

Article

Candidate Gene Variants Linked to Brown Rot Susceptibility in the European Plum Genome

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Abstract

European plum (*Prunus domestica*) is among the most important stone fruits cultivated worldwide. However, its production is significantly affected by fungal brown rot disease, caused by *Monilinia* spp. pathogens, which threaten the crop throughout the entire vegetation period. This study aimed to visually assess brown rot resistance and susceptibility in European plum and to perform whole-genome sequencing (WGS) of selected cultivars and hybrids grown in Lithuania, with the goal of identifying candidate single-nucleotide polymorphisms (SNPs) associated with disease response. WGS was performed for 20 European plum cultivars and hybrids with known resistance or susceptibility profiles, generating over 1,4 million SNPs. These SNPs were filtered to identify genetic variants associated with brown rot disease. Three candidate SNPs were found to be significantly associated with disease response (located on chromosomes G5 and G8) and one linked to susceptibility (on chromosome G5). Identified SNPs were located in genes encoding alcohol dehydrogenase family enzymes (resistant cultivars, G5 chromosome) and beta-glucosidase family enzymes (variants found in both resistant and susceptible cultivars, G5 chromosome), which are important for plant biotic stress response. The findings of this study provide a valuable foundation for the development of molecular markers for identifying resistant and susceptible cultivars and may inform future European plum breeding programs.

Keywords: *Prunus domestica*; single-nucleotide polymorphism (SNP); brown rot; *Monilinia* spp.; whole-genome sequencing (WGS)



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1. Introduction

Plums are an important component of global stone fruit production, ranking second only to peaches and nectarines in terms of production volume [1]. The European plum originated in southeastern Europe and western Asia [2]. In Europe, the European plum is the most important species cultivated for fresh and dried plum production [3]. Plums are valued for their flavor, high sugar content, late blooming, and high productivity; however, they are susceptible to spring frost and diseases [3]. The European plum (*Prunus domestica* L.) belongs to the *Prunus* genus, Rosaceae family [2]. The genus *Prunus* is characterized by a fundamental chromosome number of $x = 8$. It is a hexaploidy ($2n = 6x = 48$) hybrid of the diploid ($2n = 2x = 16$) cherry plum (*Prunus cerasifera* Ehrh.) and tetraploid ($2n = 4x = 32$) sloe (*Prunus spinosa* L.) [4–7]. The polyploidy of *Prunus* genus plants arose naturally from interspecific hybridization (autopolyploid) during phylogeny [8]. In total, about 6000 plum cultivars, belonging to up to 40 plums species, are identified all over the world [2]. One of the most important fungal diseases of stone and pome fruits is caused by *Monilinia*

spp. pathogens [9]. In total, six *Monilinia* spp. pathogen species are found worldwide: *M. laxa* (Aderhold and Ruhland) Honey, *M. fructigena* (Aderhold and Ruhland) Honey, *M. fructicola* (Winter) Honey, *M. polystroma* (G. Leeuwen), *M. mumeicola* (Y. Harada, Y. Sasaki & Sano), and *M. yunnanensis* (M.J. Hu & C.X. Luo) [9–11]. The most economically damaging *Monilinia* species in Europe are *M. laxa*, *M. fructigena*, and *M. fructicola* [10]. These pathogens can infect the host plant during the whole vegetation period, causing blossom blight, branch infections, twig canker, and fruit rot before and post-harvest [10,12].

During fungal infection, two main mechanisms in host plants are observed. One of them is the resistance mechanism, showing the host plant's ability to limit pathogen multiplications [13], and the second is the susceptibility to the pathogen by facilitating the infection and supporting host plant–pathogen compatibility [14].

The European plum genome is approximately 1399 Gb and contains 27,870 scaffolds. It is available in the genome database for Rosaceae (GDR) [15] (Callahan et al., 2021). As this genome is still incomplete, it cannot be used as a reference genome. Therefore, for genetic analysis of European plum, the *P. persica* genome is an option as a reference genome within the *Prunus* genus in genetic analysis studies [16] (Zhebentyayeva et al., 2019).

