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Mapping of Fire Blight Resistance QTL in the European Pear (*Pyrus communis* L.) Cultivar 'Petersbirne'

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ABSTRACT

The breeding of pear (*Pyrus communis*) cultivars that meet market requirements and are at the same time resistant to fire blight is a challenging task beacuse appropriate resistance donors are scarce. To identify valuable resistance sources, phenotypic screening and genetic characterization are indispensable. We established an F_1 population by crossing two moderately resistant pear cultivars, 'Petersbirne' and 'Harrow Sweet', to identify loci for resistance in 'Petersbirne' and to evaluate if the combination of two resistant cultivars will lead to a higher resistance level in the progeny compared with a cross with the susceptible 'Conference'. The 'Petersbirne' × 'Harrow Sweet' population had a lower average percent lesion length (PLL), 17.8, compared with 34.3 of the 'Harrow Sweet' × 'Conference' population. Mapping of the severity of fire blight in 'Petersbirne' revealed one resistance QTL on linkage group (LG) 02, which shares the same resistance haplotype as determined for 'Harrow Sweet'. Further, progenies homozygous for the resistance haplotype for the LG02 QTL had a significantly lower PLL value than the heterozygous progenies. Additionally, we identified a previously unidentified putative minor QTL on LG14 in 'Harrow Sweet' but could not confirm previously detected QTL on LGs other than LG02. Although a new resistance locus could not be identified in 'Petersbirne', the combination of two resistant cultivars seems to enhance the number of fire blight-resistant progenies and thus breeding success.

1 | Introduction

The bacterial disease, fire blight, is caused by *Erwinia amylovora* (Burrill) Winslow et al. (1920) and has devastating effects on pome fruit species, including pears (*Pyrus* spp.). The widely grown pear cultivars, such as 'Conference' and 'Bartlett', are highly susceptible to this disease (Maag et al. 2026). The main symptoms of fire blight are necrotic shoots with a scorched appearance, formation of a 'shepherd's crook' at the shoot tip (Figure 1) and formation of polysaccharide ooze drops, from which the bacteria can be spread. The primary infection sites are flowers, but an infection may also occur through wounds (Montanari et al. 2016). Wind, rain and insects may also help in spreading the bacterium, as well as contaminated soil and water (Peil et al. 2009; Santander et al. 2020).

Fire blight is a dreadful disease that is capable of destroying whole orchards within one vegetation period (Bonn and van der Zwet 2000). Most control measures are unsustainable or ineffective (Evran et al. 2025; Steiner 2000). For example, the application of antibiotics, which is forbidden in many countries, is effective only for the blossom blight stage of the infection (Emeriewen et al. 2014), and the application of copper and biological compounds and biological control agents, such as yeasts, bacteria and bacteriophages, are a few other less effective measures employed (Gayder et al. 2024; Peil et al. 2009; Seibold et al. 2004; Stockwell et al. 2011). The regular monitoring of orchards and host plants and the cultivation of resistant or at least tolerant cultivars are considered the most effective measures to control this disease. Unfortunately, resistant/tolerant cultivars have not reached significant commercial influence (Korban 2019).

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FIGURE 1 | A 'shepherd's crook' formed on an infected shoot tip.

Evaluations of fire blight response in progenies of different breeding pedigrees have shown that the resistance to this disease in pear is quantitative and polygenic (Korban 2019). Therefore, it is important to identify the loci determining this trait. The most detected and examined fire blight resistance quantitative trait locus (QTL) in pear germplasms is the QTL that is located on linkage group 02 (LG02) in 'Harrow Sweet' that was presumably inherited from 'Old Home' (Le Roux et al. 2012; Maag et al. 2025; Montanari et al. 2016). This QTL was detected in different works and explains between 15.7% and 38.8% of the phenotypic variation in different pear populations (Dondini et al. 2004; Gabay et al. 2021; Le Roux et al. 2012; Maag et al. 2025). A crucial requirement for mapping QTL is the availability of genetic maps of the parental lines, which are established using different marker systems. Dondini et al. (2004) mapped QTLs on LG02, LG04 and LG09 of the cultivar 'Harrow Sweet' using maps based on amplified fragment length polymorphism (AFLP), resistance gene analog (RGA) and simple sequence repeat (SSR) markers. In a follow-up study, Le Roux et al. (2012) confirmed the QTLs on LG02 and LG04 of 'Harrow Sweet' using an improved genetic map, which was comprised primarily of apple (*Malus*) and *Pyrus* SSR markers. In addition, the pear LG02 QTL was further identified by Gabay et al. (2021) in 'Harrow Sweet', following high-throughput SNP genotyping-by-sequencing that resulted in a SNP-dense genetic map of this cultivar. These authors also reported QTLs on LG07, LG13 and LG15. In a recent study, Maag et al. (2025) also identified the LG02 QTL in 'Harrow Sweet', and two additional QTLs on LG05 and LG11 in a population with a different genetic background, genotyped using the pear 70K Axiom SNP-Array (Montanari et al. 2019). Furthermore, using a SNP- and SSR-based genetic map, Montanari et al. (2016) identified the LG02 QTL in a different cultivar, 'Moonglow', suggesting that the QTL co-localizes with the LG02 QTL in 'Harrow Sweet'.

Interestingly, the cultivar 'Moonglow' shares the same resistance allele for the marker TsuENH017 on LG02 as 'Harrow Sweet' and 'Old Home'. As shown by Le Roux et al. (2012), 'Harrow Sweet' is a second-generation descendant of 'Old Home'. The resistance of 'Moonglow', as shown by Montanari et al. (2016), originated from 'Roi Charles de Wurtemberg'. Up to now, it has not been possible to clarify the missing link between 'Old Home' and 'Roi Charles de Wurtemberg' because it appears that both have a common ancestor, which remains unknown. Another cultivar that has the common QTL on LG02 with 'Moonglow' and 'Harrow Sweet' is 'Potomac' (Zurn et al. 2020), since 'Moonglow' is one of its parents (Gottschalk et al. 2024; Montanari et al. 2020).

For progress in breeding pear cultivars resistant to fire blight, knowledge about potential resistance donors is crucial. Studies have been conducted to characterize European pear germplasms for fire blight resistance and susceptibility (Korba et al. 2013; Maag et al. 2026; Ozrenk et al. 2012; Przybyla et al. 2012). Potential donors of resistance identified so far include 'Harrow Sweet', 'Old Home', 'Harrow Delight', 'Milchbirne', 'Punktierter Sommerdorn', 'Rüti Birne', 'Schoggolabirne' (Maag et al. 2026) and 'Hessle' (Przybyla et al. 2012).

