

Article

Biotechnological and Oenological Potential of Advanced Genetic Lines of Grapevine Resistant to Powdery Mildew (*Erysiphe necator*)

Phillip Ormeño-Vásquez ^{1,2}, Viviana Sosa-Zuniga ³, Mariona Gil-Cortiella ^{4,5}, Rene Morales-Poblete ^{1,6}, Carolina Vallejos ⁶, Consuelo Medina ⁷, Claudio Meneses ^{1,2} and Patricio Arce-Johnson ^{5,*}

¹ Departamento de Fruticultura y Enología, Facultad de Agronomía y Sistemas Naturales, Pontificia Universidad Católica de Chile, Av. Vicuña Mackenna 4860, Macul, Santiago 7820436, Chile; paormeno@uc.cl (P.O.-V.); remorales1@uc.cl (R.M.-P.); claudio.meneses@uc.cl (C.M.)

² Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Av. Libertador Bernardo O'Higgins 340, Santiago 8331150, Chile

³ Centro de Investigación e Innovación, Viña Concha y Toro, Fundo Poca s/n, Km10 Ruta K650, Penciahue 355000, Chile; viviana.sosa@conchaytoro.cl

⁴ Departament de Bioquímica i Biotecnologia, Facultat d'Enologia, Universitat Rovira i Virgili, 43007 Tarragona, Spain; mariona.gil@urv.cat

⁵ Centro de Investigación e Innovación, Instituto de Ciencias Aplicadas, Facultad de Ingeniería, Universidad Autónoma de Chile, Av. Del Valle 534, Santiago 8580658, Chile

⁶ Instituto de Ciencias Aplicadas, Universidad Autónoma de Chile, 5 Poniente 1670, Talca 3467987, Chile; cgvallej@uc.cl

⁷ Dirección de Investigación, Universidad Autónoma de Chile, Santiago 8580658, Chile; maria.medina01@uautonoma.cl

* Correspondence: patricio.arce@uautonoma.cl; Tel.: +56-9-7767-5621



Academic Editors: Arif Atak, Mahmood Ghasemnezhad, Qiong Zhang and Monica Marilena Miazzi

Received: 24 September 2025

Revised: 20 October 2025

Accepted: 27 October 2025

Published: 30 October 2025

Citation: Ormeño-Vásquez, P.; Sosa-Zuniga, V.; Gil-Cortiella, M.; Morales-Poblete, R.; Vallejos, C.; Medina, C.; Meneses, C.; Arce-Johnson, P. Biotechnological and Oenological Potential of Advanced Genetic Lines of Grapevine Resistant to Powdery Mildew (*Erysiphe necator*). *Agriculture* **2025**, *15*, 2267. <https://doi.org/10.3390/agriculture15212267>

Copyright: © 2025 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

Abstract

The development of grapevine varieties combining powdery mildew (*Erysiphe necator*) resistance with acceptable wine quality represents an important goal for sustainable viticulture. This study evaluated the oenological potential of five advanced breeding lines carrying *Run1* or *Run1Ren1* resistance loci, developed through marker-assisted selection to achieve 99.2–99.6% *Vitis vinifera* genome content. Genotypes were assessed under Chilean conditions during the 2024–2025 seasons, analyzing disease resistance, berry characteristics, and wine chemical parameters. All resistant genotypes exhibited complete powdery mildew resistance (OIV scores 9) without fungicide applications. Wine analyses showed pH 3.4–3.9, titratable acidity 3.7–7.8 g/L, and total phenolics 229.2–1356.1 mg GAE/L, values within ranges reported in the literature for commercial wines. Two genotypes evaluated across both seasons showed different patterns of year-to-year variation, with AJ-T2 showing 4.7% variation in anthocyanin content, while AJ-T6 exhibited greater variation in phenolic parameters. HPLC analysis revealed anthocyanin profiles dominated by malvidin-3-glucoside without diglucoside forms, consistent with *V. vinifera* patterns. These preliminary results from single-plant evaluations suggest that marker-assisted breeding may contribute to developing disease-resistant varieties with wine chemical parameters within commercial ranges, though multi-plant trials with appropriate controls are essential for validation.

Keywords: oenological; grapevine; marker-assisted selection; performance; powdery mildew; resistance locus; *Run1*

1. Introduction

Grapevine powdery mildew, a disease caused by the fungus *Erysiphe necator*, is considered one of the most economically damaging diseases in viticulture worldwide. It has been responsible for significant yield losses and necessitates intensive fungicide applications, which account for 30–40% of total pesticide use in vineyard management [1]. The development of resistant cultivars through conventional breeding programs, which incorporate resistance loci from wild *Vitis* species, offers a sustainable alternative to chemical control methods. This approach addresses both environmental concerns and increasing regulatory restrictions on pesticide use [2].

The *Run1* (Resistance to *Uncinula necator* 1) locus, originally identified in *Vitis rotundifolia*, confers complete resistance to powdery mildew through a hypersensitive response mechanism that prevents fungal colonization [3]. The *RUN1* gene, which confers the majority of resistance to powdery mildew in the *Run1* locus, has been successfully mapped and characterized. This has enabled its introgression into *V. vinifera* backgrounds through directed pollinations and tracking by marker-assisted selection [3,4]. Similarly, the *Ren1* (Resistance to *Erysiphe necator* 1) locus from *V. vinifera* cv. ‘Kishmish vatkana’ provides an alternative source of resistance, offering opportunities for stacking multiple resistance genes to enhance durability [5]. Recent literature has reinforced the importance of the *Run1* and *Ren1* loci in durable resistance strategies [6] review to powdery mildew and other grapevine pathogens, highlighting the role of marker-assisted selection and the need to combine multiple loci to achieve long-term, sustainable resistance. Similarly, Vezzulli et al. [7] report on a genetics-assisted breeding program at the Fondazione Edmund Mach (FEM), which is focused on resistance to downy mildew, powdery mildew, and phylloxera.

Nevertheless, a major challenge in breeding disease-resistant grapevines is maintaining the oenological characteristics typical of *V. vinifera* cultivars. Historical attempts at developing resistant varieties through interspecific hybridization often resulted in wines with altered sensory attributes, including “foxy” aromas [8,9] and modified phenolic profiles [10,11], which affected their commercial adoption in premium wine markets [2,12]. These quality differences were associated with a significant proportion of the non-*vinifera* genome inherited from wild grapevine donors, which may have disrupted the biochemical pathways responsible for producing quality-determining metabolites [13,14].

Recent advances in precision breeding, combining high-density molecular markers with extensive backcrossing programs, have enabled the development of advanced genetic lines. An important step has been the obtention of PIWI varieties through crosses between European and American varieties carrying natural resistance [15]. These lines potentially overcome the traditional trade-off between quality and resistance. Through six to seven generations of backcrossing to elite *V. vinifera* parents, it is now possible to recover over 99% of the *Vitis vinifera* genome while retaining the resistance locus, theoretically preserving the genetic architecture underlying wine quality [16].

Chile, as the fourth-largest wine exporter globally, along with other major wine-producing regions worldwide, faces mounting challenges in controlling powdery mildew under climatic conditions increasingly favorable for pathogen development [17,18]. The development of resistant varieties offers significant potential to reduce fungicide dependency and environmental impact while maintaining the quality standards demanded by competitive international markets [19]. Given the prominent position of Chile in the global wine trade [20], the evaluation of resistant germplasm under local environmental conditions provides valuable insights into the stability and expression of resistance and quality traits in Chilean terroirs.

The objectives of this study were to: (1) evaluate the oenological potential of advanced breeding lines carrying *Run1* or *Run1Ren1* resistance loci through comprehensive chemical

analysis of wines produced under standardized conditions; (2) characterize the stability of quality parameters across consecutive vintages to assess environmental plasticity; (3) confirm the effectiveness of introgressed resistance under natural disease pressure; and (4) identify superior genotypes suitable for commercial wine production that combine complete powdery mildew resistance with wine quality comparable to traditional *V. vinifera* cultivars. This research addresses the critical need for sustainable viticulture practices while maintaining the quality expectations of modern wine consumers and meeting increasingly stringent environmental regulations regarding pesticide use in agriculture.