The European plum germplasm has been genetically identified by random amplified polymorphic DNA (RAPD) [17], restriction fragment length polymorphism (RFLP) [18–20], markers, and fingerprinted by simple sequence repeats (SSRs) [21,22]. A recently performed transcriptome analysis of the European plum, infected with *M. fructigena*, revealed candidate genes for the European plum's susceptibility to brown rot disease [23]. Single-nucleotide polymorphisms (SNPs) have previously been identified in the European plum's genome, using the genotyping by sequencing (GBS) method [24]. However, whole-genome sequencing (WGS) is necessary for more accurate SNP detection to enable the association analysis of these variants with brown rot resistance. Unlike GBS, which sequences only a fraction of the genome, WGS provides comprehensive coverage, allowing for the identification of all variants across coding and non-coding regions [25,26].

It is already known that brown rot susceptibility in peaches is polygenic and a quantitative inheritance [27,28]. Genome-wide association studies (GWAS) were performed for identifying associations of genotypes with different phenotypes by analyzing the allele frequency of genetic variation in peach [27–29] (Uffelman et al., 2021), (Fu et al., 2021, Martinez-Garcia et al., 2023). However, European plum resistance and susceptibility to brown rot disease has not yet been analyzed by WGS or GWAS technologies.

The identification of single-nucleotide polymorphisms in polyploids is challenging due to the need to distinguish homologous and allelic SNPs [25]. Homologous SNPs are polymorphic positions found across all subgenomes, and allelic SNPs are polymorphic positions found within a single subgenome among individuals [25,30]. Next-generation sequencing (NGS) technologies have greatly enhanced the feasibility of whole-genome analysis and the identification of genetic variations in polyploid genomes [25].

For cultivar improvement, the ability to predict phenotypic traits based on genotype, like susceptibility to brown rot, is the main object for molecular breeding [25]. The identification of significant SNPs, associated with resistance/susceptibility to the *Monilinia* spp. disease in the European plum would provide new insights for breeding programs and the development of plum cultivars less susceptible to brown rot [31]. However, the genetic basis of resistance or susceptibility to brown rot in European plum has been poorly investigated, and further research is needed to identify single-nucleotide polymorphisms associated with this trait. The aim of this study was to visually evaluate brown rot resistance and susceptibility in European plum and sequence whole genomes of selected cultivars and hybrids grown in Lithuania, with the goal of identifying SNPs linked to disease response.

2. Materials and Methods

2.1. Brown Rot Susceptibility Evaluation in European Plum Cultivars

The resistance to brown rot disease was evaluated for 10 European plum (*P. domestica*) cultivars and 10 hybrids in the Lithuanian Research Centre for Agriculture and Forestry institute of horticulture orchards, in the years 2022 and 2023 (Table 1). The plums were evaluated visually at the commercial maturity stage by counting plum fruits with brown rot symptoms according to the 1–9 scale: 1 being very resistant (1–5 fruits damaged); 2 being moderately resistant (<10% fruits damaged); 3 being moderately susceptible (10–25% fruits damaged); and 5 (25–50% fruits damaged), 7 (50–75% fruits damaged), and 9 (>75% fruits damaged) being very susceptible [32,33]. The evaluation was performed on four trees of the same plum cultivar or hybrid (biological replicates).

Table 1. European plum cultivars and hybrids with resistance levels.

Resistance/Susceptibility	European Plum Cultivar/Hybrid
Susceptible	Kometa
	212 (Amitar × Jure)
	250 (Harmonija × Jure)
	251 (Aleksona × Jure)
Moderately susceptible	252 (6002a × Jure)
	Ive
	Jubileum
	Valor
Moderately resistant	Victoria
	249 (2134 × Harmonija)
	Opal
	241 (Vilniaus Vengrine × Harmonija)
Resistant	Hanita
	Staro Vengrine
	Stenley
	Top
	216 (Vilniaus Vengrine × Jure)
	244 (Tarantovskaja krasavica × Jure)
	245 (Dabrowicka × Jure)
	293 (Free pollination of Cacanska najbolja)

2.2. Plant Material for Molecular Analysis

For DNA extraction, leaf samples were collected from 20 European plum cultivars/hybrids, classified as resistant (8) or moderately resistant or (2) moderately susceptible (5) or susceptible (5) (Table 1). The European plum leaves were collected from one-year-old shoots in the spring from a single plum tree for each analyzed plum cultivar in 2023. Leaves were frozen with liquid nitrogen and stored at −70 °C until further analysis.

