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Bunch compactness, rot incidence, and stenospermocarpy gradient: A five-year evaluation of six Pinot blanc clones in northeast Italy

Umberto Malossini[1], Pier Luigi Bianchedi[1], Tomas Roman[1], Duilio Porro[1], Massimo Bertamini[2], Michele Faralli[2,*]

[1] Technology Transfer Centre, Fondazione Edmund Mach, via Mach 1, 38098 San Michele all'Adige (TN), Italy
[2] Center Agriculture Food Environment (C3A), University of Trento, Via Mach 1, 38098 San Michele all'Adige (TN), Italy

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*correspondence:
michele.faralli@unitn.it

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ABSTRACT

In viticulture, bunch rot is considered a major issue due to the elevated intrinsic varietal susceptibility, leading to significant yield and quality losses. Pinot blanc can be severely affected by late-season bunch rot, primarily due to its characteristically compact bunch structure. While several vineyard management practices can induce looser bunch architecture, clonal selection offers the potential to identify individuals with naturally less compact bunches without major penalties on yield or juice chemical parameters. In this study, six Pinot blanc clones (namely, ersa140, 141, and 142; Lb16 and 18; and SMA102), trained to “pergola semplice”, were evaluated over five years in an experimental vineyard in the Trentino region. The evaluation focused on traits associated with yield and its components, bunch compactness, juice chemical parameters, and bunch rot incidence. The results revealed contrasting traits among clones, with a gradient in yield and related components across the tested material. Although differences in bunch compactness were observed—expressed as the ratio between bunch weight and rachis length (ranging from 6 to 15 g/cm)—the loose bunch trait was primarily associated with reduced yield and was linearly related to an increased number of stenospermocarpic berries. Clones with looser bunches exhibited higher °Brix and pH levels, likely due to berry dehydration (potentially driven by accelerated ripening following an unbalanced leaf-to-fruit ratio) and increased potassium uptake, respectively. Bunch rot frequency and the number of bunches exhibiting high rot incidence varied among clones, potentially due to two non-mutually exclusive mechanisms: (i) looser bunch architecture and (ii) specific properties of the berry skin. This study provides evidence of a strong relationship between bunch characteristics and yield potential in the six Pinot blanc clones evaluated, which should be considered in future vineyard planning. Intermediate clones, such as Lb18 and especially SMA102, were characterised by moderate vine productivity levels (~3 kg per vine) combined with good tolerance to bunch rot, suggesting their suitability for environments with moderate disease pressure without incurring severe yield penalties.

KEYWORDS: *Vitis vinifera*, yield, juice composition, clonal selection, intravarietal diversity, bunch rot susceptibility

INTRODUCTION

Pinot blanc is an internationally important grapevine variety with around 16,000 hectares of total cultivated area worldwide (OIV, 2023). France, Germany, and Italy are the main producer countries, mainly in Alsace, Baden, and the north-east regions, respectively. Austria, Hungary, the Czech Republic, and Slovakia are also important producing countries; most of the Pinot blanc is confined to cool-wet viticultural areas where pre-harvest rainfall increases the probability of yield and quality losses following bunch rot occurrence (Molitor *et al.*, 2018; Wilcox 2016; Molitor *et al.*, 2016). Indeed, in grape berries, bunch rot causes economic loss to grape and wine production worldwide, generally boosted by high humidity around the bunch zone (Wilcox *et al.*, 2015). The organisms responsible are largely filamentous fungi, the most common of these being *Botrytis cinerea* (grey mould), *Aspergillus* spp., *Penicillium* spp., and fungi found in warmer climates (*e.g.*, *Greeneria uvicola* (bitter rot)) (Steel *et al.*, 2013). While breeding for fungi resistance provided several novel hybrid varieties, with marker-assisted selection being the core technique for their fast development, to date, there is only preliminary knowledge on a putative resistance locus, for example, resistance to *Botrytis cinerea* (Sapkota *et al.*, 2019). Present variety development focuses on berry physical barriers, for example, a thick berry skin or hydrophobic berry surface (Gabler *et al.*, 2003). Therefore, while environmental conditions play an important role in fungi proliferation, fungicide spray, canopy management (*e.g.*, bunch-zone defoliation to reduce relative humidity around berries) and nitrogen nutrition (lower berry split) are still some of the agronomic practices extensively used in the short-term to reduce the incidence and severity of the disease (Tello & Ibanez, 2018).