2. Materials and Methods

2.1. Plant Material and Experimental Site

The study evaluated five advanced grapevine breeding lines with previously characterized resistance loci: four genotypes carrying the *Run1* resistance locus and one genotype carrying both *Run1* and *Ren1* resistance loci (Table 1). In the early stages of our breeding program, we performed extensive crosses between resistant parental lines carrying the two resistance loci, *Run1* and *Ren1*, and emblematic Chilean wine grape genotypes: Carménère, Merlot, and Cabernet Sauvignon, generating progenies of over 500 individuals. After initial molecular screenings and resistance evaluations under greenhouse conditions, we selected resistant lines that were subsequently planted in the field. From these, five advanced lines were chosen for this work. The genetic background and resistance profile of these lines had been established through prior molecular characterization using SSR markers as part of the breeding program development (Table 1). Resistant genotypes were developed through conventional breeding, employing marker-assisted selection. This approach led to the attainment of 99.2–99.6% *Vitis vinifera* genome content after six to seven backcross generations. The experimental field was situated in Curacaví, Chile (33°24′01.0″ S, 71°03′17.6″ W) (Figure 1). The environmental variability between 2023–2024 and 2024–2025, particularly in terms of thermal regime, humidity, and water availability, created distinct ripening conditions based on data from the La Aurora agrometeorological station in Curacaví (Supplementary Data S1) [21].

Table 1. Genetic background and resistance profile of advanced grapevine breeding lines carrying powdery mildew resistance loci.

ID	Genotype	Resistance Locus/Loci	Female Parent	Male Parent	Backcross Number	Estimated % of <i>V. vinifera</i> Genome	OIV Resistance
AJ-T6	P09-CAR	<i>Run1Ren1</i>	BC5(02-2) × 91-4/27	Carménère	BC7	99.6%	9
AJ-T2	P09-107-113	<i>Run1</i>	BC5(02-2)	91-4/27	BC6	99.2%	9
AJ-B1	P09-107-147	<i>Run1</i>	BC5(02-2)	91-4/27	BC6	99.2%	9
AJ-T3	P09-105-81	<i>Run1</i>	BC5(02-2)	91-4/27	BC6	99.2%	9
AJ-T5	P09-EN69	<i>Run1</i>	BC5(02-2) × 91-4/27	Crimson Seedless	BC7	99.6%	9

The table presents the breeding codes, genotype identifications, resistance loci present (*Run1* and/or *Ren1*), parental lineages, backcross generation numbers, and estimated percentage of *Vitis vinifera* genome content achieved through marker-assisted selection.

The vines were trained using a pergola system, with 2.5 m between rows and 1.0 m between plants. Vine management was conducted according to standard viticultural practices, except for the withholding of powdery mildew fungicide, which was employed to assess the vines' inherent resistance to powdery mildew inoculation disease.

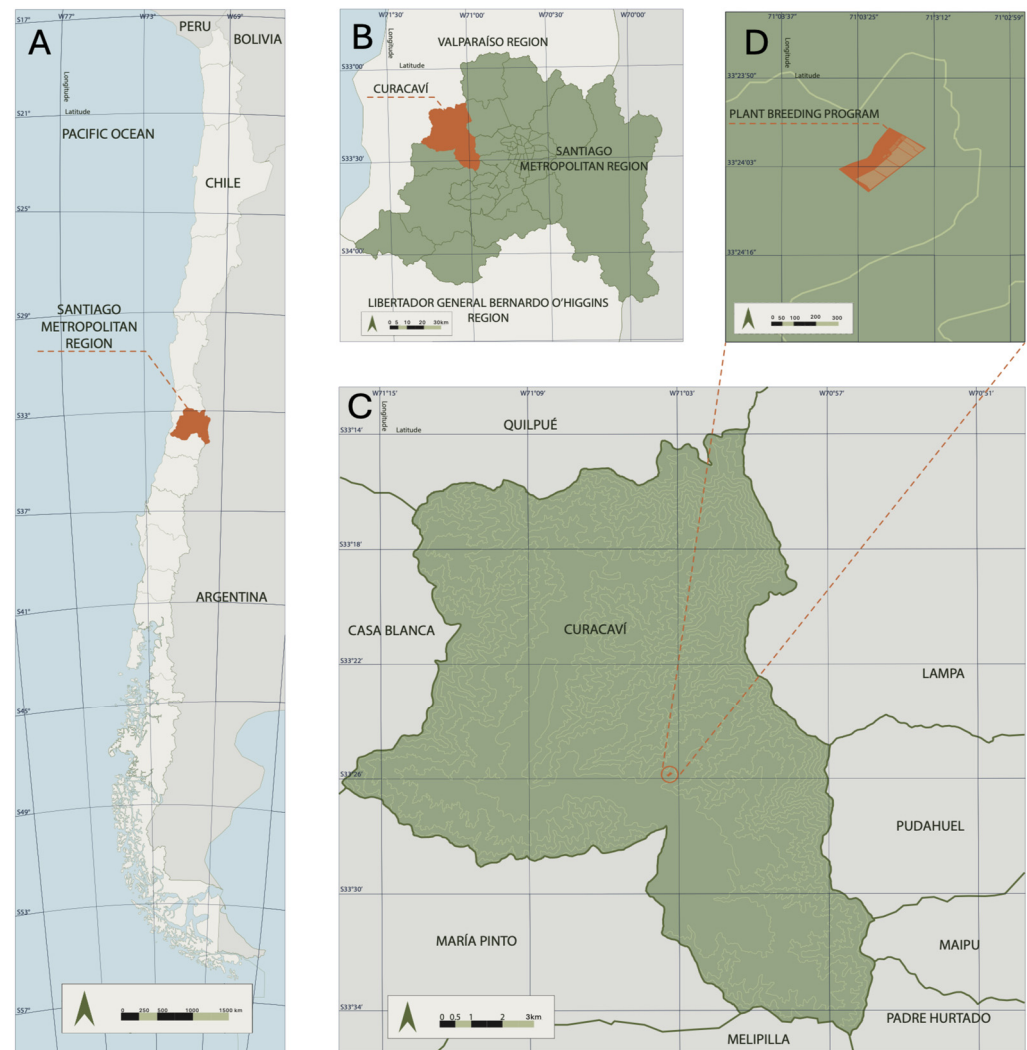


Figure 1. Experimental site location for field evaluation of *Run1* and *Run1Ren1*-carrying grapevine genotypes. (A) Overview of Chile showing the location of the Santiago Metropolitan Region. (B) Santiago Metropolitan Region highlighting Curacaví county. (C) Detailed view of Curacaví. (D) Specific location of the experimental vineyard (highlighted in orange) situated at coordinates 33°24'01.0" S, 71°03'17.6" W. The site provides representative Mediterranean climate conditions for assessing disease resistance and enological potential under commercial viticultural conditions typical of Chile's central wine-producing valleys.

2.2. Disease Resistance Evaluation

Powdery mildew (*Erysiphe necator*) resistance was evaluated under controlled greenhouse conditions (photoperiod (16 h light: 8 h dark, 26 °C, 60% relative humidity) using dry inoculation (airborne dispersion of conidia from infected leaves with, following the approach of Ciubotaru et al. [22], which has been shown to yield more effective infections than wet spray inoculation. Susceptible control genotypes (*V. vinifera* cvs. Chardonnay and Carménère) were included to validate inoculation effectiveness. Disease severity was assessed using the International Organization of Vine and Wine descriptor 452-1, with scores ranging from 1 (very low resistance, dense sporulation) to 9 (total resistance, no visible symptoms). Evaluations were performed on 10 randomly selected leaves per plant, and final resistance scores were calculated as the mean of all assessments.

2.3. Harvest and Grape Analysis

The grapes designated as AJ-T6, AJ-T2, and AJ-T3 were harvested at sugar content levels ranging from 22.9 to 25 °Brix. In the case of the AJ-B1 genotype, harvest occurred at 21 °Brix, as it was the only white variety. Brix measurements were taken twice per week from veraison to harvest using an optical refractometer (Sudelab, Barcelona, Spain). The AJ-T5 genotype was harvested at 17.2 °Brix, which is clearly below the optimal ripeness level. This was due to the limited number of berries available for maturity assessment, as we aimed to minimize sample consumption and preserve enough grapes for the winemaking trial. In this case, the sampled berries were likely not representative of the overall ripeness of the clusters from plant. Therefore, since the ripeness level of this genotype at harvest did not correspond to the optimal maturity typically required for winemaking, the evaluation of its oenological potential should be interpreted with caution.

Breeding material was very limited, and at the time of this work, we had only one plant per genotype, at the fruit stage. Therefore, the different clusters were considered technical replicates for the purpose of assessing within-plant variation in cluster weight. Following the harvest, three clusters per genotype were selected randomly for weighing. The quantity of berries per cluster was meticulously enumerated and categorized based on their health status, distinguishing between healthy and dehydrated raisins. Subsequently, the berries were separated from the cluster by means of a scratch, and the berries and stems were weighed separately. The berries from all clusters were then amalgamated, with three groups of 50 random berries being created for the purpose of recording their mass and volume. The volume of 50 berries was obtained by calculating the water displacement caused by a group of 50 berries in a half-filled 500 mL glass graduated cylinder. In the next stage of the process, the different batches of destemmed grapes were prepared, and each batch was crushed separately. The grape paste (consisting of must, skins, and seeds) was then introduced into each of the fermenters.