Evaluations of fire blight resistance have also been performed in other *Pyrus* species to introgress these resistance sources despite the possible linkage drag that may bring a lot of unwanted negative traits. Bokszczanin et al. (2012) identified two *P. ussuriensis* accessions and one *P. pyrifolia* accession for the breeding of pear cultivars that are resistant to fire blight. Bell et al. (2004) identified the *P. ussuriensis* accession 'Prairie Gem' and the *P. calleryana* × *P. betulifolia* hybrid '950104', which showed very low infection following artificial inoculations with the pathogen. Thus, accessions of other *Pyrus* species can also be considered valuable resources for breeding pear cultivars with resistance to fire blight, although several generations of backcrossings will be necessary to eliminate linkage drag (Peil et al. 2021).

In general, donors for fire blight resistance in the *Pyrus* gene pool, and specifically in European pear (*P. communis*) cultivars, are rare (Maag et al. 2026).

Different pear cultivars from the German Fruit Genebank (GFG) and its partners have been tested for fire blight resistance and susceptibility using the *E. amylovora* strain Ea222 (Maag et al. 2026). The cultivar 'Petersbirne' showed low disease incidence to this pathogen strain. Therefore, there is high interest to integrate this cultivar in a breeding programme with the objective to breed cultivars with resistance to fire blight. To study the inheritance and genetics of the resistance of 'Petersbirne' and to increase the likelihood of obtaining breeding clones that would have the aptitude to become cultivars for commercial production, an F_1 population was established by crossing the Canadian fire blight-resistant pear cultivar 'Harrow Sweet' with 'Petersbirne'.

Our aim with this study is to characterize the resistance to fire blight found in the cultivar 'Petersbirne' and to evaluate whether crossing two low-susceptibility cultivars increases the proportion of less susceptible progeny.

2 | Materials and Methods

2.1 | Plant Material and DNA Isolation

We established an F_1 population with 103 individuals that were derived by crossing 'Petersbirne' with 'Harrow Sweet'. All genotypes are maintained in the orchard of the Julius Kühn-Institute, Dresden-Pillnitz, Germany. Young leaves of all genotypes, including two replicates of 'Petersbirne' and 'Harrow Sweet' as internal controls, were harvested from trees, lyophilized and sent to SGS Institute Fresenius, TraitGenetics Section, Seeland, Germany, for DNA isolation and genotyping with the pear Axiom 70K SNP array (Montanari et al. 2019). For SSR analyses, leaf samples were collected, and DNA was isolated using the Extract-N-Amp extraction and Extract-N-Amp dilution solution (Sigma-Aldrich, Darmstadt, Germany) as described in (Maag et al. 2025). DNA was thereafter diluted 1:20 and stored in −20°C until required for PCR analysis.

2.2 | Phenotyping

Artificial shoot inoculation of the 'Petersbirne' × 'Harrow Sweet' progeny was performed as described by (Maag et al. 2025). At least 10 replicates (i.e., a range of 10 to 27 replicates) per genotype were grafted on the rootstocks 'Kirchensaller Mostbirne' and/or 'Bartlett' due to the lack of rootstocks. Actively growing shoots were inoculated with *E. amylovora* strain Ea222 once they reached a height of approximately 25 cm. The plants were grown in a cold house. Shoot inoculation was done by cutting off the tips from the two youngest leaves with scissors that were dipped into the bacterial suspension (10^9 cfu/mL). Disease severity on replicates was assessed 28 days post-inoculation (dpi) by measuring fire blight lesion length (cm) and converted to percent lesion length (PLL) by dividing necrotic shoot length by total shoot length multiplied by 100.

2.3 | Genotyping of the F_1 Population

2.3.1 | SNP Genotyping

The analysis of the Axiom 70K SNP array for *Pyrus* (Montanari et al. 2019) was done by SGS Institute Fresenius, TraitGenetics Section, Gatersleben, Germany, following the protocol of the manufacturer. Data were analysed with the Axiom Analysis Suite (AxAS) software (Thermo Fisher Scientific, Santa Clara, CA, USA) using the default settings. A set of 71,363 SNPs in total was obtained. SNPs monomorphic in the progenies, SNPs with missing data in a parent and SNPs that differed between the two replicates of 'Petersbirne' were deleted. Afterwards, all markers were sorted according to the segregation type. Distortion of segregation of markers was calculated by the χ^2 test. All markers that were heterozygous in only one parent and had a χ^2 value higher than 5.39 and SNPs that were heterozygous in both parents and had a χ^2 value higher than 5.99 were deleted. Next, if the data for a genotype did not match the possible segregation pattern of a SNP, the data were replaced with missing data, and all SNPs with more than four missing data were deleted. SNPs were renamed using the physical positions on the respective linkage group given by Montanari et al. (2019). SNP sequences of SNP markers for which Montanari et al. (2019) did not give a physical position were blasted against the double haploid 'Bartlett' genome assembly (Linsmith et al. 2019) and the 'd'Anjou' genome (Yocca et al. 2024). In general, the best hit was used, but if a hit did not fit into the right LG, the best hit that matched the correct LG was used. These SNPs were named by group and position in the assemblies of 'Bartlett' or 'd'Anjou', for example, LG02_8237422 or A_LG09_1577498, respectively.

2.3.2 | SSR Genotyping

SSR markers TsuENH001, TsuENH017 and NH033b associated with the fire blight resistance QTL on LG02 (Le Roux et al. 2012), SSRs CH02f06, CH05c07, NB130b and NB129a that are associated with the fire blight resistance QTL on LG02, LG09 and LG15 (Montanari et al. 2016), and SSRs LG02_3080407, LG02_4812003, LG02_4980102, LG02_5239998, LG05_15675952, LG05_16346072, LG05_20199748, LG05_21929601, LG11_1530980, LG11_2996458, LG17_14400600 and LG17_15106863 associated with the fire blight resistance QTL on LG02, LG05, LG11 and LG17 (Maag et al. 2025) were applied to both parents and the progeny. Forward primers were either labelled with fluorescent dyes or tailed with an adapter at the 5′-end to allow amplification with a fluorescent dye (Table S1). PCR was performed using the Type-It Kit (Qiagen, Hilden, Germany) in a volume of 10 μL consisting of 1× Mastermix, 0.5× Q-solution, 0.2-μM primer and 0.2-μM adapter labelled with fluorescent dye in PCR with unlabelled forward primer, and 10 ng of DNA in multiplexes or with unlabelled forward primer as a single PCR. The amplification conditions for SSRs from Maag et al. (2025) were used, namely, 95°C for 5 min, followed by 34 cycles of 95°C for 30 s, 60°C for 1 min 30 s, 72°C for 30 s and a final extension of 30 min at 60°C. PCR conditions for the other SSRs were as described by Le Roux et al. (2012) and Montanari et al. (2016). PCR products were multiplexed (MP—Table S1) for fragment analysis on an ABI 3500 XL Genetic Analyser (Life Technologies, Darmstadt, Germany). Then 2.5 μL each of PCR with markers CH02f06, CH05c07 and NH033b and 10 μL each of PCRs with markers NB129a, NB130b, TsuENH001 and TsuENH017 were added to MPs in a total volume of 100 μL. One microlitre of each PCR product of LG02_4812003 and LG02_4980102 was used in an MP with a total volume of 40 μL, and from all other SSR products, 1 μL was used in a total volume of 100 μL. For the separation of PCR fragments, 1 μL of an MP was mixed with 9-μL HiDi formamide and 0.05 μL of size standard GeneScan LIZ 600 (Life Technologies, Darmstadt, Germany). Samples were denatured for 5 min at 95°C before loading on the ABI Genetic analyser (Life Technologies, Darmstadt, Germany). SSR alleles were analysed with GeneMapper Software 6 (Life Technologies, Darmstadt, Germany).