2.3. DNA Extraction and Whole-Genome Sequencing of the European Plum

From the collected European plum leaves, DNA was extracted using a modified [34] cetyltrimethylammonium bromide (CTAB) method [35]. DNA quantification and quality check was performed using the Nanodrop Implen GmbH spectrophotometer (Implen, Munich, Germany) and Qubit 1X dsDNA HS (High Sensitivity) assay kit (Thermo Fisher Scientific, Waltham, MA, USA). In total, 20 DNA samples, with OD_{260/280} = 1.8–2.0 and concentration ≥ 10 ng/μL, were sent for library preparation and sequencing to Novogene (Cambridge, UK). Whole-genome sequencing was performed using the Illumina NovaSeq x Plus Series (PE150) sequencing platform. The accession number of Bioproject in the

National Center for Biotechnology Information (NCBI) database is PRJNA1269969 (<http://www.ncbi.nlm.nih.gov/bioproject/1269969>) (accessed on 30 May 2025).

2.4. SNP Identification and Statistical Analysis

Cleaned reads from 20 sequencing libraries were aligned to the peach (*Prunus persica*) reference genome from the NCBI database (GCF_000346465.2) using BWA-MEM2 (v2.2.1) [36]. Joint variant calling was performed on the resulting alignment files using Freebayes (v1.3.9) [37] and the variants were annotated using Variant Effect Predictor (v114.0) [38]. After annotation, a custom python script was used to filter for genetic variants in genes, that are known to be differentially expressed when the plum fruit comes in contact with the *M. fructigena* pathogen. Genes selected for filtering were based on the study by Antanyrienė et al. [23], and are functionally implicated in plant defense responses, alpha-linolenic acid metabolism, mitogen-activated protein kinase (MAPK) signaling, and plant hormone signal transduction and biosynthesis of various plant secondary metabolites pathways. To identify SNPs significantly associated with disease resistance in *P. persica*, we compared variant presence in two groups of cultivars, resistant and susceptible, and applied Fisher's exact test to assess whether the distribution of the alternate allele between the two mentioned groups was statistically significant. A significance threshold of 0.05 was chosen to determine whether the SNP is potentially associated with disease resistance.

The statistical analysis for cultivar and hybrid resistance evaluation was performed with SAS Version 9.3 (Statistical Analysis System) (2011) [39]. The plotting was performed with Science and Research Online Plot, n.d. (SRplot) online software [40] and ggplot2 version 3.5.2 in R software (4.4.3) [41].

3. Results

3.1. Brown Rot Susceptibility Evaluation

Susceptibility and resistance to brown rot were evaluated in 20 European plum cultivars and hybrids in the years 2022 and 2023 (Table 1). However, no significant differences were observed between the two years of evaluation. Among the analyzed plum cultivars, 40% exhibited resistance to brown rot, while 25% were classified as susceptible and 25% as moderately susceptible (Figure 1). The smallest proportion (10%) was categorized as moderately resistant.

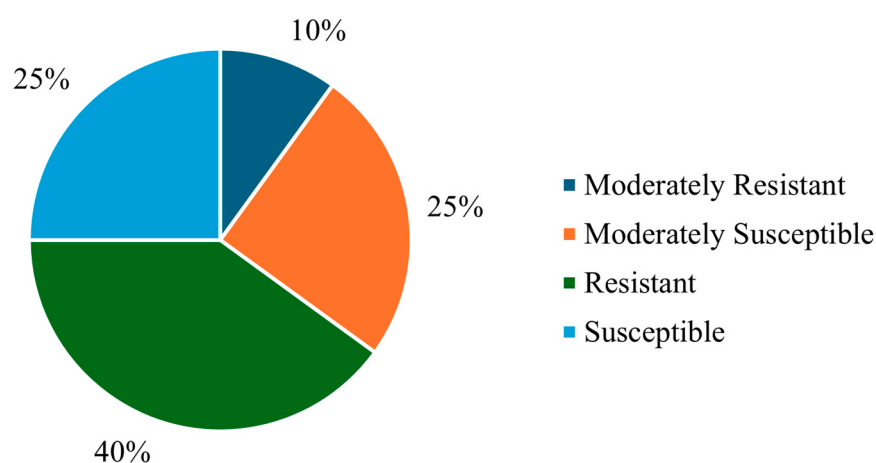


Figure 1. Resistance and susceptibility of European plum cultivars and hybrids to brown rot.