2.4. Microvinification

Microvinification procedures were differentiated according to the type of wine. For red wine genotypes (AJ-T6, AJ-T2, AJ-T3, AJ-T5), grapes were manually destemmed and crushed, and the resulting must (including juice, skins, and seeds) was transferred to Pyrex bottles for fermentation, with a maceration period of two weeks. After maceration, the solid components were separated by filtration. For the white grape genotype (AJ-B1), grapes were pressed immediately after destemming and crushing, and only the juice was used for fermentation in Pyrex bottles. In both red and white winemaking processes, alcoholic fermentation was initiated by inoculating commercial *Saccharomyces cerevisiae* yeast (Lalvin QA23, Lallemend, Rancagua, Chile), rehydrated according to the manufacturer's instructions, and added at a concentration of 20 g/hL on the same day the berries were harvested and processed (approximately one hour after crushing). The bottles were maintained at 22 °C in a temperature-controlled incubator. Fermentation progress was monitored daily by measuring density and temperature using a portable densimeter (DensitoPro, Mettler Toledo, Barcelona, Spain), and was considered over when the density remained stable for two consecutive days. Upon completion of alcoholic fermentation, all wines were sulfited (50 mg/L SO₂) to prevent oxidation and microbiological spoilage. After two weeks of natural settling, the clarified wines were transferred to clean bottles of different capacities according to the final volume obtained.

For red wines, fermentation proceeded with skin contact for enhanced phenolic extraction, followed by a two-week maceration period. Subsequently, solid components were separated by filtration. For white wine, fermentation was conducted without skin contact to prevent excessive phenolic extraction and color development. Upon completion of

alcoholic fermentation, all wines underwent sulfiting (50 mg/L SO₂) to prevent oxidation and microbiological spoilage before final clarification and bottling.

2.5. Basic Oenological Analyses

Standard oenological parameters were determined according to OIV official methods. pH was measured using a calibrated pH meter FE20 (Mettler Toledo, Greifensee, Switzerland). Titratable acidity was determined by titration with 0.1 N NaOH to a pH 7.0 endpoint and expressed as g/L tartaric acid. Alcohol content was determined by distillation using a portable densimeter, DensitoPro (Mettler Toledo, Barcelona, Spain). All analyses were performed in triplicate.

2.6. Phenolic Composition Analysis

Total phenolic content was determined by the OD 280 value [23]. Wine samples were diluted 1:50 with distilled water, and absorbance was measured at 280 nm. The results were expressed as mg/L gallic acid equivalents (GAE) using a commercial gallic acid standard curve (0–500 mg/L). Total anthocyanins were measured by the SO₂ bleaching procedure [23]. Anthocyanin content was expressed as mg/L malvidin-3-glucoside equivalents. Total tannins were determined by the LA method (Tannin Assay, [23]) with results expressed as g/L epicatechin equivalents.

2.7. Color Parameters

Wine color intensity (CI) was calculated as the sum of absorbances at 420, 520, and 620 nm using 1 mm path length cuvettes. Hue was calculated as the ratio A₄₂₀/A₅₂₀. CIELab coordinates (L*, a*, b*) were determined through the measurement of absorbances at 450, 520, 570, and 630 nm, and employing the software MSCV[®] (2001–2012) [24].

2.8. HPLC Analysis of Individual Anthocyanins

Individual anthocyanins were analyzed by reverse-phase high-performance liquid chromatography with diode-array detection (RP-HPLC-DAD), using an Agilent 1200 system equipped with a C18 reverse-phase column (250 × 4.6 mm, 5 µm). The method involved the direct injection of 30 µL of wine, previously filtered through a 0.22 µm syringe-driven filter. The mobile phases were (A) water/formic acid (90:10) and (B) acetonitrile/formic acid (90:10). Gradient elution was carried out at 25 °C with a flow rate of 1 mL/min as follows: 0–40 min, 10–25% B; 40–45 min, 25–40% B; 45–50 min, 40–10% B. The full UV-Vis spectrum (220–600 nm) was recorded, with detection and quantification performed at 520 nm. Anthocyanins were identified by comparing retention times with standards and by matching UV-Vis spectra reported in the literature. Quantification was based on external calibration curves of malvidin-3-O-glucoside, and results were expressed as mg/L of malvidin-3-O-glucoside equivalents. HPLC analysis of individual anthocyanins was conducted exclusively on the 2025 vintage samples due to sample availability constraints.

2.9. Statistical Analysis

Given the single-plant per genotype design, three clusters per plant were analyzed as technical replicates to characterize within-plant measurement precision. For genotypes assessed in two seasons (AJ-T6 and AJ-T2), descriptive statistics summarize year-to-year behavior within the same plant. Formal hypothesis testing across genotypes or seasons was not undertaken; therefore, reported means ± standard error denote within-plant precision, and any contrasts among genotypes are presented descriptively. Conclusions are framed accordingly and will be further evaluated in forthcoming multi-plant, multi-year trials.

3. Results

3.1. Disease Resistance Performance

All *Run1*-carrying genotypes and the *Run1Ren1*-carrying genotype exhibited complete resistance to powdery mildew in greenhouse evaluations, with OIV resistance scores of 9, indicating complete resistance. Under field conditions without fungicide applications, no powdery mildew symptoms were observed on these resistant genotypes, confirming the greenhouse results. Conversely, the susceptible controls, Chardonnay and Carménère, demonstrated a need for standard fungicide programs to maintain berry health in the field. The *Run1Ren1* stacked resistance genotype (AJ-T6) maintained complete resistance under both greenhouse and field conditions. No resistance breakdowns were observed, even under the high disease pressure conditions of the 2024–2025 field season.

3.2. Ampelographic and Cluster Characteristics

A substantial degree of phenotypic variation was identified among the *Run1*-carrying and *Run1Ren1*-carrying genotypes with respect to cluster and berry characteristics (Table 2, Figure 2). Ampelographically, the clusters showed moderate variability in size, shape, and compactness across genotypes and seasons. AJ-B1 (white) presented medium–large, conical clusters of moderate compactness with a short–medium peduncle and spherical green–yellow berries of medium size and even distribution. AJ-T2 (red) presented large, cylindrical–conical clusters with a discreet shoulder, compact to very compact, borne on a medium–long peduncle; berries were uniform, black–blue, with evident bloom. AJ-T6 (2024, red) presented medium, conical clusters of low to moderate compactness with a short peduncle and slight within-cluster berry-size heterogeneity. AJ-T6 (2025, red) presented small–medium, short-conical, compact clusters without wings; berries were small to medium, black–blue, and uniform.

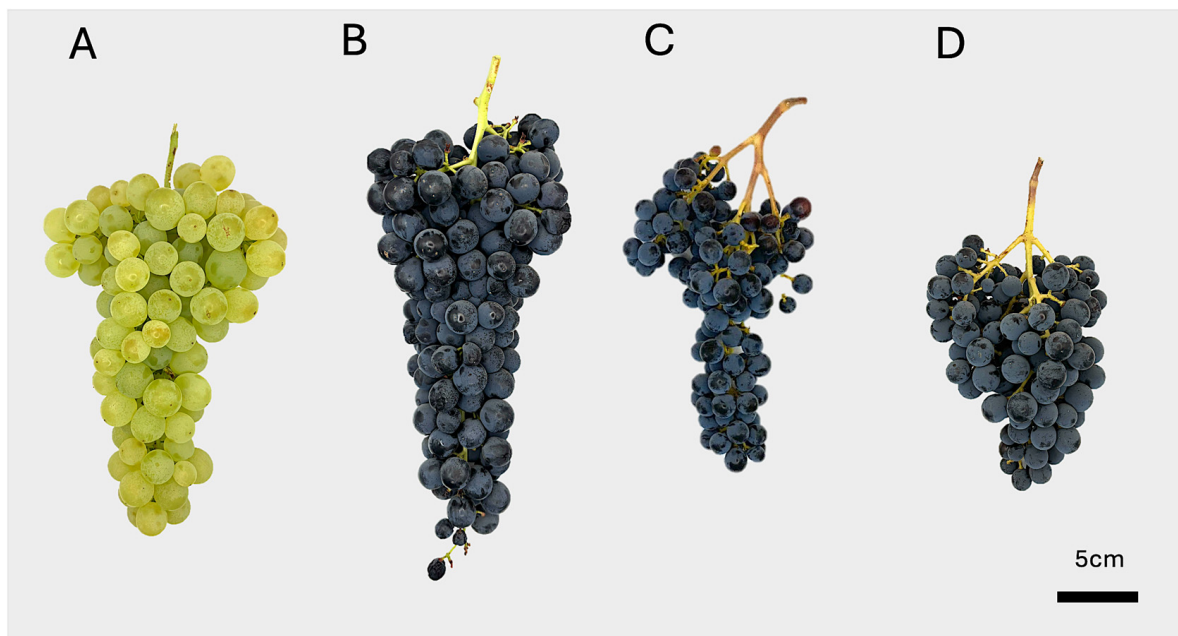


Figure 2. Morphological characterization of clusters from advanced breeding lines carrying powdery mildew resistance loci. Representative clusters showing (A) AJ-B1 white wine genotype with 99.2% *V. vinifera* genome content; (B) AJ-T2 red wine genotype (BC6 generation); (C) AJ-T6 stacked resistance genotype (*Run1Ren1*, BC7 generation) harvested in 2024; (D) AJ-T6 (2025) demonstrating phenotypic consistency across seasons. Scale bar = 5 cm.