2.4 | Genetic Mapping and QTL Mapping

The SNP and SSR genotypic data were used to create parental maps for 'Petersbirne' and 'Harrow Sweet' using JoinMap 5.0 (van Ooijen 2018).

Settings in JoinMap 5.0 were regression mapping and Haldane's function using independence LOD for grouping. For the initial

mapping, only SNP markers that were heterozygous in only one parent, and polymorphic SSR markers were chosen. Identical SNP markers were excluded with the JoinMap automatic exclusion function. The data of the preliminary maps were edited. Implausible double recombinants were corrected, and missing data were replaced with plausible data that fit the segregation pattern. After the second mapping, markers that were heterozygous in both parents were selected to fill gaps larger than one centimorgan (cM) for each parental map. Therefore, SNP markers were selected according to their physical position in the corresponding LG, added to the JoinMap 5.0 input files and the final maps were calculated.

The final genetic maps and the average PLL of each offspring were used to determine the marker–phenotype association with Kruskal–Wallis analysis, and subsequent interval mapping was carried out with the software MapQTL5 (van Ooijen 2004). The genome-wide and the chromosome-wide thresholds were calculated using the permutation test with 1000 iterations on MapQTL 5.0. To determine whether the alleles of a marker show significant differences in PLL, the SAS procedure glimmix (generalized linear mixed model) (Schabenberger 2005) was used.

2.5 | Reconstruction of Pedigrees and Determination of Resistance Haplotype

For the pedigree construction of cultivars that are assumed to be resistant to fire blight, data published by Montanari et al. (2020) and public data from the National Clonal Germplasm Repository from the United States Department of Agriculture (USDA-ARS 2017) were used (Table S2). To identify the haplotype responsible for the resistance on LG02, SNPs were used that had been mapped to LG02 in the region between the SSRs TsuENH017 and TsuENH001 markers in 'Harrow Sweet' (Maag et al. 2025) and in both 'Harrow Sweet' and 'Petersbirne' in this study.

3 | Results

3.1 | Phenotyping

The average PLL of both parents and each individual of the progeny derived from the cross 'Petersbirne' × 'Harrow Sweet' is shown in Figure 2.

The phenotypic assessment of both parents yielded average PLL values of 15.5, with a standard deviation of 25.7 and 14.4, with a standard deviation of 26.2, for 'Petersbirne' and 'Harrow Sweet', respectively. The average and the median values of the progenies were 17.8, with a standard deviation of 29.1, and 13.9, respectively. Five individuals showed no symptoms of fire blight, and the maximal value of 63.7 PLL was shown by one individual.

3.2 | Genotyping With SNPs and SSRs

After the removal of all monomorphic SNP markers, SNPs with more than four missing data and markers with a distorted segregation pattern, a set of 22,812 SNPs (i.e., 32% of the markers on the 70K SNP array chip) was used for further analysis. Of these, 13,302 SNPs and 15,981 SNPs were used to establish genetic linkage maps for 'Petersbirne' and 'Harrow Sweet', respectively. Six thousand four hundred seventy-one SNPs were heterozygous in both parents, whereas 6831 SNPs were heterozygous only in 'Petersbirne' and 9510 SNPs were heterozygous only in 'Harrow Sweet'. Of the 18 SSR markers that were applied to the progeny, all SSRs were polymorphic in 'Harrow Sweet' and 16 SSRs in 'Petersbirne'. The SSR marker LG02_3080407 detected two loci in both parents, the SSR-marker LG02_5239998 had two loci in 'Harrow Sweet', and the SSR marker LG05_20199748 had two loci in 'Petersbirne' and three loci in 'Harrow Sweet'. One individual with 9328 missing SNP data was excluded from further analyses.

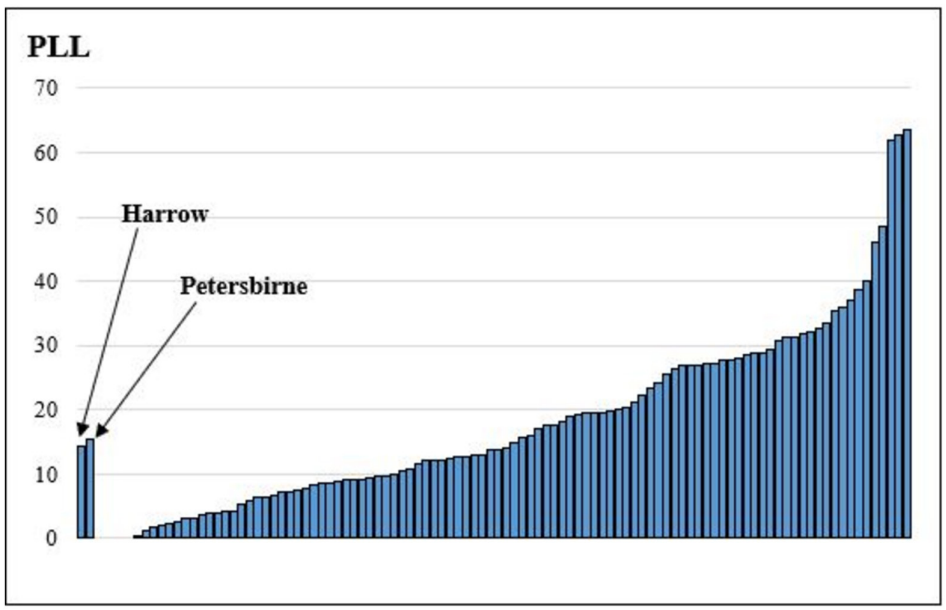


FIGURE 2 | Distribution of the average PLL (percent lesion length) values of 102 progenies of 'Petersbirne' × 'Harrow Sweet' after inoculation with *Erwinia amylovora* strain Ea222.

3.3 | Construction of Genetic Maps

SNP and SSR data were loaded onto JoinMap 5.0 to calculate the linkage maps. Seventeen LGs were grouped for 'Petersbirne' and 'Harrow Sweet' at LODs of 12 and 21, respectively. The linkage map of 'Petersbirne' consists of 1597 SNP markers and 18 loci from 16 SSRs, with a length of about 1268 cM.

The 17 linkage groups of 'Harrow Sweet' consist of 1591 SNPs and 22 loci from 18 SSR markers. The total length of this map is about 1378 cM. Table 1 gives an overview of the number of SNPs and SSRs per LG, the largest gap in each LG and the number of markers per cM for both parental maps.

