9*	*11.2*	*20.46 – 31.56*
		F17	**18.92**	**14.3**	**37.3**	**16.52 – 22.48**
	ASM	*T13*	*0.40*	*3.3*	*3.3*	*0.00 – 6.80*
		F3	*13.36*	*3.9*	*5.4*	*8.25 – 18.54*
		F11	*26.31*	*5.4*	*6.9*	*20.98 – 33.17*
		F12	*24.82*	*3.7*	*7.9*	*20.46 – 31.56*
		F17	**18.92**	**19.2**	**33.7**	**16.52 – 20.90**
Ea-1430_2	water	T1	7.64	1.5	-	-
		T3	**27.16**	**5.0**	**9.4**	**21.57 – 32.02**
		T5	*63.66*	*4.1*	*6.3*	*57.93 – 65.65*
		T7	3.19	1.1	-	-
		T15	*29.70*	*3.6*	*9.3*	*21.68 – 32.50*
		F1	29.65	1.1	-	-
		F5	*47.65*	*4.4*	7.4	42.08 – 61.62
		F7	65.12	1.8	-	-
		F15	*86.70*	*3.2*	*4.2*	*81.15 – 92.65*
	ASM	*T1*	*0.40*	*3.3*	*5.1*	*0.00 – 58.27*
		T3	15.93	1.3	-	-
		T5	*49.55*	*5.1*	*5.3*	*43.24 – 53.14*
		T7	*23.12*	*4.1*	*4.5*	*15.73 – 29.10*
		T15	40.23	2.5	-	-
		F1	**26.12**	**5.9**	**7.0**	**15.4 – 31.63**
		F5	*47.65*	*3.9*	*9.1*	*42.08 – 61.62*
		F7	63.13	1.6	-	-
		F15	96.57	1.1	-	-

Supplementary Table S6. Interactions between significant and suggestive QTLs identified in Vi-B04_2, Vi-B04_2$_{qT1-}$ and Ea-1430_2 experiments.

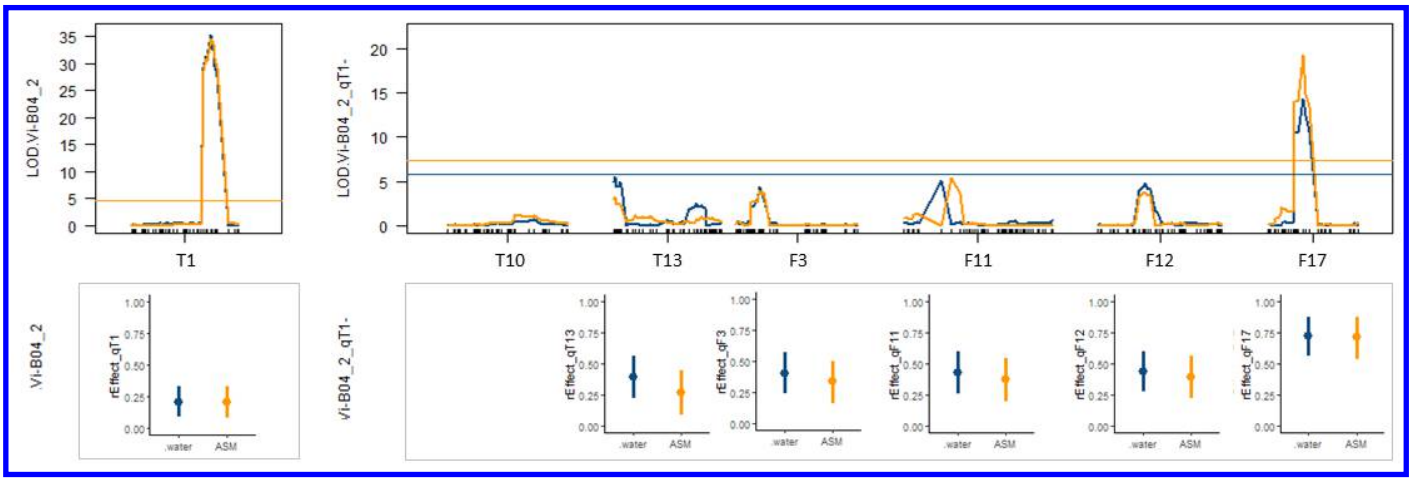
		water					ASM				
Trait	**QTLs combination**	**AA:AA**	**AB:AA**	**AA:AB**	**AB:AB**	**F-value [a]**	**AA:AA**	**AB:AA**	**AA:AB**	**AB:AB**	**F-value [a]**
Vi-B04_2	qF11:qF17	29.8	33.2	11.1	20.6	5.4 *	-	-	-	-	-
	qT1:qF17	-	-	-	-	-	17.0	0.5	5.9	-0.1	5.5 *
Vi-B04_2$_{qT1-}$	qT13:qF11	56.3	65.1	64.6	84.3	9.0 **	-	-	-	-	-
	qT13:qF17	78.1	97.2	53.0	63.7	7.7 **	-	-	-	-	-
	qF12:qF17	90.1	83.7	65.8	47.9	5.0 *	-	-	-	-	-
Ea-1430_2	qT3:qT15	4.0	5.0	3.8	3.9	10.5 **	-	-	-	-	-
	qT5:qF5	4.0	3.7	5.0	4.1	7.0 **	-	-	-	-	-
	qT1:qF5	-	-	-	-	-	1.8	1.8	2.4	1.9	4.8 *
	qF1:qF5	-	-	-	-	-	1.9	1.8	2.4	1.8	4.0 *

[a] F-value of the variance analysis Fisher-test where stars represent the significance of the test at the risk of 0.05 (*), 0.01 (**) or 0.005 (***).