Table 2. Cluster and berry characteristics of powdery mildew-resistant grapevine genotypes.

Genotype	Year	Type	100-Berry Mass (g)	100-Berry Volume (mL)	°Brix	pH	Titrateable Acidity (g/L)	% Healthy Berries (Count)	% Healthy Berries (Mass)	% Rachis Mas
AJ-T6	2024	Red	139.9 ± 5.1	116 ± 4	22.9	ND	ND	97.3 ± 0.1	93.8 ± 0.1	5.75 ± 0.3
AJ-T6	2025	Red	178.1 ± 4.2	161.7 ± 3.3	22.0	3.5	5.2	ND	ND	ND
AJ-T2	2024	Red	307.6 ± 10.3	286.7 ± 6.6	24.9	3.5	7.1	92 ± 4.7	95.7 ± 4.7	2.31 ± 0.7
AJ-T2	2025	Red	396.6 ± 11.5	368 ± 6.1	22.3	3.6	4.8	ND	ND	ND
AJ-B1	2024	White	265.4 ± 5.3	273.3 ± 23.4	21.0	3.4	5.0	94.9 ± 1.7	91.5 ± 1.7	2.64 ± 0.2
AJ-B1	2025	White	353.2 ± 13.3	323.3 ± 13.3	21.1	3.7	4.1	ND	ND	ND
AJ-T3	2024	Red	99.7 ± 2.1	92.7 ± 1.8	24.7	3.4	7.1	82.1 ± 3.2	80.7 ± 3.2	6.87 ± 0.3
AJ-T5	2024	Red	235.8 ± 1.5	222 ± 1.2	17.2	ND	ND	93.9 ± 1.6	95.4 ± 1.6	1.99 ± 0.1

Values were expressed as mean ± standard error (n = 3 biological replicates). °Brix: soluble solids content; ND: not determined due to insufficient sample volume; Titrateable acidity expressed as g of tartaric acid equivalents per liter. “% Healthy Berries (count)” refers to % of non-defective berries counted; “% Healthy Berries (mass)” refers to % mass contribution of healthy berries relative to total cluster mass. Three genotypes (AJ-T2, AJ-T6 and AJ-B1) were evaluated across two consecutive seasons (2024–2025) due to consistent fruit production. Remaining genotypes were assessed in single seasons due to insufficient fruit yield for comprehensive analysis.

The 100-berry mass ranged from 99.7 ± 2.1 g in AJ-T3 to 307.6 ± 10.3 g in AJ-T2 in 2024, demonstrating considerable diversity in berry size among resistant lines. This three-fold variation in berry mass was accompanied by proportional differences in berry volume (80.0 ± 3.1 to 286.7 ± 6.6 mL). Three genotypes (AJ-T2, AJ-T6, and AJ-B1) were evaluated across two consecutive seasons (2024–2025) due to consistent fruit production. Remaining genotypes were assessed in single seasons due to insufficient fruit yield for comprehensive analysis.

Technological maturity parameters indicated that grapes achieved appropriate harvest conditions for their respective wine styles. Red wine genotypes (AJ-T2, AJ-T3, and AJ-T6) reached °Brix levels of 22.9–24.9, consistent with optimal sugar accumulation for red wine production (standard range: 23–25 °Brix), while the white wine genotype (AJ-B1) showed °Brix values of 21.0–21.1, appropriate for white wine elaboration (standard range: 21–23 °Brix). The pH values ranged from 3.4 to 3.7, while titratable acidity varied from 4.1 to 7.1 g/L tartaric acid equivalents, indicating suitable acidic balance for quality wine production across both red and white wine types.

Berry health assessment revealed high percentages of healthy berries (82.1–97.3%), demonstrating successful deployment of both single (*Run1*) and stacked (*Run1Ren1*) introgressed resistance loci against their primary target, powdery mildew, under natural field pressure without fungicide applications for this pathogen. Berry deterioration levels remained within acceptable ranges for quality wine production, with observed losses attributable to secondary fungal pathogens such as *Botrytis cinerea*, against which standard fungicide treatments were applied, as the genotypes lack resistance to this pathogen. This pattern confirms the precision and effectiveness of the powdery mildew resistance mechanisms, with all genotypes carrying *Run1* (single locus) or *Run1Ren1* (dual loci) showing complete protection against the target pathogen. The rachis mass percentage was consistently low (1.99–6.87%), indicating well-filled clusters with minimal stem contribution.

3.3. Oenological Parameters and Wine Quality

Wines produced from *Run1*-carrying and *Run1Ren1*-carrying genotypes exhibited acceptable oenological parameters comparable to premium *V. vinifera* standards (Table 3). The pH values of finished wines ranged from 3.4 to 3.9, maintaining the acidic character necessary for wine freshness, microbiological stability, and aging potential. Titratable acidity varied between 4.5 and 7.8 g/L (tartaric acid equivalents), with most genotypes showing balanced acidity levels suitable for both immediate consumption and aging.

Total phenolic content revealed successful maintenance of biochemical diversity across resistant genotypes, with concentrations ranging from 229.2 to 1356.1 mg/L gallic acid equivalents. This broad spectrum demonstrates that the breeding program effectively preserved natural phenolic variation while introducing resistance traits. Red wine genotypes achieved commercially relevant phenolic levels, exemplified by AJ-T2 with 1356.1 mg/L in 2024—concentrations that provide a robust foundation for quality wine production with enhanced aging potential and antioxidant properties.

Anthocyanin contents in red wines showcased retained biosynthetic capacity, with concentrations spanning 15.6 to 261 mg/L malvidin-3-glucoside equivalents. The genotype carrying dual resistance loci (*Run1Ren1*, AJ-T6: 84.2–231.0 mg/L) and single *Run1* locus genotypes (AJ-T2: 248.7–261.0 mg/L; AJ-T3: 130.9 mg/L) achieved anthocyanin levels fully compatible with quality wine standards. Notably, AJ-T2 reached 261 mg/L, confirming that resistance introgression preserved rather than compromised the genetic architecture underlying color development.

Table 3. Enological parameters and phenolic composition of wines produced from powdery mildew-resistant grapevine genotypes.

Genotype	Year	Type	Winemaking Type	Titrateable Acidity (g/L)	pH	Total Phenolics (GA eq.)	Total Anthocyanins (mg/L MV3G eq.)	Total Tannins (g/L EC eq.)	CI	Tone	% Yellow	% Red	% Blue
AJ-T6	2024	Red	Red	5.8 ± 0.3	3.60 ± 0.02	1091.4 ± 20.8	84.2 ± 6.2	712.6 ± 8.5	7.3 ± 0.3	0.7 ± 0.0	36.2 ± 5.3	36.2 ± 6.9	10.3 ± 0.1
AJ-T6	2025	Red	Red	5.5 ± 0.1	3.70 ± 0.07	231 ± 20.8	231 ± 40.5	-	8.8 ± 0.4	0.6 ± 0.0	34.3 ± 0.2	53.3 ± 0.4	12.4 ± 0.1
AJ-T2	2024	Red	Red	6.5 ± 0.1	3.70 ± 0.00	1356.1 ± 62.3	261 ± 16.0	815.7 ± 40.7	12.4 ± 0.6	0.6 ± 0.0	34 ± 3.0	54.1 ± 2.1	11.9 ± 0.1
AJ-T2	2025	Red	Red	4.5 ± 0.1	3.90 ± 0.02	1005.8 ± 4.5	248.7 ± 16.0	-	3.5 ± 0.2	0.6 ± 0.0	33.5 ± 1.2	55.2 ± 1.8	11.3 ± 0.0
AJ-B1	2024	White	White	6.2 ± 0.1	3.40 ± 0.01	229.2 ± 4	-	-	0.2 ± 0.0	2.4 ± 0.1	61.1 ± 1.0	25.6 ± 0.6	13.3 ± 0.2
AJ-T3	2024	Red	Red	6.5 ± 0.0	3.50 ± 0.00	632 ± 31.5	130.9 ± 1.0	188.1 ± 16.8	6.5 ± 0.6	0.7 ± 0.0	37.1 ± 0.1	49.7 ± 0.2	13.2 ± 0.3
AJ-T5	2024	Red	Red	7.8 ± 0.8	3.40 ± 0.06	420.8 ± 6.1	15.6 ± 3.6	69.3 ± 40.8	4.0 ± 0.1	0.8 ± 0.0	38.8 ± 5.5	53.5 ± 7.2	10.3 ± 0.1
AJ-T6	2024	Red	Red	5.8 ± 0.3	3.60 ± 0.02	1091.4 ± 20.8	84.2 ± 6.2	712.6 ± 8.5	7.3 ± 0.3	0.7 ± 0.0	36.2 ± 5.3	36.2 ± 6.9	10.3 ± 0.1