The physical positions of 141 and 159 SNPs mapped to the maps of 'Petersbirne' and 'Harrow Sweet', respectively, were not provided by Montanari et al. (2019). The position of 8 and 24 SNPs missing in 'Petersbirne' and 'Harrow Sweet', respectively, were presented in Maag et al. (2025). The physical position of the remaining SNPs could be determined after blasting against the genomes from 'Bartlett' and 'd'Anjou'. The complete maps of both 'Petersbirne' and 'Harrow Sweet' containing the SNP numbers of the array and their physical position are presented in Table S3. For 'Harrow Sweet', 21 SNP positions could not be identified in the 'Bartlett' genome. All of them were identified in the 'Anjou' genome assembly. Eleven of these markers mapped on the top of LG09, including nine SNPs with a position in 'Anjou' on LG17.

For 'Petersbirne', the physical positions for 26 SNPs could not be determined in the genome of 'Bartlett'. All of them were identified in the 'd'Anjou' genome.

The order of the SNPs on both genetic maps, in general, is in accordance with their physical position. Some markers were assigned by blasting to a linkage group that does not correspond to the linkage group in the genetic map. These markers are highlighted in Table S3.

A total of three SSRs were multi-locus markers. The SSR LG02_3080407 mapped two loci, LG02 and LG15, in both 'Petersbirne' and 'Harrow Sweet'. LG02_5239998 mapped with one locus in 'Petersbirne' on LG02 and with two loci in 'Harrow Sweet' on LG02 and LG15. Mapping of SSR marker LG05_20199748 resulted in two loci, LG05 and LG10, in 'Petersbirne' and three loci, LG05 and two on LG10, in 'Harrow Sweet'.

3.4 | QTL Mapping

Kruskal–Wallis analysis was performed with the mean PLL values for each genotype using the genetic linkage maps of

TABLE 1 | Summarized characteristics of the genetic maps from the pear cultivars 'Petersbirne' and 'Harrow Sweet'.

	Petersbirne					Harrow Sweet				
	No. of		Length		Largest	No. of		Length		Largest
LG	SNPs	SSRs	(cM)	Markers/cM	gap	SNPs	SSRs	(cM)	Markers/cM	gap
1	82		62.7	1.3	2.4	67		64.4	1.0	3.7
2	80	7	73.3	1.2	5.7	89	8	83.2	1.2	3.7
3	109		94.4	1.2	5.5	101		93.6	1.1	9.9
4	79		63.3	1.2	4.5	84		71.5	1.2	4.3
5	110	3	90.9	1.2	8.2	110	3	105.3	1.1	3.7
6	75		56.5	1.3	3.2	61		73.8	0.8	4.1
7	86		77.5	1.1	15.8	114		80.1	1.4	5.2
8	81		60.1	1.3	3.0	92		72.3	1.3	7.2
9	78	2	66.5	1.2	3.4	69	2	64.1	1.1	8.5
10	106	1	80.7	1.3	4.0	58	2	54.5	1.2	3.8
11	108	2	69.4	1.6	3.5	121	2	87.8	1.4	5.1
12	98		71.6	1.4	4.3	100		70.4	1.4	5.2
13	91		78.1	1.2	3.5	93		83.4	1.1	11.7
14	87		63.0	1.4	2.7	90		86.8	1.0	7.9
15	140	1	110.4	1.3	6.0	150	3	121.0	1.3	3.9
16	83		73.5	1.1	3.6	83		86.4	1.0	10.8
17	106	2	76.5	1.4	2.9	109	2	79.6	1.4	3.6
Total	1597	18	1268.4			1591	22	1378.2		

both parents to determine marker–phenotype associations. The most significant marker–phenotype associations were found in both 'Petersbirne' and 'Harrow Sweet' on LG02. Further significant associations were found on LG14 in 'Harrow Sweet' (Table 2). Although significant LOD scores were identified for LG09 (LOD = 2.8, chromosome-wide threshold 2.7 in 'Petersbirne') and LG12 (LOD = 3.1) in both parents, as the peaks passed the chromosome-wide threshold of 2.8 for 'Petersbirne' and 3.0 for 'Harrow Sweet', significant marker–trait associations with the Kruskal–Wallis test could not be determined for these LGs.

In 'Petersbirne', a QTL on LG02 was identified by interval mapping with an LOD score of 5.2, which explained 21.1% of the phenotypic variation. This QTL exceeds the genome-wide threshold of an LOD of 4.4.

A QTL with an LOD of 5.2 at the same position on LG02 was identified in 'Harrow Sweet', explaining 21% of the phenotypic variation. Whereas the QTL on LG02 exceeds the genome-wide threshold of 4.3, another QTL identified on LG14 only exceeded the chromosome-wide threshold of 2.9. SNP LG14_19998520 underlying this QTL explained 13.2% of the phenotypic variation, with an LOD of 3.1. Both QTL together explain around 33.2% of the phenotypic variation (Table 2).

Four SSR markers chosen to flank the QTL on LG02 span around 11 cM (Figure 3). An overview of the markers with the highest association to the QTLs is presented in Table 2.

The analyses with SAS showed that individuals which had inherited only the QTL on LG02 from 'Petersbirne' and individuals that had both the QTL from 'Harrow Sweet' and 'Petersbirne'

TABLE 2 | Overview of the markers with the highest LOD of the detected QTL and allele sizes of SSRs and the genetic position of the markers linked to resistance.

Marker[a]	Allele/SNP linked to QTL[b]	Position on the LG (cM)	LOD	KW	%expl.	PLL associated with		SNP name on array
						Resis.	Susc.	
LG02		Petersbirne						
LG02_3080407_180	180	8.6						
TsuENH017	235	8.7						
LG02_3981399[b]	**T**/C	11.8	5.2	15.6	21.1	11.5	32.2	AX-171947526
LG02_4812003_162	162	14.9						
TsuENH001	207	20.0						
LG02		Harrow Sweet						
LG02_3080407_180	216	12.0						
TsuENH017	179	12.0						
LG02_4058739[b]	**A**/G	16.6	5.2	16.7	21.0	10.7	32.2	AX-172367621
LG02_4812003_162	162	19.7						
TsuENH001	207	22.8						
LG14								
LG14_18697554	T/**C**	67.9						AX-172002174
LG14_19998520[b]	T/**G**	78.8	3.1	7	13.2	13.9	23.0	AX-172031527
LG14_20695225[b]	A/**C**	81.2	3.1	13.6	13.1	13.1	22.9	AX-171886591
LG14_21569042	A/**G**	86.8						AX-172149739