Another important target for reducing bunch rot incidence is achieving a lower bunch compactness, a trait that can be reached via either genetic improvement or agronomic practices (Tello & Ibanez, 2018; Belfiore *et al.*, 2024; Wegher *et al.*, 2022). Indeed, a compact bunch has been shown to directly affect susceptibility to bunch rot but also ripening dynamics, with detrimental consequences on berry composition and wine quality. In a compact bunch, the spatial arrangement of the berries, generally in close contact, can: i) restrict the development of waxy cuticle and reduce the functionality of a thick cuticle against rot fungi (Tello & Ibanez, 2018; Gabler *et al.*, 2003; Kretschmer *et al.*, 2007); ii) increase the surface wetness due to poor ventilation leading to higher pathogen proliferation (Gabler *et al.*, 2003; Becker & Knoche, 2012); iii) increase the probability of microcracking and juice outflow and therefore providing water and nutrients for mould development which can be temporally rapid (Tello & Ibanez, 2018; Hed *et al.*, 2009). Overall, several agronomical practices, mostly to be applied pre- or during flowering, are available for viticulturist to achieve a loose bunch: i) early flowering stage source-limitation (both via antitranspirant application or basal leaf defoliation) can reduce berry number or size (the latter, potentially via an induction in stenospermocarpy, *i.e.*, the production of incompletely developed seeds with normal, yet smaller, development of the berry) (Palliotti *et al.*, 2012; Tello & Ibanez, 2018); ii) gibberellic acid (GA3) application, depending on stage of application (*i.e.*, pre or early flowering) can increase rachis length or reduce berry number (Tello & Ibanez, 2018; Wegher *et al.*, 2022). All these practices can provide bunches with reduced mass per unit of rachis length, hence equating to a lower compactness. The presence of intra and inter-varietal natural variation for bunch compactness is also known and has been extensively used as a source of variability for clonal selection or breeding programs (Portu *et al.*, 2024; Belfiore *et al.*, 2024; Tello *et al.*, 2015). Large variation for such traits has already been observed in several varieties such as Riesling (Molitor *et al.*, 2016; Molitor *et al.*, 2018), Pinot noir (Richter *et al.*, 2020), and Pinot gris (Belfiore *et al.*, 2024). However, the genetic basis of intra-varietal variation is still elusive, although: i) mutations for single or multiple SNPs (Emanuelli *et al.*, 2010; Bertamini *et al.*, 2021) were able to explain monoterpene accumulation in Chardonnay berries; ii) the presence of a virus (particularly GFLV) modified the length of internodes, length and size of leaves and bunches, leading to yield reduction in Gewürztraminer (Malossini *et al.*, 2006). Traditionally, the management of bunch rot in grapevine has relied heavily on the application of synthetic fungicides (Diez-Mendez *et al.*, 2024). However, the emergence of fungicide-resistant strains of pathogens such as *Botrytis cinerea*, in conjunction with increasing environmental and regulatory pressures, has increased the need to develop more environmentally and economically sustainable disease control strategies. Moreover, climate change – characterised by elevated temperatures and altered precipitation regimes (Faralli *et al.*, 2024) – is exacerbating grapevine susceptibility to rot-inducing pathogens (*e.g.*, Diez-Mendez *et al.*, 2024). In this context, the reduction of bunch compactness through various viticultural practices or breeding approaches has emerged as a critical factor in mitigating disease incidence.

The Pinot family includes several varieties derived from distinct somatic variants (Pinot noir, Pinot gris, Pinot blanc, Pinot meunier, Pinot teinturier) (Regner *et al.*, 2000; Vezzulli *et al.*, 2012). Pinot cultivars are typically characterised by highly compact cluster morphology, which significantly increases their susceptibility to rot (Belfiore *et al.*, 2024; Richter *et al.*, 2020). A unique intra-varietal natural variation is known to be present within Pinot with bunch compactness, quality, and phenology being the major traits for clonal selection: to date, up to a thousand Pinot clones have been registered worldwide (Robinson *et al.*, 2012). In Pinot blanc, a few studies provided evidence of significant variation for wine characteristics and productivity (Regner *et al.*, 2018), while comparative studies regarding the sensitivity of different clones to bunch rot are lacking, such as for other cool-climate varieties like Riesling (Molitor *et al.*, 2018).