Wine chemical composition, including titrateable acidity (g/L tartaric acid), pH, total phenolic content (mg/L gallic acid equivalents), total anthocyanins (mg/L malvidin-3-glucoside equivalents), total tannins (g/L epicatechin equivalents), color intensity (CI), tone, and chromatic composition (% yellow, red, and blue contributions). Values were expressed as mean ± standard error (n = 3).

Color intensity profiles confirmed successful retention of chromatic diversity throughout the resistance breeding program, with red wine genotypes spanning 3.5 to 12.4 absorbance units. Tone values (0.6–0.8) remained within optimal parameters for red wine with low oxidation, demonstrating preserved color balance despite extensive backcrossing and the small volume of winemaking batches.

Comprehensive colorimetric analysis validated the breeding program's success in maintaining color complexity, with C^* values ranging from 40.6 to 68.1 and hue angles spanning 9.6–32°, indicating retention of the full spectrum of color expression potential. This broad chromatic range provides winemakers with diverse stylistic options while maintaining disease resistance. The white wine genotype AJ-B1 achieved ideal white wine color parameters (CI: 0.2, L^* : 96.3), confirming that resistance introgression preserved varietal color integrity across both red and white wine types.

HPLC analysis of individual anthocyanins showed profiles consistent with *V. vinifera* wines, with malvidin-3-glucoside as the predominant anthocyanin across all red wine genotypes. The presence of acylated anthocyanins suggests potential for color stability during wine aging, indicating preservation of anthocyanin biosynthetic pathways in resistant selections. HPLC analysis of 2025 vintage samples revealed total anthocyanin concentrations of 206.63–229.57 mg/L, which fell within the range determined by spectrophotometric measurements across both vintages (84.2–261 mg/L), demonstrating the analytical reliability of both methods. The anthocyanin profiles of resistant genotypes matched those of traditional *V. vinifera* cultivars, with characteristic absence of diglucoside forms, confirming successful preservation of *V. vinifera* species-specific biosynthetic pathways (Table 4).

Table 4. Individual anthocyanin composition of wines produced from powdery mildew-resistant grapevine genotypes (2025 vintage).

Anthocyanin	AJ-T6	AJ-T2
delp-3-gluc	3.15 ± 0.54	1.24 ± 0.09
cyan-3-gluc	0.27 ± 0.09	1.06 ± 0.1
petun-3-gluc	9.48 ± 1.42	4.66 ± 0.85
peon-3-gluc	3.16 ± 1.21	16.99 ± 2.25
malv-3-gluc	120.47 ± 16.45	128.85 ± 30.29
delp-3-gluc Ac	0.94 ± 0.08	0.57 ± 0.05
cyan-3-gluc Ac	1.26 ± 0.25	-
petun-3-gluc Ac	2.6 ± 0.39	-
peon-3-gluc Ac	2.03 ± 0.45	2.58 ± 0.29
malv-3-gluc Ac	55.01 ± 7.87	3.78 ± 0.3
delp-3-gluc coum	1.64 ± 0.05	1.59 ± 0.1
cyan-3-gluc coum	1.81 ± 0.4	1.57 ± 0.15
petun-3-gluc coum	0.94 ± 0.15	0.35 ± 0.04
peon-3-gluc coum	1.63 ± 0.31	17.53 ± 2.1
malv-3-gluc coum	23.69 ± 4.59	25.86 ± 2.37
TOTAL	229.57 ± 32.52	206.63 ± 15.65

Values were expressed as mean ± standard error (n = 3). Individual anthocyanins quantified by RP-HPLC-DAD analysis. Results expressed as mg/L malvidin-3-glucoside equivalents. “-” indicates concentrations below detection limit. AJ-T6: Run1Ren1-carrying genotype; AJ-T2: Run1-carrying genotype. gluc: glucosylated forms; Ac: acetylated forms; coum: coumaroylated forms.

Two-season evaluation of genotypes AJ-T2 and AJ-T6 revealed contrasting patterns of seasonal variation. AJ-T2 demonstrated relatively stable anthocyanin production across vintages (261.0 mg/L in 2024 vs. 248.7 mg/L in 2025; 4.7% variation), while maintaining consistent total phenolic levels (1356.1 vs. 1005.8 mg/L GAE). In contrast, AJ-T6 showed greater seasonal responsiveness, with notable variation in total phenolics (1091.4 vs. 231.0 mg/L GAE) and anthocyanin content (84.2 vs. 231.0 mg/L).

4. Discussion

The development of grapevine lines carrying *Run1* and *Run1Ren1* resistance loci while retaining 99.2–99.6% *Vitis vinifera* genome content is consistent with recent advances in sustainable viticulture. Our results show that marker-assisted backcrossing can introgress disease resistance genes from wild *Vitis* species without compromising the superior oenological qualities that define quality wine grapes. While several resistant cultivars have achieved commercial success in specific regions (e.g., PIWI varieties in Europe), this work advances the marker-assisted breeding approach in a program that uses local genotypes.

The phenolic composition of wines produced from *Run1*-carrying and *Run1Ren1*-carrying genotypes ranged from 229.2 to 1356.1 mg/L GAE across both red and white wine types, falling within the range reported for *V. vinifera* cultivars in the literature. Red wine genotypes reached levels of 231.0–1356.1 mg/L GAE, while the white genotype showed phenolic content consistent with its wine style. These results contrast with previous generations of resistant varieties that often exhibited reduced phenolic content. The phenolic levels observed suggest that selection of *vinifera* parents and extensive backcrossing (BC6–BC7) may have contributed to preserving biochemical pathways responsible for phenolic synthesis while retaining the resistance trait.

HPLC analysis of 2025 vintage samples revealed detailed anthocyanin profiles characteristic of quality *V. vinifera* wines, with total concentrations of 206.63–229.57 mg/L malvidin-3-glucoside equivalents. Malvidin-3-glucoside predominated across all red wine genotypes, with AJ-T6 achieving 120.47 mg/L and AJ-T2 reaching 128.85 mg/L. The presence of acylated and coumaroylated derivatives (15.6–55.01 mg/L) indicated excellent potential for color stability during wine aging, confirming preservation of sophisticated anthocyanin biosynthetic pathways in resistant selections.

Our findings align with recent reports on advanced resistant varieties while demonstrating competitive outcomes in key parameters. While Casanova-Gascón et al. [25] reported phenolic contents of 1200–1800 mg/L in resistant varieties grown in Spain, our *Run1* and *Run1Ren1* red lines achieved values up to 1356.1 mg/L, suggesting that intensive selection and marker-assisted breeding can maintain high phenolic potential. Similarly, Pedneault and Provost [2] noted that many resistant varieties showed 20–30% lower anthocyanin content compared to *V. vinifera* standards, whereas our results demonstrate levels within the range of traditional cultivars (15.6–261 mg/L).