3.2. Whole-Genome Sequencing of European Plum

The whole-genome sequencing for 20 libraries was performed for the identification of genetic variants in the European plum genome (Table S1). In total, over 505 million

high-quality raw reads were generated, averaging more than 24 million reads per sample, corresponding to 75.9 G of raw sequencing data. On average, 98.85% were retained as clean reads. The proportion of bases with a Phred quality score ≥ 30 (Q30) ranged from 96.06% to 96.91%. The guanine–cytosine (GC) content across samples ranged from 38.48% to 41.06%.

As the assembled genome of the European plum is not available, the *P. persica* genome—a model plant within the *Prunus* genus—was used as the reference genome for read alignment [42] (Table S2). The mapping rate of reads to the reference genome ranged from 65.78% to 82.81% across samples. The average sequencing depth ranged from $9.67\times$ to $10.15\times$, and genome coverage at $1\times$ depth varied between 69.68% and 73.48%.

3.3. SNPs Detection Across European Plum Genome

On average, more than 1.4 million SNPs were identified across the 20 sequenced European plum cultivars, including 815 SNPs originating from the chloroplast genome and 2828 unlocalized SNPs. To assess the potential functional impact of these variants, the average number of SNPs per sample were classified based on their genomic locations (Figure 2). The majority of variants were located in intronic regions (34.52%), followed by exonic regions (29.53%). SNPs located within the >2 kb of intergenic regions accounted for 12.75% of the SNPs, while SNPs located within the <2 kb intergenic regions, which is in 1 kb downstream or upstream of the genes, accounted for 5.35% and 5.83%, respectively. Variants within untranslated regions (UTRs) were observed in 3'UTR (5.44%) and 5'UTR (4.89%) and both untranslated regions jointly (5'UTR/3'UTR) (5.83%). A small proportion of variants were located in splicing regions (0.05%) and in regions encompassing both upstream and downstream flanks of genes (1.64%).

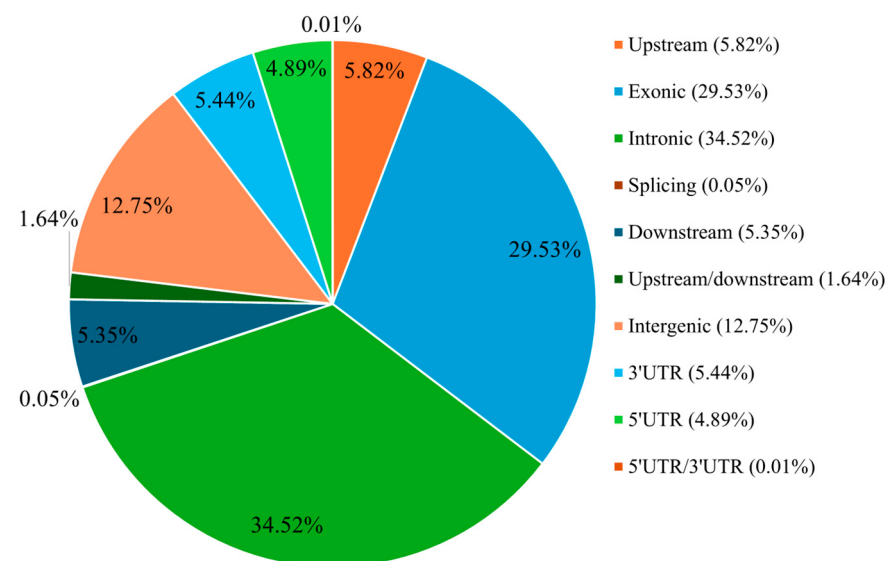


Figure 2. Categorization of SNPs by their genomic regions across all samples of the European plum cultivars and hybrids.

Six major types of SNP variants were identified across all European plum cultivars and hybrids. Among these, the most frequent mutation types were T:A > C:G (transitions from T to C and A to G) and C:G > T:A (transitions from C to T and G to A), representing the highest proportions of total SNP detected across all samples (Figure 3). The distribution of SNP variant types was consistent among all cultivars and hybrids, indicating a conserved mutational pattern within the European plum genome.