Therefore, the present study was carried out in five consecutive vintages (2019–2023) in an experimental vineyard located in a relatively cool and wet macroclimatic area of Trentino Alto-Adige (Valsugana, please see "Materials and methods") with the aim of: 1) detecting variation for agronomic (productivity, shoot fertility, bunch weight) and juice composition (sugar, acidity, yeast available nitrogen, potassium) traits between five commercially available Pinot blanc clones and one novel Pinot blanc clone (SMA102) selected within the clonal selection activities of Fondazione Edmund Mach; 2) evaluating bunch compactness and relative underlying traits associated with loose bunches (*i.e.*, number of berries per unit of rachis length, weight of berries per unit of rachis length); 3) assessing possible relationships between environmental conditions in different vintages, bunch rot incidence and cluster characteristics. The work provides evidence of clones characterised by a limited bunch rot sensitivity via a loose bunch while maintaining an appropriate productivity per plant.

MATERIALS AND METHODS

1. Vineyard establishment and experimental design

The experiments were conducted in an experimental vineyard over five vintages (2019, 2020, 2021, 2022, 2023) in Vigalzano (46.075381, 11.231058, Trento, Italy). The site is located at 520 m above sea level, has a sandy-loam soil with around 20 % slope, and it is south-southwest exposed. The vineyard was established in 2011 with five clones of Pinot blanc selected both at the Laimburg research Centre (Lb) and the Agenzia Regionale per lo Sviluppo Rurale ERSA (CREAVIT-ERSA, ersa) along with Friuli-Venezia Giulia region and CREA-VE: specifically, Lb16 and 18 and ersa140, 141, and 142. Additional information for each clone can be found in the national Italian database (http://catalogoviti.politicheagricole.it/result.php?codice=193). An additional biotype still not included in the national register and selected in San Michele all'Adige, was also planted (SMA102). Clones were assigned within the vineyard in a randomised design in blocks (seven vines per clone per block), and all vines were trained to "pergola semplice" with 3 m distance between rows and 0.7 m distance between vines. These materials were all grafted on Kober 5BB (up to 570 vines) rootstock. To exclude any potential influence of viral infections, and in accordance with the Italian phytosanitary regulations, all nursery materials employed in the study were tested for the presence of grapevine viruses using ELISA tests (Agritest, Bari; Faggioli *et al.*, 2013). The results confirmed that both the clonal selections and rootstocks were free from Grapevine fanleaf virus (GFLV), Arabis mosaic virus (ArMV), Grapevine leafroll-associated virus 1 (GLRaV-1), Grapevine leafroll-associated virus 3 (GLRaV-3), and Grapevine virus A (GVA). All the analyses listed below were performed on 50 vines per clone, spatially selected within at least five blocks per analysis (seven vines per block) to take into account the variability existing within the field. Vines were irrigated during the growing seasons via drip irrigation according to evapotranspiration requirements and via farm irrigation scheduling. Winter pruning was applied every year by the same operators, and the number of total buds was maintained similar between clones, while summer pruning and crop protection treatments were applied according to farm schedules.

2. Environmental data and bioclimatic indices

Environmental data, including mean temperature and precipitation were obtained from the Fondazione Edmund Mach weather station located approximately 150 m from the site (Pergine Valsugana, https://meteo.fmach.it/meteo/mappa.php) and growing degree days—weather-based indicator for assessing crop development—were calculated as the difference between the daily mean temperature and the base temperature (10 °C) and successively indicated as GDD10, by considering the period April to October. When the mean temperature was below the base temperature, a value of 0 was automatically assigned.