Abbreviations: cM, centimorgan; %expl., percent phenotypic variation explained; KW, Kruskal–Wallis; LOD, logarithm of odds; PLL, percent lesion length; resis, resistance; susc, susceptibility.
[a]The first number after the LG is the position on the respective LG in Bartlett.
[b]The name of the marker and the nucleotide (fragment) of the marker with the highest LOD score associated to resistance is printed in bold.
[Correction added on 18 June 2026, after first online publication: In Table 2, under the "SNP name on array" column, all instances of "AXE-" have been corrected to "AX-"]

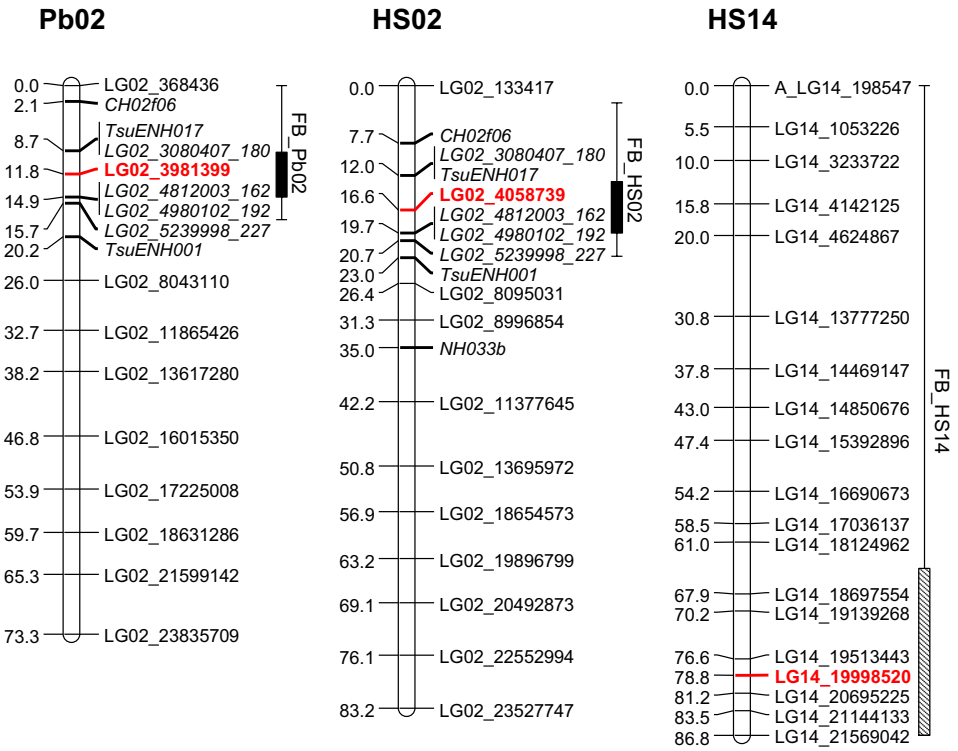


FIGURE 3 | QTL positions that are associated with fire blight resistance in simplified linkage groups. SSRs are marked in italics, and markers expressing the highest LOD are marked red. 1-LOD interval is represented by bars, and 2-LOD interval by lines. Black bars represent QTL that passed the genome-wide threshold, and dashed bars represent the QTL that have passed only the chromosome-wide threshold. The figure was generated with the software MapChart 2.3 (Voorrips 2002).

had a significantly lower PLL, namely, 14.7 and 12.0, respectively, than individuals that only had the QTL from 'Harrow Sweet', PLL = 20.8, or no QTL, PLL = 30.5. Although the combination of both QTLs on LG02 and the QTL from 'Petersbirne' showed no significant difference, the PLL of individuals that only have the QTL from 'Harrow Sweet' differs significantly from the PLL of individuals that have neither QTL. We compared the PLL of individuals inheriting contrasting alleles of single SNPs within the QTL regions. Individuals who inherited the resistance alleles of these SNPs in a homozygous manner had significantly lower PLL than individuals who inherited these alleles in a heterozygous manner. The significant difference in PLL between individuals of these two categories was higher when compared with individuals who inherited the susceptible allele in a homozygous manner (Figure 4). In general, individuals who inherited marker alleles associated with resistance showed significant differences in PLL values. For example, individuals who inherited the resistance allele of the marker LG02_3216333 (heterozygous in 'Petersbirne') showed a PLL of 13.4 (lm) compared with those with the other allele (ll) with a PLL of 23.6. This was similar for the marker LG02_3458490 (heterozygous in 'Harrow Sweet'), where individuals with the resistance allele (np) showed PLL values of 16.6 compared with individuals with the other allele (nn) with a PLL of 20.6.

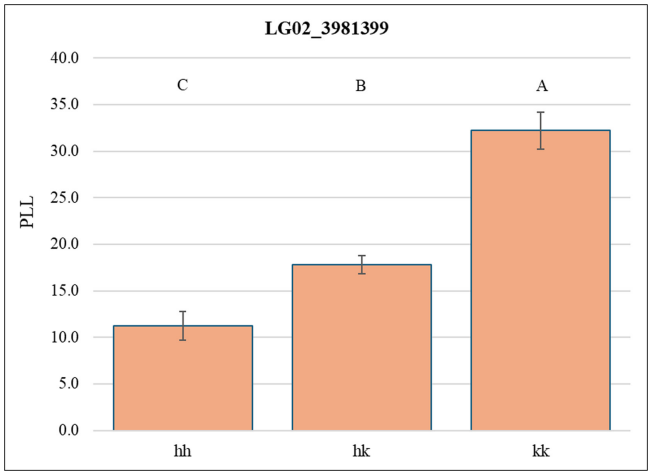


FIGURE 4 | The mean PLL values of the individuals who inherited alleles of the marker LG02_3981399 in homozygous resistant manner (hh), heterozygous manner (hk) and homozygous susceptible manner (kk). Letters above the bars indicate statistically significant difference in mean PLL.

3.5 | Determination of Resistance Haplotype and Reconstruction of Pedigrees

We used SNPs that map in the intervals between SSRs TsuENH017 and TsuENH001 in both 'Harrow Sweet' and 'Petersbirne' to reconstruct the resistance haplotypes using data from the current study and from Maag et al. (2025). The SNPs identified in this interval span a region of around 4.07 Mb (i.e., 3.22 Mb for LG02_3218883 to 7.29 Mb for LG02_7292910 in both 'Harrow Sweet' and 'Petersbirne', Table S3). The resistant haplotype shared by the cultivars 'Harrow Sweet', 'Petersbirne', 'Rousselet de Reims', 'Seckel', 'Elliot', 'Green Sugar Pear' ('Sucre Verte'), 'Old Home', 'Roi

Charles de Wurtemberg', 'Duchesse de Angouleme', 'White Doyenne', 'Potomac', 'Anjou' and 'Moonglow' ranges from 3.49 Mb (LG02_3492529) to 4.96 Mb (LG02_4955390), which has a length of approximately 1.46 Mb. SNP data of four replicates of 'Harrow Sweet' (Montanari et al. 2020, Maag et al. 2025 and this study) and SNP data of two and three replicates, respectively, for 'Moonglow' (Montanari et al. 2020) and 'Petersbirne' (Montanari et al. 2020), were included in the analysis (Table 3). Some of the SNPs in the replicates were not identical (Table 3).