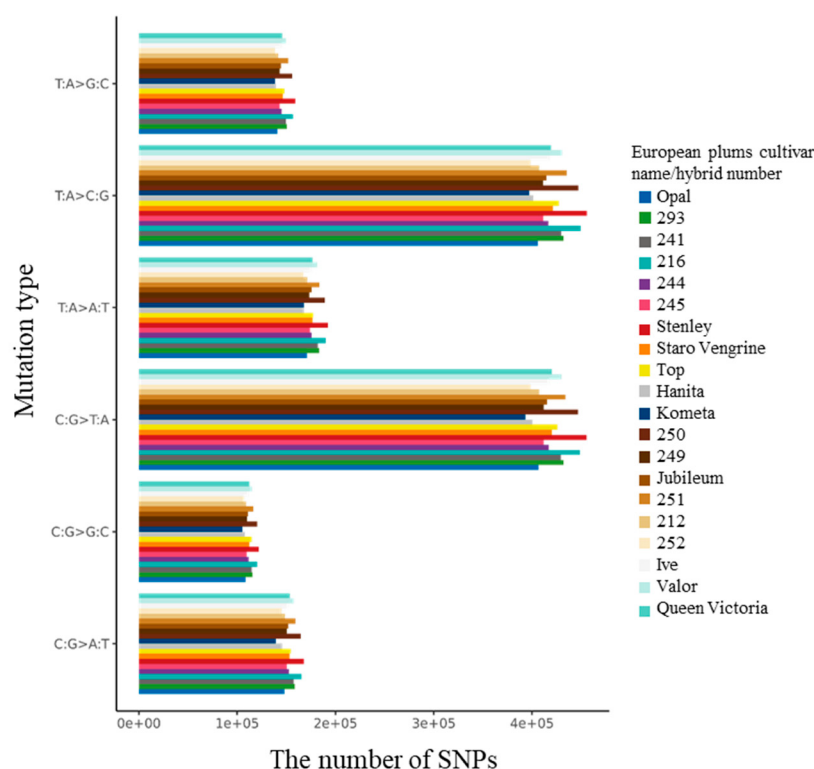


Figure 3. Frequency of SNP mutations across the genomes of European plum cultivars and hybrids. The cultivars and hybrids are represented by distinct color-coded bars.

In the European plum genome, SNPs were distributed across all eight chromosomes. The mean SNP density across all samples was approximately 1 SNP per 12.162 kb (Figure 4, Table S3). Among the chromosomes, the highest SNP density was observed on chromosome G2 (1 SNP per 11.225 kb), while the lowest was on chromosome G5 (1 SNP per 13.589 kb). On average, 343,265 SNPs were detected per chromosome, ranging from 251,358 on chromosome G5 to 616,383 SNPs on chromosome G1. The relatively uniform distribution of SNPs across chromosomes supports the robustness and consistency of the variant detection analysis.

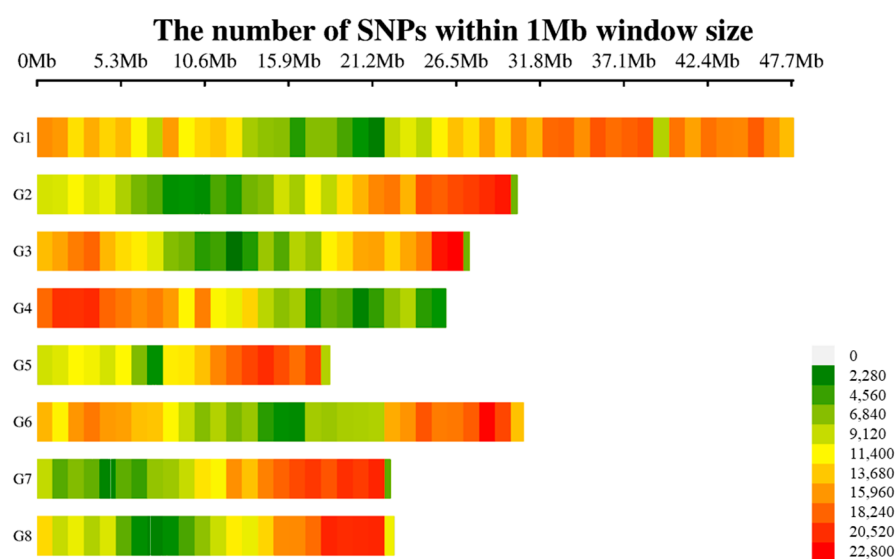


Figure 4. SNP density across European plum chromosomes, representing the number of SNPs within a 1 Mb window size.