Two-season analysis revealed genotype-specific stability patterns, with the *Run1* genotype AJ-T2 showing remarkable consistency in anthocyanin production (4.7% variation), contrasting with findings of Van Heerden et al. [26], who reported seasonal variations of up to 35% in resistant cultivars. According to our on-site climate records (Supplementary Data S1), the inter-annual shifts in anthocyanin concentration were consistent with climatic modulation of the flavonoid pathway during ripening. Seasons characterized by high evaporative demand and accelerated ripening compressed the accumulation window and increased berry-skin temperatures—conditions known to limit anthocyanin biosynthesis and/or enhance degradation—yielding lower color despite rapid sugar loading. By contrast, seasons with a milder spring onset and greater soil-moisture reserves favored a more gradual ripening trajectory, cooler night-time temperatures, and extended time above the biosynthetic threshold, supporting higher anthocyanin accumulation. Elevated UV-solar radiation levels modulate the expression of key genes in the phenylpropanoid pathway, leading to an increased accumulation of anthocyanins and other polyphenols [27,28]. Within this framework, the pyramided *Run1Ren1* genotype (AJ-T6) exhibited a wider year-to-year amplitude in anthocyanin concentration, whereas AJ-T2 remained comparatively stable, consistent with a genotype-by-environment effect that merits confirmation in multi-plant, multi-year trials. In the broader regional context, Chile has exhibited a sustained warming

trend [29], which is expected to extend infection-favorable windows for *Erysiphe necator* and intensify disease pressure; consequently, the deployment of *Run1*/*Ren1* pyramided resistant lines becomes particularly relevant to sustain yields and wine composition without increasing fungicide inputs.

Our findings align with recent studies that have evaluated the oenological performance of powdery mildew-resistant grape varieties. Gratl et al. [30] conducted extensive phenolic profiling of various resistant hybrid lines in Italy, finding that many achieved comparable polyphenol and anthocyanin profiles across vintages. Similarly, studies on resistant white grape varieties have demonstrated that their aromatic and phenolic profiles can approach those of traditional cultivars when appropriate viticultural and winemaking practices are employed [2]. These results, combined with our observations, suggest that advanced resistant lines developed through marker-assisted breeding have the potential to meet quality standards for commercial wine production, though validation through comprehensive multi-environment trials remains essential.

The complete resistance to powdery mildew (OIV scores 9) achieved by all *Run1*-carrying and *Run1Ren1*-carrying genotypes corroborates the effectiveness of these resistance loci previously reported by [31], Agurto et al. [4] and Sosa-Zuniga et al. [6]. The stacked resistance in genotype AJ-T6 represents an advanced approach beyond single-locus resistance, addressing concerns about durability in commercial viticulture. This dual-locus strategy is particularly important as pathogen populations evolve and potentially overcome a single resistance gene [32].

Stacking multiple resistance loci, such as *Run1* and *Ren1*, reduces the likelihood of resistance breakdown, as pathogens would need to simultaneously overcome multiple distinct defenses—an event that is statistically far less probable than overcoming a single resistance gene [33,34].

The combination of *Run1* and *Ren1* is not merely additive; it generates a synergistic immune response, enhancing ROS production, callose deposition, programmed cell death, and activation of defense-related genes compared to each locus individually. This synergistic effect provides a stronger and long-lasting barrier against *E. necator*. This strategy is critical because resistance conferred by individual loci, such as *Run1*, can be overcome by co-evolving pathogen strains [35,36]. Stacking loci with different mechanisms and origins may help reduce selection pressure on the pathogen population, providing a potentially more resilient and durable form of resistance for sustainable viticulture [6,37].

Reducing fungicide applications is a key factor for sustainable wine production, a goal directly addressed by resistant grapevine cultivars [38]. Conventional programs for *Vitis vinifera* often require an average of 12–15 preventive sprays per season. In contrast, resistant varieties can be managed with just 2–4 applications, a strategy that also preserves the durability of the resistance [39]. Literature indicates that these varieties may decrease vineyard treatments by half (50%) [40], with some studies highlighting a maximum potential reduction of up to 80% in pesticide use [41]. Field trials confirm this sharp contrast, showing a 60–90% reduction in fungicide treatments [39]. This decrease also lowers the environmental load of copper and sulfur, with the exact savings depending on the R-loci and vintage conditions [1,42].

The ability to maintain quality wine characteristics in resistant varieties is a primary factor that influences their potential adoption by producers who prioritize wine standards. The oenological parameters achieved by *Run1*-carrying and *Run1Ren1*-carrying wines, including pH (3.4–3.9), phenolic content (229.2–1356.1 mg GAE/L), and anthocyanin levels (15.6–261.0 mg/L), fall within ranges reported for quality wine production. However, comprehensive comparisons with traditional *V. vinifera* cultivars grown and vinified under

identical conditions would be necessary to fully assess their relative quality potential and market acceptance.

This introgression program builds upon established marker-assisted selection methodologies, utilizing high-density molecular markers to achieve precise tracking of the resistance locus through multiple backcross generations while simultaneously selecting against undesirable non-*vinifera* alleles [43]. The successful application of these breeding technologies to achieve >99% *vinifera* genome recovery while maintaining complex resistance demonstrates their effectiveness for developing commercially viable resistant cultivars [44].

The identification of genotype AJ-T6 carrying both *Run1* and *Ren1* loci demonstrates the potential for stacking resistance genes without discernible negative effects on wine quality. The inclusion of sensory analysis is fundamental to validate the enological potential of these resistant lines. Duley et al. [45] analyzed wines made from disease-resistant hybrid cultivars, concluding that their phenolic and aromatic profiles can approach those of traditional *V. vinifera* wines, provided that proper vinification protocols are applied. Similarly, Vecchio et al. [46] demonstrated that consumers in different markets favorably accept wines produced from resistant varieties, especially when their origin and environmental benefits are clearly communicated.

In the climatic context of climate change, recent trends in Chilean wine regions demonstrate an increase in average temperature and a shift towards warmer nights [29], which increases agroclimatic risks and reinforces the importance of adopting resistant materials, such as those carrying *Run1* and *Ren1*, to ensure future resilience. From an economic and environmental vantage, the adoption of these varieties can markedly curtail reliance on fungicides and decrease the carbon footprint, thereby fortifying the rationale for their large-scale implementation.

This approach is consistent with the European PIWI movement, which advocates for the promotion of resistant varieties as a sustainable innovation. The market share of this movement is increasing, partly because it offers environmental and marketing benefits that resonate with environmentally conscious consumers [47].

While our results are highly encouraging, several limitations must be acknowledged. The evaluation was conducted at a single location over two seasons, and broader multi-environment trials would strengthen conclusions about stability and adaptability. Additionally, although chemical analyses provide strong indicators of quality potential, sensory evaluation by trained panels and consumer acceptance studies remain essential for full validation. Future breeding efforts should consider incorporating resistance to other pathogens, particularly *Plasmopara viticola* and *Botrytis cinerea*, to develop truly sustainable varieties requiring minimal chemical inputs. Long-term monitoring of resistance durability under commercial production conditions will be crucial for sustainable deployment.

In conclusion, the *Run1* and *Run1Ren1* grapevine lines evaluated in this study showed disease resistance combined with wine chemical characteristics within reported ranges for commercial wines. The estimated 99.2–99.6% *V. vinifera* genome content suggests these materials could produce wines with chemical profiles resembling traditional cultivars, while reducing fungicide applications for powdery mildew control. These initial findings add to accumulating evidence that marker-assisted breeding approaches may contribute to addressing the trade-off between disease resistance and wine quality, indicating potential for more sustainable wine production practices.

5. Conclusions

The introgression of *Run1* and *Run1Ren1* resistance loci into advanced grapevine breeding lines resulted in complete powdery mildew resistance (OIV scores 9) in the conditions of this assay while maintaining 99.2–99.6% *V. vinifera* genome content. Oenological

analyses showed phenolic content ranging from 229.2 to 1356.1 mg GAE/L and anthocyanin profiles characterized by malvidin-3-glucoside predominance without diglucoside forms, consistent with *V. vinifera* biosynthetic pathways. Two-season observations indicated genotype-specific variation in seasonal response. AJ-T2 showed 4.7% variation in anthocyanin content between years, while AJ-T6 displayed greater variation in phenolic parameters. The results indicate that marker-assisted breeding can produce grapevine varieties combining powdery mildew resistance with oenological parameters within commercial ranges. This approach could reduce fungicide applications while maintaining wine chemical composition compatible with quality production. These findings require validation through replicated multi-environment trials. The current evaluation, limited to single plants per genotype at one location, provides initial data that warrant expanded testing. Future studies should include adequate replication, multiple locations, sensory evaluation, and comparison with standard cultivars under identical conditions to determine commercial viability.

Supplementary Materials: The following supporting information can be downloaded at <https://www.mdpi.com/article/10.3390/agriculture15212267/s1>: Data S1: Climate data.