TABLE 3 | Haplotype of SNP markers shared within the resistance locus interval on LG02 by 'Petersbirne', 'Harrow Sweet' and cultivars presumed to be resistant to fire blight.

Nr.	Marker	Position in Harrow Sweet[4]	LOD in Harrow Sweet[4]	Position in Harrow Sweet[3]	LOD in Harrow Sweet[3]	Position in Petersbirne[3]	LOD Petersbirne[3]	Haplotype linked to resistance	Harrow Sweet[3]	Harrow Sweet[4]	Harrow Sweet[5]	Harrow Sweet[5]	Petersbirne[3]	Petersbirne[3]	Petersbirne[5]	Rousselet de Reims[5]	Seckel[5]	Elliot[5]	Green Sugar Pear[5]	Bergamotte d' Autopmne[5]	Old Home[5]	Roi Charles de Wurtemberg[5]	Duchesse de Angouleme[5]	White Doyenne[5]	Potomac[5]	Anjou[5]	Moonglow[5]	Moonglow[5]	Clairegeaus Butterbirne[5]	Bartlett[5]	Michigan-US 437[5]	Howell Sport[5]	Vermont Beauty[5]	Conference[4]	Conference[5]
	TsuENH017	6.8	7.7	12.0	3.8	8.7	3.8																												
1	LG02_3218883[1]	8.0	7.6					T	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|T	T|C	T|C	T|C	T|C	C|C	T|T	C|C	C|C	C|C	C|C	T|C	T|C
2	LG02_3386359[1]	8.1	7.5	12.8	4.2			G	G|A	G|A	G|A	G|A	A|A	A|A	G|A	G|A	A|A	G|A	A|A	A|A	G|A	G|G	G|A	G|A	G|A	G|A	A|A	G|G	A|A	A|A	A|A	A|A	G|A	G|A
3	LG02_3409592[2]			12.8	4.2			A	A|G	A|G	A|G	G|G	A|G	A|G	G|G	A|G	A|G	G|G	A|G	A|A	G|G	G|G	A|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G
4	LG02_3386359[1;]	8.1	7.5	12.8	4.2			G	G|A	G|A	G|A	G|A	A|A	A|A	G|A	G|A	A|A	G|A	A|A	A|A	G|A	G|G	G|A	G|A	G|A	G|A	A|A	G|G	A|A	A|A	A|A	A|A	G|A	G|A
5	LG02_3547016[1;]	8.2	7.5	14.0	4.5			A	A|G	A|G	A|G	A|G	A|A	A|A	A|G	A|G	A|G	A|G	A|G	A|A	A|G	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	G|G	G|G	G|G	G|G	A|G	A|G
6	LG02_3458490[2]			14.0	4.5			C	C|A	C|A	C|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	C|A	A|A	A|A	C|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A
7	LG02_3492529[2]					10.1	4.5	C	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|C	C|T	C|T	C|T	C|T	C|T	C|C	C|T	C|T	C|T	C|T	C|T	C|T	T|T	C|C	T|T	T|T	T|T	T|T	C|T	C|T
8	LG02_3493221[1]	8.2	7.5					C	C|T	C|T	C|T	C|T	C|C	C|C	C|T	C|C	C|T	C|T	C|T	C|T	C|T	C|C	C|T	C|T	C|T	C|T	C|T	C|T	T|T	C|C	T|T	T|T	T|T	T|T	C|T	C|T
9	LG02_3533452[1]	8.4	7.5					C	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|C	C|A	C|A	C|A	C|A	C|A	A|A	C|C	A|A	A|A	A|A	A|A	C|A	C|A
10	LG02_3675804[2]					11.2	5.2	T	T|C	T|C	T|C	T|C	T|C	T|C	T|T	T|T	T|C	T|C	T|C	T|C	T|C	T|T	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	C|C	C|C	C|C	C|C
11	LG02_3266194[1]	8.9	8.5					A	A|C	A|C	A|C	A|C	A|C	A|C	A|A	A|C	A|C	A|C	A|C	A|A	A|C	A|A	A|A	A|C	A|C	A|C	A|C	C|C	A|A	A|C	A|C	C|C	C|C	A|C	A|C
12	LG02_3904487[1]	9.9	8.2					G	G|A	G|A	G|A	G|A	G|A	G|A	G|G	G|G	G|A	G|A	G|A	G|A	G|A	G|G	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	A|A	A|A	A|A	A|A
13	LG02_3981399[2]					11.8	5.2	T	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|T	T|C	T|T	T|T	T|C	T|C	T|C	T|C	C|C	T|C	C|C	C|C	C|C	C|C	C|C	C|C
14	LG02_4409816[2]					12.3	5.0	C	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|C	C|T	C|T	C|T	C|T	C|T	T|T	C|T	T|T	T|T	T|T	T|T	T|T	T|T
15	LG02_4058739[2]			16.6	5.2			A	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|A	A|G	A|G	A|G	A|G	A|G	A|G	A|G	G|G	G|G	G|G	G|G	G|G	G|G
16	LG02_4579806[2]			18.6	4.7			G	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|G	--	G|A	G|A	G|A	G|A	A|A	G|A	A|A	A|A	A|A	A|A	A|A	A|A
17	LG02_4850990[1]	10.8	8.4					C	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T
18	LG02_4955390[1]	11.6	7.9					G	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A
19	LG02_4996930[2]			19.7	3.7	14.9	3.8	A	A|C	A|C	A|C	C|C	A|C	A|C	C|C	A|C	A|C	A|C	A|C	A|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C
20	LG02_5395324[2]					15.4	3.5	T	T|C	T|C	T|C	C|C	T|C	T|C	C|C	T|C	T|C	T|C	--	T|T	C|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	T|C	C|C	C|C	C|C	C|C	C|C	C|C	C|C
21	LG02_5659298[1]	12.7	7.8					G	G|T	G|T	G|T	T|T	G|T	G|T	T|T	G|T	G|T	G|T	G|T	G|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T	T|T
22	LG02_5702459[2]					16.2	3.2	A	A|G	A|G	A|G	A|G	A|G	A|G	A|G	A|A	A|G	A|G	A|G	A|A	A|G	A|A	A|A	A|G	A|G	A|G	--	G|G	A|G	G|G	G|G	G|G	G|G	G|G	G|G
23	LG02_5827102[2]			21.2	3.2			T	T|G	T|G	T|G	G|G	T|T	T|T	G|G	T|G	T|G	T|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G
24	LG02_5953648[1]	13.5	7.5					A	A|G	A|G	A|G	G|G	A|G	A|G	G|G	A|A	A|G	A|G	A|G	A|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G
25	LG02_6184538[1]	15.1	7.4					T	T|G	T|G	T|G	G|G	T|G	T|G	G|G	T|G	T|G	T|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	G|G	T|G	T|G
26	LG02_6091103[1]	15.3	7.1					G	G|A	G|A	G|A	A|A	G|A	G|A	A|A	G|G	G|A	G|A	G|A	G|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	G|A	G|A
27	LG02_6144924[2]			21.6	2.8			G	G|A	G|A	G|A	G|A	G|G	G|G	G|A	G|A	G|A	G|A	A|A	A|A	G|A	G|A	G|A	G|A	G|A	G|A	G|A	A|A	A|A	A|A	A|A	A|A	A|A	G|A	G|A
28	LG02_6197805[1]	15.4	7.7					A	A|C	A|C	A|C	A|C	A|A	A|A	A|C	A|A	A|C	A|C	A|C	A|A	A|C	A|A	A|A	A|C	A|C	A|C	A|C	C|C	A|C	C|C	C|C	C|C	C|C	A|C	A|C
29	LG02_6206423[1]	15.5	7.7					G	G|A	G|A	G|A	A|A	G|A	G|A	A|A	G|A	G|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	--	A|A	A|A	A|A	A|A	A|A	A|A	G|A	G|A
30	LG02_6101664[1]	15.9	6.4					C	C|A	C|A	C|A	A|A	C|A	C|A	A|A	C|A	C|A	C|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	C|A	C|A
31	LG02_6818590[1]	16.1	7.2					G	G|A	G|A	G|A	A|A	G|A	G|A	G|A	G|A	G|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	A|A	G|A	A|A	G|A	G|A	A|A	A|A	A|A	A|A
32	LG02_6407404[1]	16.3	7.4					G	G|T	G|T	G|T	G|T	G|G	G|G	G|T	G|G	G|T	G|T	G|T	G|G	G|T	G|G	G|G	G|G	G|T	G|T	G|T	G|T	T|T	G|T	T|T	T|T	T|T	T|T	G|T	G|T
33	LG02_6538103[1]	16.5	7.5					C	C|A	C|A	C|A	C|A	C|C	C|C	C|C	C|A	C|A	A|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	C|A	A|A	C|A	C|A	A|A	A|A	C|A	C|A
34	LG02_6427809[1]	16.5	7.5					C	C|T	C|T	C|T	C|T	C|C	C|C	C|C	C|C	C|T	C|T	C|T	C|C	C|T	C|C	C|C	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	T|T	T|T	C|T	C|T
35	LG02_6564408[1]	16.9	7.7					T	T|C	T|C	T|C	C|C	T|C	T|C	T|T	T|C	T|C	C|C	C|C	C|C	T|C	T|C	T|C	T|C	C|C	T|C	C|C	T|C	C|C	T|C	C|C	C|C	T|C	T|C
36	LG02_6936520[1]	17.4	7.0					G	G|T	G|T	G|T	T|T	G|G	G|G	G|G	G|T	G|T	T|T	G|T	G|T	G|T	G|T	G|T	G|T	G|T	T|T	G|T	T|T	G|T	T|T	G|T	G|T	T|T	T|T	G|T	G|T
37	LG02_6739458[1]	17.6	6.7					C	C|T	C|T	C|T	C|T	C|C	C|C	C|C	C|C	C|T	C|T	C|T	C|C	C|T	C|C	C|C	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	C|T	T|T	T|T	C|T	C|T
38	LG02_7246018[1]	17.9	6.2					A	A|G	A|G	A|G	G|G	A|A	A|A	A|A	A|G	A|G	G|G	A|G	A|G	A|G	A|G	A|G	A|G	A|G	G|G	A|G	G|G	A|G	A|G	G|G	G|G	A|G	A|G	G|G	A|G	A|G
39	LG02_7292910[2]			22.8	2.3			T	T|G	T|G	T|G	G|G	T|T	T|T	T|G	T|G	T|G	G|G	T|G	T|G	T|G	T|G	T|G	T|G	T|G	G|G	T|G	T|G	G|G	G|G	G|G	G|G	G|G	G|G	T|G	T|G
40	TsuENH001[12]	18.2	6.2	23.0	2.1	20.0	2.1																												