3.4. SNPs Associated with Brown Rot Identification

SNPs identified in the sequenced European plum genomes were annotated in relation to genes previously associated with resistance or susceptibility to brown rot [21] and were found distributed across all eight chromosomes (Figure 5). In total, 45 statistically significant variants ($p < 0.05$) were detected, with the highest $-\log_{10}(p)$ values observed in chromosomes G5 and G8. The highest number of significant SNPs were located in chromosomes G1 and G5, with 10 SNPs in each. Notably, two SNPs were found exclusively in resistant cultivars (on chromosome G8), while one SNP was detected only in susceptible cultivars (on chromosome G5).

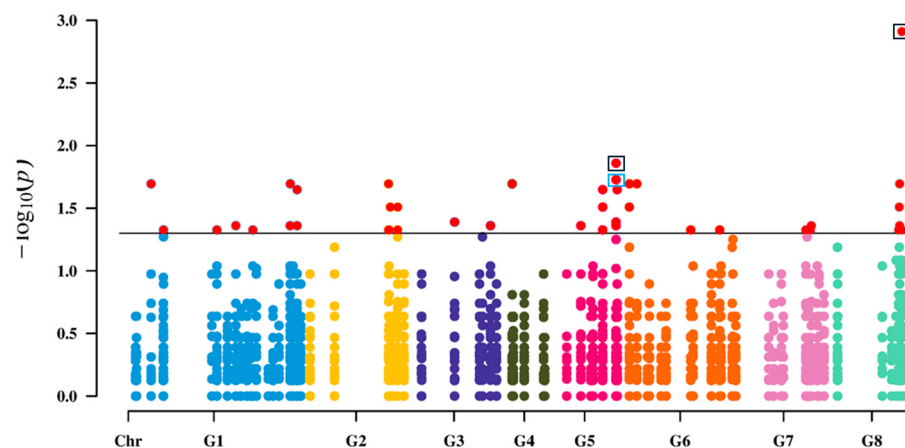


Figure 5. Manhattan plot showing the distribution of candidate SNPs associated with resistance or susceptibility to *Monilinia* spp. pathogens across the eight chromosomes (G1–G8) of European plum. Each point in different colors represents a single SNP across chromosomes. Red points indicate SNPs with statistical significance ($p < 0.05$). SNPs outlined in black were detected exclusively in resistant cultivars, while SNPs outlined in blue were found only in susceptible cultivars. The y-axis represents the $-\log_{10}(p\text{-value})$, and the horizontal line denotes the significance threshold.

The first resistance-associated SNP was located on chromosome G8 (NC_034016.1:19373021), representing a G to A substitution. This SNP appeared in a homozygous alternate state exclusively in resistant cultivars and is annotated as a downstream variant of the alcohol dehydrogenase gene (Gene ID: 18766308). This gene is found in alpha-linolenic acid metabolism. The second resistance-associated SNP was identified on chromosome G5 (NC_034013.1:17594665) as a C to T transition, occurring in a heterozygous alternate state in resistant cultivars. It is positioned downstream of the beta-glucosidase 44 (BLU44) gene (Gene ID: 18777625). The beta-glucosidase 44 gene is functionally expressed in the biosynthesis of various plant secondary metabolites pathway.

Additionally, a homozygous alternate SNP located on chromosome G5 (NC_034013.1:17584892) was identified in six cultivars (five susceptible and one moderately susceptible). This T to A substitution is annotated as a downstream variant near another putative beta-glucosidase 44 (BGLU44) gene (Gene ID: 18776263), potentially implicating it in susceptibility and also found in the biosynthesis of various plant secondary metabolites pathway.