Author Contributions: P.O.-V.: conceptualization, original draft, writing—review & editing. V.S.-Z.: formal analysis, methodology, writing—review & editing. R.M.-P.: methodology, visualization. M.G.-C.: formal analysis, methodology. C.V.: writing—review & editing. C.M. (Consuelo Medina): project administration, writing—review & editing. C.M. (Claudio Meneses): supervision, writing—review & editing. P.A.-J.: funding acquisition, supervision, writing—review & editing. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by PROYECTO ANID Investigación Tecnológica, Grant No. IT23I0007. The funding provided essential resources for field sampling activities, laboratory analyses and oenological characterization. P.O.-V. was supported by ANID doctoral fellowship 21231208 and PRONABEC-Perú. We thank AgriJohnson Ltda. for providing the plant materials and Universidad Autónoma de Chile, Talca Campus, for providing their facilities.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data supporting the findings of this study are available from the corresponding author upon reasonable request.

Acknowledgments: The authors acknowledge the invaluable collaboration of AgriJohnson Ltda workers was essential for the successful completion of this research.

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

Abbreviations

The following abbreviations are used in this manuscript:

OIV	Organisation Internationale de la Vigne et du Vin
ND	Not determined
SE	Standard error
GAE	Gallic acid equivalents
MV3G eq	Malvidin-3-glucoside equivalents
EC eq	Epicatechin equivalents
PCA	Principal components analysis
ANOVA	Analysis of variance
DNA	Deoxyribonucleic acid

References

- Pertot, I.; Caffi, T.; Rossi, V.; Mugnai, L.; Hoffmann, C.; Grando, M.S.; Gary, C.; Lafond, D.; Duso, C.; Thiery, D. A Critical Review of Plant Protection Tools for Reducing Pesticide Use on Grapevine and New Perspectives for the Implementation of IPM in Viticulture. *Crop Prot.* **2017**, *97*, 70–84. [\[CrossRef\]](#)
- Pedneault, K.; Provost, C. Fungus Resistant Grape Varieties as a Suitable Alternative for Organic Wine Production: Benefits, Limits, and Challenges. *Sci. Hortic.* **2016**, *208*, 57–77. [\[CrossRef\]](#)
- Barker, C.L.; Donald, T.; Pauquet, J.; Ratnaparkhe, M.B.; Bouquet, A.; Adam-Blondon, A.F.; Thomas, M.R.; Dry, I. Genetic and Physical Mapping of the Grapevine Powdery Mildew Resistance Gene, Run1, Using a Bacterial Artificial Chromosome Library. *Theor. Appl. Genet.* **2005**, *111*, 370–377. [\[CrossRef\]](#) [\[PubMed\]](#)
- Agurto, M.; Schlechter, R.O.; Armijo, G.; Solano, E.; Serrano, C.; Contreras, R.A.; Zúñiga, G.E.; Arce-Johnson, P. RUN1 and REN1 Pyramiding in Grapevine (*Vitis vinifera* Cv. Crimson Seedless) Displays an Improved Defense Response Leading to Enhanced Resistance to Powdery Mildew (*Erysiphe necator*). *Front. Plant Sci.* **2017**, *8*, 758. [\[CrossRef\]](#) [\[PubMed\]](#)
- Hoffmann, S.; Di Gaspero, G.; Kovács, L.; Howard, S.; Kiss, E.; Galbács, Z.; Testolin, R.; Kozma, P. Resistance to *Erysiphe necator* in the Grapevine ‘Kishmish Vatkana’ Is Controlled by a Single Locus through Restriction of Hyphal Growth. *Theor. Appl. Genet.* **2008**, *116*, 427–438. [\[CrossRef\]](#)
- Sosa-Zuniga, V.; Valenzuela, Á.V.; Barba, P.; Cancino, C.E.; Romero-Romero, J.L.; Arce-Johnson, P. Powdery Mildew Resistance Genes in Vines: An Opportunity to Achieve a More Sustainable Viticulture. *Pathogens* **2022**, *11*, 703. [\[CrossRef\]](#)
- Vezzulli, S.; Zulini, L.; Stefanini, M. Genetics-Assisted Breeding for Downy/Powdery Mildew and Phylloxera Resistance at Fem. In *Proceedings of the BIO Web of Conferences*; EDP Sciences: Les Ulis, France, 2019; Volume 12.
- Sun, Q.; Gates, M.J.; Lavin, E.H.; Acree, T.E.; Sacks, G.L. Comparison of Odor-Active Compounds in Grapes and Wines from *Vitis vinifera* and Non-Foxy American Grape Species. *J. Agric. Food Chem.* **2011**, *59*, 10657–10664. [\[CrossRef\]](#)
- Slegers, A.; Angers, P.; Ouellet, É.; Truchon, T.; Pedneault, K. Volatile Compounds from Grape Skin, Juice and Wine from Five Interspecific Hybridgrape Cultivars Grown in Québec (Canada) for Wine Production. *Molecules* **2015**, *20*, 10980–11016. [\[CrossRef\]](#)
- Springer, L.F.; Sacks, G.L. Protein-Precipitable Tannin in Wines from *Vitis vinifera* and Interspecific Hybrid Grapes (*Vitis* Ssp.): Differences in Concentration, Extractability, and Cell Wall Binding. *J. Agric. Food Chem.* **2014**, *62*, 7515–7523. [\[CrossRef\]](#)
- Nicolle, P.; Marcotte, C.; Angers, P.; Pedneault, K. Pomace Limits Tannin Retention in Frontenac Wines. *Food Chem.* **2019**, *277*, 438–447. [\[CrossRef\]](#)
- Montaigne, E.; Coelho, A.; Khelifi, L. Economic Issues and Perspectives on Innovation in New Resistant Grapevine Varieties in France. *Wine Econ. Policy* **2016**, *5*, 73–77. [\[CrossRef\]](#)
- Liang, Z.; Owens, C.L.; Zhong, G.-Y.; Cheng, L. Polyphenolic Profiles Detected in the Ripe Berries of *Vitis vinifera* Germplasm. *Food Chem.* **2011**, *129*, 940–950. [\[CrossRef\]](#) [\[PubMed\]](#)
- Ruiz-Garcia, Y.; Romero-Cascales, I.; Gil-Munoz, R.; Fernández-Fernández, J.I.; López-Roca, J.M.; Gomez-Plaza, E. Improving Grape Phenolic Content and Wine Chromatic Characteristics through the Use of Two Different Elicitors: Methyl Jasmonate versus Benzothiadiazole. *J. Agric. Food Chem.* **2012**, *60*, 1283–1290. [\[CrossRef\]](#) [\[PubMed\]](#)
- Scariolo, F.; Gabelli, G.; Magon, G.; Palumbo, F.; Pirrello, C.; Farinati, S.; Curioni, A.; Devillars, A.; Lucchin, M.; Barcaccia, G.; et al. The Transcriptional Landscape of Berry Skin in Red and White PIWI (“Pilzwiderstandsfähig”) Grapevines Possessing QTLs for Partial Resistance to Downy and Powdery Mildews. *Plants* **2024**, *13*, 2574. [\[CrossRef\]](#)
- Töpfer, R.; Hausmann, L.; Harst, M.; Maul, E.; Zyprian, E.; Eibach, R. New Horizons for Grapevine Breeding. *Fruit Veg. Cereal Sci. Biotechnol.* **2011**, *5*, 79–100.
- Bois, B.; Zito, S.; Calonnec, A.; Ollat, N. Climate vs Grapevine Pests and Diseases Worldwide: The First Results of a Global Survey. *J. Int. Des. Sci. De La Vigne Et Du Vin* **2017**, *51*, 133–139.
- Caffarra, A.; Rinaldi, M.; Eccel, E.; Rossi, V.; Pertot, I. Modelling the Impact of Climate Change on the Interaction between Grapevine and Its Pests and Pathogens: European Grapevine Moth and Powdery Mildew. *Agric. Ecosyst. Environ.* **2012**, *148*, 89–101. [\[CrossRef\]](#)
- Merli, R.; Preziosi, M.; Acampora, A. Sustainability Experiences in the Wine Sector: Toward the Development of an International Indicators System. *J. Clean Prod.* **2018**, *172*, 3791–3805. [\[CrossRef\]](#)
- Matus, J.T. Development and Status of the Chilean Wine Industry. In *Grapevine Breeding Programs for the Wine Industry*; Reynolds, A.G., Ed.; Woodhead Publishing: Cambridge, UK, 2016; pp. 385–409.
- Agrometeorología INIA Red Agrometeorológica INIA. Available online: <https://agrometeorologia.cl> (accessed on 17 October 2025).
- Ciubotaru, R.M.; Franceschi, P.; Vezzulli, S.; Zulini, L.; Stefanini, M.; Oberhuber, M.; Robatscher, P.; Chitarrini, G.; Vrhovsek, U. Secondary and Primary Metabolites Reveal Putative Resistance-Associated Biomarkers against *Erysiphe Necator* in Resistant Grapevine Genotypes. *Front. Plant Sci.* **2023**, *14*, 1112157. [\[CrossRef\]](#)
- Ribéreau-Gayon, P.; Glories, Y.; Maujean, A.; Dubourdieu, D. *Handbook of Enology, Volume 2: The Chemistry of Wine Stabilization and Treatments*; John Wiley & Sons: Hoboken, NJ, USA, 2021; ISBN 111958776X.