Note: SNPs filled with yellow are different amongst the same replicates of the same cultivar. SNPs framed with lines indicate cultivars sharing the resistance haplotype from LG02_3492529 to LG02_4955390.

[1]Marker from Maag et al. (2025).

[2]Marker from this study.

[3]Data from this study.

[4]Data from Maag et al. (2025).

[5]Data from Montanari et al. (2020)

-- missing data.

[Correction added on 6 June 2026, after first online publication: In the footnote of Table 3, the superscripts were corrected from letters to numbers.]

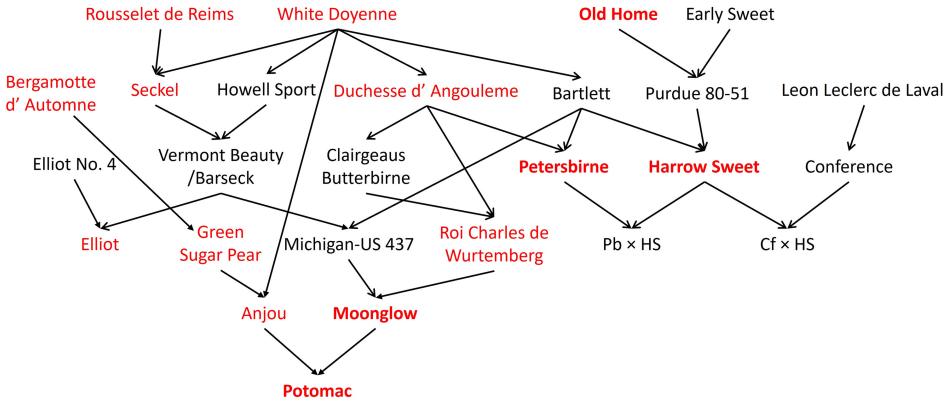


FIGURE 5 | Pedigree of cultivars with assumed resistance to fire blight. Pear cultivars sharing the resistant haplotype on LG02 are in red, the cultivars with QTL determined on LG02 are in bold red.

The construction of the pedigrees of pear cultivars presumed to be resistant to fire blight, for some of which resistance QTLs have already been described, is shown in Figure 5.

4 | Discussion

The 70K Axiom SNP array (Montanari et al. 2019) has proven to be a significant tool for genetic studies in pear. We applied this technology in our study to genotype an F_1 population derived from the cross 'Petersbirne' × 'Harrow Sweet' to construct genetic maps that enhance the dissection of the inheritance of fire blight resistance. We successfully developed genetic maps of both parents using the SNP data derived from genotyping their progenies. The genetic maps developed in this study are comparable with those developed by Maag et al. (2025) using a population with 'Harrow Sweet' as a parent. Importantly, SNP genotyping data allowed for a genome-wide map, which represent the 17 chromosomes of *Pyrus*, as well as a comparative study of the inheritance of SNP haplotypes of interest. This is especially necessary to decipher previously unknown pedigrees and will be important for future studies.