4. Discussion

Whole-genome sequencing is a powerful tool for SNPs discovery and for investigating resistance or susceptibility to fungal diseases such as brown rot in plums. To date, WGS has not been applied for SNP detection in European plum, whereas previous studies have employed genotyping by sequencing (GBS) technology [16]. For example, Zhebentyayeva et al. [16] identified 129,110 SNPs, including 400 SNPs from the chloroplast genome, using

GBS, with an average of 4.93 million reads per sample. In contrast, our WGS-based study yielded more than 24 million reads per sample—approximately 4.8 times higher—and identified over 1.4 million SNPs, including 815 from the chloroplast genome, representing 10.8-fold increase in SNP detection. This substantial increase in variant discovery is attributed to the broader and more uniform genome coverage provided by WGS, as GBS is inherently limited to genome regions adjacent to restriction sites [43].

In this study, 20 European plum cultivars and hybrids with varying levels of resistance to brown rot were analyzed. It is well established that environmental conditions, including climate and geographical location, significantly influence the prevalence and severity of *Monilinia* spp. infections [44]. In our Lithuanian trials, conducted in 2022 and 2023, no statistically significant differences in resistance levels were observed between the two years, suggesting relative environmental stability across seasons and indicating an inherent susceptibility or resistance among the cultivars. The cultivar responses to brown rot in our study differed from those reported in previous studies. For instance, the ‘Kometa’ cultivar was classified as susceptible and ‘Victoria’ as moderately susceptible in our evaluations. However, studies conducted in Latvia between 1996 and 2006 reported both cultivars as resistant to *Monilinia* spp. pathogens [45]. The cultivar ‘Jubileum’ was identified as moderately susceptible in Lithuania, which aligns with Latvian observations that fruit rot occurred primarily in very moist summers [45]. In contrast, ‘Jubileum’ was reported as highly susceptible in Romania during the 2020 growing season [44]. Similarly, the ‘Stanley’ cultivar, considered resistant in our study, was among the most affected by brown rot in Romania [44]. These inconsistencies highlight the complexity of breeding and evaluating disease resistance. Climate change and differences in environmental factors—such as humidity, temperature, and pathogen strain diversity—can significantly affect the outcomes. Variations in disease expression across countries and years highlight the combined influence of genetic factors and local environmental conditions on disease spread.

Resistance of European plum to *Monilinia* spp. is governed by both constitutive and inducible defense mechanisms, involving genetically regulated responses [46]. To date, no direct association between simple sequence repeats (SSRs) and resistance to *Monilinia* spp. has been established in plums [47]. Previous transcriptomic analysis using RNA-seq of the moderately resistant ‘Victoria’ cultivar identified 41 differentially expressed genes (DEGs) involved in defense responses, including those encoding pathogenesis-related (PR) proteins and the mildew resistance locus O (MLO) family. DEGs were enriched in pathways associated with plant defense: MAPK signaling pathway, plant hormone signal transduction, biosynthesis of various plant secondary metabolites, and alpha-linolenic acid metabolism [23]. In the present study, three candidate SNPs associated with brown rot resistance were identified. Notably, these SNPs corresponded to genes previously recognized as DEGs in transcriptomic analyses and Kyoto Encyclopedia of Genes and Genomes (KEGG) database, suggesting their involvement in plant–pathogen interaction [23]. This overlap provides strong evidence for their potential functional relevance and highlights the value of integrating genomic and transcriptomic data to elucidate resistance mechanisms in European plum.

In resistant to brown rot European plum cultivars, a homozygous alternate variant was identified in the alcohol dehydrogenase gene (Gene ID: 18766308), which encodes a key enzyme involved in the reduction in acetaldehyde to ethanol. This enzyme plays a critical role during both abiotic and biotic stress responses. Overexpression of alcohol dehydrogenase in various plant species has been linked to enhanced tolerance to salt, drought, cold, and pathogen infections [48].