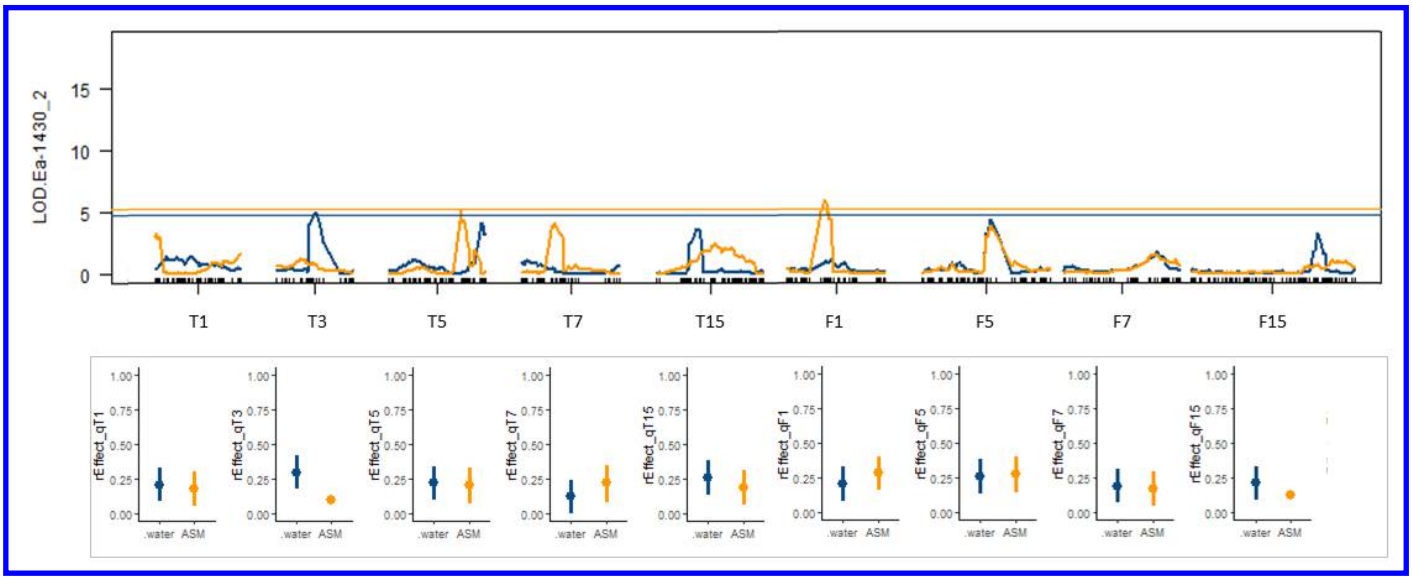
Supplementary Figure S1. Relationship between disease severity (BLUP estimates) for water- and ASM- treated individuals of the TxF progeny in (A) Vi-B04_2 and (B) Ea-1430_2 experiments. Distributions of BLUPs are shown in the upper (water control) and right (ASM treatment) part of each graph where the complete population is represented in grey and the sub-population qT1- (i.e., individuals selected as not-carrying the resistance allele of the major QTL qT1) in green. The same color code is used in the graph where the green dots are superimposed on the grey dots. Control and parental genotypes are shown with triangles in orange (TN10-8), red (Fiesta) and black (Gala and Golden Delicious). Cor is the Pearson coefficient of correlation between water and ASM BLUPs. Value for the sub-population qT1- is indicated within brackets.



Supplementary Figure S2. LOD score curves of QTLs involved in resistance against scab (Vi-B04_2) for each treatment identified in the TxF progeny (upper part) and relative effects (rEffects) of these QTLs (lower part). Blue and orange colors represent respectively the water control and ASM treatment. LOD score thresholds are drawn as horizontal lines with the respective colors. In each rEffect plot, mean and standard deviation of each rEffect, calculated with bootstrapping, are represented by a point and a vertical bar respectively, with the respective blue and orange color for water-control and ASM-treatment respectively.



Supplementary Figure S3. LOD score curves of QTLs involved in resistance against fire blight (Ea-1430_2) for each treatment identified in the TxF progeny (upper part) and relative effects (rEffects) of these QTLs (lower part). Blue and orange colors represent respectively the water control and ASM treatment. LOD score threshold are drawn as horizontal lines with the respective colors. In each rEffect plot, mean and standard deviation of each rEffect, calculated with bootstrapping, are represented by a point and a vertical bar respectively, with the respective blue and orange color for water-control and ASM-treatment respectively.



Supplementary Table S3. Summary of the genetic map of the TxF progeny. For each linkage group of each parent, SNP markers are ordered according to their genetic position given in centimorgan (cM).