The two parental cultivars in this study have consistently shown very low susceptibility to fire blight in previous experiments (Maag et al. 2026). 'Harrow Sweet', on the one hand, has been proven to carry the pear fire blight QTL on LG02 (Maag et al. 2025; Dondini et al. 2004; Le Roux et al. 2012). Zurn et al. (2020) identified a major QTL in a similar position on LG02 in 'Old Home', which is one parent of 'Harrow Sweet', although the position of the QTL shifted between the 2 years of analyses by about 10 cM. 'Petersbirne', on the other hand, has not previously been used in any fire blight mapping studies; thus, it was unknown what resistance QTL alleles this cultivar expresses. Phenotypic evaluation of the resultant progenies from this cross showed that the number of completely blighted individuals was reduced compared with Maag et al. (2025). The approach of crossing two parents that show low susceptibility to fire blight in pear breeding programme appears to be a logical and useful one, as the comparison of the results shown in the study published by Maag et al. (2025), and the current study indicates that the segregating F_1 population that is derived from the cross 'Petersbirne' × 'Harrow Sweet' did show significantly lower mean PLL value (18.2) ($p < 0.0001$) than the population that was derived from the cross 'Conference' × 'Harrow Sweet' (34.3). 'The cultivar 'Conference' is highly susceptible to fire blight. Moreover, these results were supported by molecular analyses, where the genotypes having the beneficial alleles from both resistant parents showed lower fire blight severity values following artificial inoculations.

In this study, we confirmed the resistance QTL on LG02 and identified a novel putative minor QTL on LG14 in 'Harrow Sweet', and simultaneously, we identified a QTL on LG02 in 'Petersbirne' in the same region as in 'Harrow Sweet'. QTL in other LGs identified in the works of Le Roux et al. (2012), Gabay et al. (2021) and Maag et al. (2025) could not be confirmed in the present study. This supports the suggestion that the LG02 locus for fire blight is the predominant locus in the *P. communis* gene pool. However, the LOD value, phenotypic variation explained, and therefore, the strength of this QTL varies from study to study. The phenomenon of different strengths of the same QTL in different populations could be affected by using different pathogen strains, as was also mentioned by Desnoues et al. (2018), concerning *Malus* species. The reasons for this phenomenon can be diverse. Because both cultivars 'Petersbirne' and 'Harrow Sweet' are tolerant/resistant to fire blight, the mapping results could have been affected because, for QTL mapping, the expression of traits of interest in the parents of the mapping populations has to be different (Dhingani et al. 2015). In Maag et al. (2025), the maximal LOD score for LG02 was 8.54, whereas in this study, the highest LOD score for 'Harrow Sweet' was 5.16. The relatively small population size of 102 individuals, though sufficient for mapping studies, can be a possible reason for differing LOD scores. Further, fire blight phenotyping is challenging due to the erratic nature of disease, where variable severity is observed between replicates. Reasons for this could be physiological parameters of the phenotyped plants, the pathogen strain used for inoculation, the inoculation method and the environment. These questions are thoroughly discussed in Maag et al. (2026).

Based on our results, it is reasonable to assume that 'Petersbirne' and 'Harrow Sweet' share a common ancestor in their pedigree. According to Montanari et al. (2020), both 'Petersbirne' and 'Harrow Sweet' are direct descendants of 'Bartlett'. However, 'Bartlett' is highly susceptible to fire blight in comparison to both 'Petersbirne' and 'Harrow Sweet' (Ozrenk et al. 2012). 'Harrow Sweet' shares the resistance allele of marker TsuENH017 with

'Old Home' on LG02 (Maag et al. 2025; Montanari et al. 2016) because 'Old Home' is an ancestor of 'Harrow Sweet'.

The reconstruction of the pedigrees and the comparison of the SNPs for the cultivars that are assumed to be resistant to fire blight did show that the haplotype for the resistance on LG02 in the cultivars is the same. This resistance haplotype ranges from the SNP-marker LG02_3492529 to SNP-marker LG02_4955390, which corresponds to a length of approximately 1.46 Mb. We propose that the gene linked to resistance is located in this interval. Furthermore, this leads to the assumption that the resistance on this LG originates from a common unknown ancestor because the ancestors and full pedigrees of 'Rousselet de Reims', 'White Doyenne', 'Old Home', 'Elliot No. 4' and 'Green Sugar Pear' are not known.

This finding stimulates the question of how diverse the variation in European pear is for loci that contribute significantly to fire blight resistance.

Because many phenotyping tests have been carried out in pear (Korba et al. 2013; Maag et al. 2026; Ozrenk et al. 2012; van der Zwet and Bell 1995), it would be an interesting outlook for the future to genotype pear collections and to conduct genome-wide association studies (GWAS) in order to unravel unknown alleles and loci that contribute to the resistance to fire blight. This could provide insight into allelic diversity and the effect alleles may contribute to the progeny. The assessment of the diversity of the alleles of markers linked to fire blight resistance and the effect of the different alleles would be crucial in order to provide an overview of the desirable alleles that could be useful for the breeding process of novel pear cultivars that are resistant to fire blight.

5 | Conclusions

The breeding of fruit trees is a process that consumes both physical resources and time. Therefore, every tool that eases the process and enables saving money and time is welcome. Crossing a resistant cultivar with another resistant cultivar led to a higher percentage of offspring less affected by *E. amylovora*. We identified a QTL for fire blight resistance on LG02 in 'Petersbirne' and also found that it shares the same resistance haplotype as in 'Harrow Sweet'. Furthermore, by comparing the resistance haplotype with other pear cultivars assumed to be resistant, we detected a region spanning around 1.46 Mb on LG02 shared by all of these cultivars.

Author Contributions

Martin Maag: investigation, writing – original draft, validation, visualization, writing – review and editing, formal analysis, data curation, software, methodology. **Holger Zetzsche:** investigation, writing – review and editing, methodology, data curation, formal analysis, validation, visualization. **Henryk Flachowsky:** conceptualization, writing – review and editing, supervision, resources. **Ofere Francis Emeriewen:** investigation, writing – original draft, writing – review and editing, validation, formal analysis, visualization, methodology. **Andreas Peil:** conceptualization, investigation, funding acquisition, writing – original draft, writing – review and editing, visualization, validation, methodology, formal analysis, software, supervision, data curation, project administration.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data that support the findings of this study are published herein and as Supporting Information. More data could be made available upon request.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Table S1:** SSRs used for genotyping the population derived from 'Petersbirne' × 'Harrow Sweet' and the adherent references in which PCR conditions were described. **Table S2:** Data from the National Clonal Germplasm Repository from the United States Department of Agriculture (USDA-ARS 2017) used for pedigree reconstruction. **Table S3:** The complete genetic maps of 'Petersbirne' and 'Harrow Sweet' containing the SNP numbers of the array, their physical positions and map positions.