In European plum cultivars, the variants in the beta-glucosidase enzyme family were detected in both resistant (Gene ID: 18777625) and susceptible (Gene ID: 18776263) to

brown rot cultivars; however, these occurred at distinct genomic positions and involved different nucleotide substitutions. The beta-glucosidase enzyme family is known to play a pivotal role in the activation of phytohormones and defense compounds, contributing to the plant's ability to respond to biotic and abiotic stresses [49,50]. Plant beta-glucosidase forms the first chemical barrier against pathogen attack by hydrolyzing relatively inert glycosidases to release various toxic compounds, such as saponins, coumarins, hydroxamic acid, rotenoids, quinones, hydrogen cyanide, etc. [51]. Their role in disease resistance has been well established in crop species such as maize and rice [49,51].

In this study, a homozygous alternate SNP located on chromosome G5 in the beta-glucosidase 44 gene (Gene ID: 1877762, position: NC_034013.1:17584892) was established exclusively in susceptible cultivars, suggesting a potential association with susceptibility to *Monilinia* spp. pathogens. In contrast, a heterozygous alternate SNP in a closely related gene, putative beta-glucosidase 44 (BGLU44) (Gene ID: 18776263, position: NC_034013.1:17594665), was identified in resistant cultivars, indicating its possible role in conferring resistance to brown rot.

In this study, visual assessments were used to evaluate tolerance to *Monilinia* spp. pathogens among European plum cultivars (Table 1). SNPs associated with either resistance or susceptibility were successfully identified in all resistant and susceptible cultivars. Notably, in the moderately susceptible cultivar 'Victoria', an SNP commonly found in susceptible cultivars was also detected. This finding suggests that 'Victoria' may, in fact, be more accurately classified as susceptible under certain environmental conditions.

This is the first study to identify candidate SNPs associated with resistance or susceptibility to *Monilinia* spp. in European plum. To date, such associations of SNPs have only been explored in peach (*P. persica*), another member of the stone fruit group [27,28]. In Spanish peach cultivars, 3 SNPs linked to brown rot susceptibility were identified in 1, 3, and 6 linkage groups. However, none of these SNPs overlapped with the variants identified in our study, suggesting species-specific resistance mechanisms or genetic divergence within the *Prunus* genus [28].

5. Conclusions

In this study, three candidate SNPs significantly associated with brown rot resistance (two SNPs in chromosomes G5 and G8) and susceptibility (one SNP in chromosome G5) were identified in the alcohol dehydrogenase gene and beta-glucosidase family enzymes in the European plum. This research also represents the first visual evaluation of European plum cultivar resistance and susceptibility to brown rot conducted in Lithuania. The phenotypic data obtained from these evaluations were used to identify SNPs associated with disease response. This is the first study to report candidate SNPs associated with brown rot in European plums. The findings provide a preliminary foundation for the SNPs linked to brown rot discovery and the development of molecular markers to distinguish resistant and susceptible cultivars. Furthermore, these results may inform future gene-editing strategies aimed at enhancing brown rot resistance in European plum breeding programs.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/agronomy15071562/s1>, Table S1: Statistics of European plum whole-genome sequencing data; Table S2. Statistics of European plum mapping to reference genome (*P. persica*); Table S3. Genomic coverage of the SNPs on the European plum chromosomes.

Author Contributions: Conceptualization, R.A., V.B. and B.F.; methodology, R.A. and B.F.; software, R.A., M.K. and B.F.; validation, R.A. and B.F.; formal analysis, R.A. and B.F.; investigation, R.A. and B.F.; data curation, R.A. and M.K.; writing—original draft preparation, R.A. and B.F.; writing—review

and editing, V.B., M.K. and B.F.; visualization, R.A. and M.K.; supervision, B.F. All authors have read and agreed to the published version of the manuscript.

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Data Availability Statement: Data are contained within the article or Supplementary Materials.

Conflicts of Interest: The authors declare no conflicts of interest.

Abbreviations

The following abbreviations are used in this manuscript:

RAPD	random amplified polymorphic DNA
RFLP	restriction fragment length polymorphism
SSR	simple sequence repeat
SNP	single nucleotide polymorphism
GBS	genotyping by sequencing
WGS	whole-genome sequencing
NGS	next-generation sequencing
CTAB	cetyltrimethylammonium bromide
NCBI	National Center for Biotechnology Information
MAPK	mitogen-activated protein kinase
UTR	untranslated region
DEG	differentially expressed gene
MLO	mildew resistance locus O
PR	pathogenesis-related
KEGG	Kyoto Encyclopedia of Genes and Genomes

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