24. Ayala, F.; Echávarri, J.F.; Negueruela, A.I. A New Simplified Method for Measuring the Color of Wines. I. Red and Rosé Wines. *Am. J. Enol. Vitic.* **1997**, *48*, 357–363. [\[CrossRef\]](#)
25. Casanova-Gascón, J.; Ferrer-Martín, C.; Bernad-Eustaquio, A.; Elbaile-Mur, A.; Ayuso-Rodríguez, J.M.; Torres-Sánchez, S.; Jarne-Casasús, A.; Martín-Ramos, P. Behavior of Vine Varieties Resistant to Fungal Diseases in the Somontano Region. *Agronomy* **2019**, *9*, 738. [\[CrossRef\]](#)
26. Van Heerden, C.J.; Burger, P.; Vermeulen, A.; Prins, R. Detection of Downy and Powdery Mildew Resistance QTL in a ‘Regent’ × ‘RedGlobe’ Population. *Euphytica* **2014**, *200*, 281–295. [\[CrossRef\]](#)
27. Serrano, A.; Espinoza, C.; Armijo, G.; Inostroza-Blancheteau, C.; Poblete, E.; Meyer-Regueiro, C.; Arce, A.; Parada, F.; Santibáñez, C.; Arce-Johnson, P. Omics Approaches for Understanding Grapevine Berry Development: Regulatory Networks Associated with Endogenous Processes and Environmental Responses. *Front. Plant Sci.* **2017**, *8*, 1486. [\[CrossRef\]](#)
28. Sunitha, S.; Loyola, R.; Alcalde, J.A.; Arce-Johnson, P.; Matus, J.T.; Rock, C.D. The Role of UV-B Light on Small RNA Activity During Grapevine Berry Development. *G3 Genes Genomes Genet.* **2019**, *9*, 769–787. [\[CrossRef\]](#)
29. Verdugo-Vásquez, N.; Orrego, R.; Gutiérrez-Gamboa, G.; Reyes, M.; Zurita-Silva, A.; Balbontín, C.; Gaete, N.; Salazar-Parra, C. Climate Trends and Variability in the Chilean Viticultural Production Zones during 1985–2015. *OENO One* **2023**, *57*, 345–362. [\[CrossRef\]](#)
30. Gratl, V.; Sturm, S.; Zini, E.; Letschka, T.; Stefanini, M.; Vezzulli, S.; Stuppner, H. Comprehensive Polyphenolic Profiling in Promising Resistant Grapevine Hybrids Including 17 Novel Breeds in Northern Italy. *J. Sci. Food Agric.* **2021**, *101*, 2380–2388. [\[CrossRef\]](#)
31. Feechan, A.; Anderson, C.; Torregrosa, L.; Jermakow, A.; Mestre, P.; Wiedemann-Merdinoglu, S.; Merdinoglu, D.; Walker, A.R.; Cadle-Davidson, L.; Reisch, B. Genetic Dissection of a TIR-NB-LRR Locus from the Wild N Orth A Merican Grapevine Species *M Uscadinia Rotundifolia* Identifies Paralogous Genes Conferring Resistance to Major Fungal and Oomycete Pathogens in Cultivated Grapevine. *Plant J.* **2013**, *76*, 661–674. [\[CrossRef\]](#) [\[PubMed\]](#)
32. Ricciardi, V.; Crespan, M.; Maddalena, G.; Migliaro, D.; Brancadoro, L.; Maghradze, D.; Failla, O.; Toffolatti, S.L.; De Lorenzis, G. Novel Loci Associated with Resistance to Downy and Powdery Mildew in Grapevine. *Front. Plant Sci.* **2024**, *15*, 1386225. [\[CrossRef\]](#) [\[PubMed\]](#)
33. Mundt, C.C. Pyramiding for Resistance Durability: Theory and Practice. *Phytopathology* **2018**, *108*, 792–802. [\[CrossRef\]](#) [\[PubMed\]](#)
34. Fresnedo-Ramírez, J.; Yang, S.; Sun, Q.; Cote, L.M.; Schweitzer, P.A.; Reisch, B.I.; Ledbetter, C.A.; Luby, J.J.; Clark, M.D.; Londo, J.P.; et al. An Integrative AmpSeq Platform for Highly Multiplexed Marker-Assisted Pyramiding of Grapevine Powdery Mildew Resistance Loci. *Mol. Breed.* **2017**, *37*, 145. [\[CrossRef\]](#)
35. Qiu, W.; Feechan, A.; Dry, I. Current Understanding of Grapevine Defense Mechanisms against the Biotrophic Fungus (*Erysiphe necator*), the Causal Agent of Powdery Mildew Disease. *Hortic. Res.* **2015**, *2*, 15020. [\[CrossRef\]](#)
36. Cadle-Davidson, L.; Chicoine, D.R.; Consolie, N.H. Variation Within and Among *Vitis* Spp. for Foliar Resistance to the Powdery Mildew Pathogen *Erysiphe Necator*. *Plant Dis.* **2011**, *95*, 202–211. [\[CrossRef\]](#)
37. Merdinoglu, D.; Schneider, C.; Prado, E.; Wiedemann-Merdinoglu, S.; Mestre, P. Breeding for Durable Resistance to Downy and Powdery Mildew in Grapevine. *OENO One* **2018**, *52*, 203–209. [\[CrossRef\]](#)
38. Trapp, O.; Avia, K.; Borrelli, C.; Eibach, R.; Merdinoglu, D.; Töpfer, R. More Sustainability in Europe’s Vineyards—Using Resistant Grapevine Varieties to Reduce the Input of Pesticides. *Plants People Planet* **2025**, *7*, 1621–1628. [\[CrossRef\]](#)
39. Eisenmann, B.; Wingerter, C.; Dressler, M.; Freund, C.; Kortekamp, A.; Bogs, J. Fungicide-Saving Potential and Economic Advantages of Fungus-Resistant Grapevine Cultivars. *Plants* **2023**, *12*, 3120. [\[CrossRef\]](#) [\[PubMed\]](#)
40. Piccoli, A.; Viganò, F. Unveiling the Motivations Behind Cultivating Fungus-Resistant Wine Varieties: Insights from Wine Growers in South Tyrol, Italy. *Sustainability* **2025**, *17*, 2615. [\[CrossRef\]](#)
41. Mian, G.; Nassivera, F.; Sillani, S.; Iseppi, L. Grapevine Resistant Cultivars: A Story Review and the Importance on the Related Wine Consumption Inclination. *Sustainability* **2023**, *15*, 390. [\[CrossRef\]](#)
42. Warneke, B.W.; Nackley, L.L.; Pscheidt, J.W. Management of Grape Powdery Mildew with an Intelligent Sprayer and Sulfur. *Plant Dis.* **2022**, *106*, 1837–1844. [\[CrossRef\]](#)
43. Brault, C.; Segura, V.; Roques, M.; Lamblin, P.; Bouckenooghe, V.; Pouzalgues, N.; Cunty, C.; Breil, M.; Frouin, M.; Garcin, L.; et al. Enhancing Grapevine Breeding Efficiency through Genomic Prediction and Selection Index. *G3 Genes Genomes Genet.* **2024**, *14*, jkae038. [\[CrossRef\]](#)
44. Tourrette, E.; Falque, M.; Martin, O.C. Enhancing Backcross Programs through Increased Recombination. *Genet. Sel. Evol.* **2021**, *53*, 25. [\[CrossRef\]](#)
45. Duley, G.; Ceci, A.T.; Longo, E.; Boselli, E. Oenological Potential of Wines Produced from Disease-Resistant Grape Cultivars. *Compr. Rev. Food Sci. Food Saf.* **2023**, *22*, 2591–2610. [\[CrossRef\]](#)

46. Vecchio, R.; Pomarici, E.; Giampietri, E.; Borrello, M. Consumer Acceptance of Fungus-Resistant Grape Wines: Evidence from Italy, the UK, and the USA. *PLoS ONE* **2022**, *17*, e0267198. [[CrossRef](#)]
47. Kiefer, C.; Szolnoki, G. Consumer Acceptance of Fungus-Resistant Grape Varieties—An Exploratory Study Using Sensory Evaluation Tests among Consumers in Germany. *Sustainability* **2023**, *15*, 10664. [[CrossRef](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.