3. Vine balance assessment, bunch rot screening, and bud fruitfulness

For all the vines selected and for every vintage, traits associated with productivity and vine balance were collected. In certain vintages (*e.g.*, 2022 and 2023), only the mean bunch weight was directly quantified under laboratory conditions, as detailed below. Firstly, starting from 2019, each vine was assessed, and unproductive or inhomogeneous vines were discarded from the experiments. At BBCH18 (Lorenz *et al.*, 1995), the number of buds and shoots per vine was manually recorded, and the percentage of burst buds calculated. The number of inflorescences was also recorded, and bud fruitfulness was calculated as the average number of potential bunches per shoot. The same protocol was applied to both fruiting canes and spurs. At harvest and for each vine, all bunches were counted and collected to assess total plant productivity and mean bunch weight. The first screening to evaluate bunch sanitary status for each clone was carried out previous to harvest for the frequency or percentage of unhealthy (*i.e.*, mouldy) clusters over total observed (up to 100 bunches) as bunches with at least one unhealthy berry via visual inspection in the vineyard. Subsequently, a random pool of 100 bunches per clone were sampled and immediately shipped to the laboratory where the degree of fungal attack was divided into seven classes of damage severity by manually counting in the laboratory the total number of berries and the total number unhealthy berries: healthy, 1 %, 2–5 %, 6–10 %, 11–25 %, 26–50 %, and 51–75 % (Townsend & Heuberger, 1943). Vine balance was monitored after harvest as the ratio between vine productivity (kg) and wood pruning weight (kg) (Ravaz index).

4. Bunch morphological characteristics, bunch compactness

At harvest, 15 to 30 representative bunches per clone were taken to the laboratory and weighed individually with a balance. Afterwards, berries were carefully separated from the rachis and counted and weighed, while the rachis length was recorded. Mean berry weight was then calculated as the total weight of berries divided by the total number of berries. Berries were then individually assessed via visual inspection to evaluate whether fully developed seeds were present and qualitatively define the degree of stenospermocarpy. Bunch compactness was subsequently calculated as the ratio between berry weight and rachis length (*i.e.*, unit of weight per cm of rachis length).

5. Juice chemical composition

Harvest was carried out according to farm schedules (23 September 2019; 21 September 2020; 24 September 2021; 30 August 2022; 13 September 2023), and 10–30 bunches from each clone were collected. Bunches were then crushed, destemmed, and pressed at the same pressure for each sample. Samples of fresh juice were then analysed for pH, total soluble solids (TSS—°Brix), titratable acidity (TA—g/L as tartaric acid), tartaric and malic acid concentration (g/L), and yeast available nitrogen (YAN) (mg/L) using a WineScan Fourier Transform Infrared (FTIR) spectrometer (FOSS, Hillerød, Denmark).

6. Statistical analysis

All the phenotypic and environmental data were analysed via RStudio (R Core Team 2018) by using either the stats, agricolae, or ggplot2 packages. All traits were subjected to two-way ANOVA and one-way ANOVA depending on factor numbers (*i.e.*, Clone and Year). In some vintages, due to operational constraints, some traits were not assessed and therefore are not reported. Association between traits was assessed via linear regression, while Random Forest was used to select the variables with the highest discriminative weight between clones via mean decrease Gini. Principal components analysis (PCA) was then applied to the selected variables. Juice chemical composition was normalised for average values, and the deviation from the mean for each clone is shown regardless of the vintage. All data were checked for normality via the Shapiro–Wilk test. When present, means separation ($p < 0.05$) was carried out via Tukey's test.

RESULTS

The dynamic of the mean air temperature of the five vintages is shown in Figure 1A. Overall, the warmer conditions were experienced in 2022 (up to 1700 GDD10 cumulated over April–October) and 2023. The coolest years were 2020 and 2021 (1500 GDD10 cumulated) (Figure 1B). Average cumulative precipitation was similar between vintages (around 800 mm over April–October), with only 2022 showing a generally lower total amount (651 mm) (Figure 1C). However highest cumulative precipitation during August–September (*i.e.*, the period of maximum susceptibility of bunch to late rot due to structural changes, *i.e.*, post-veraison) was observed in 2022 (up to 250 mm) and 2020 (up to 200 mm), while the lowest was observed in 2023 (140 mm).

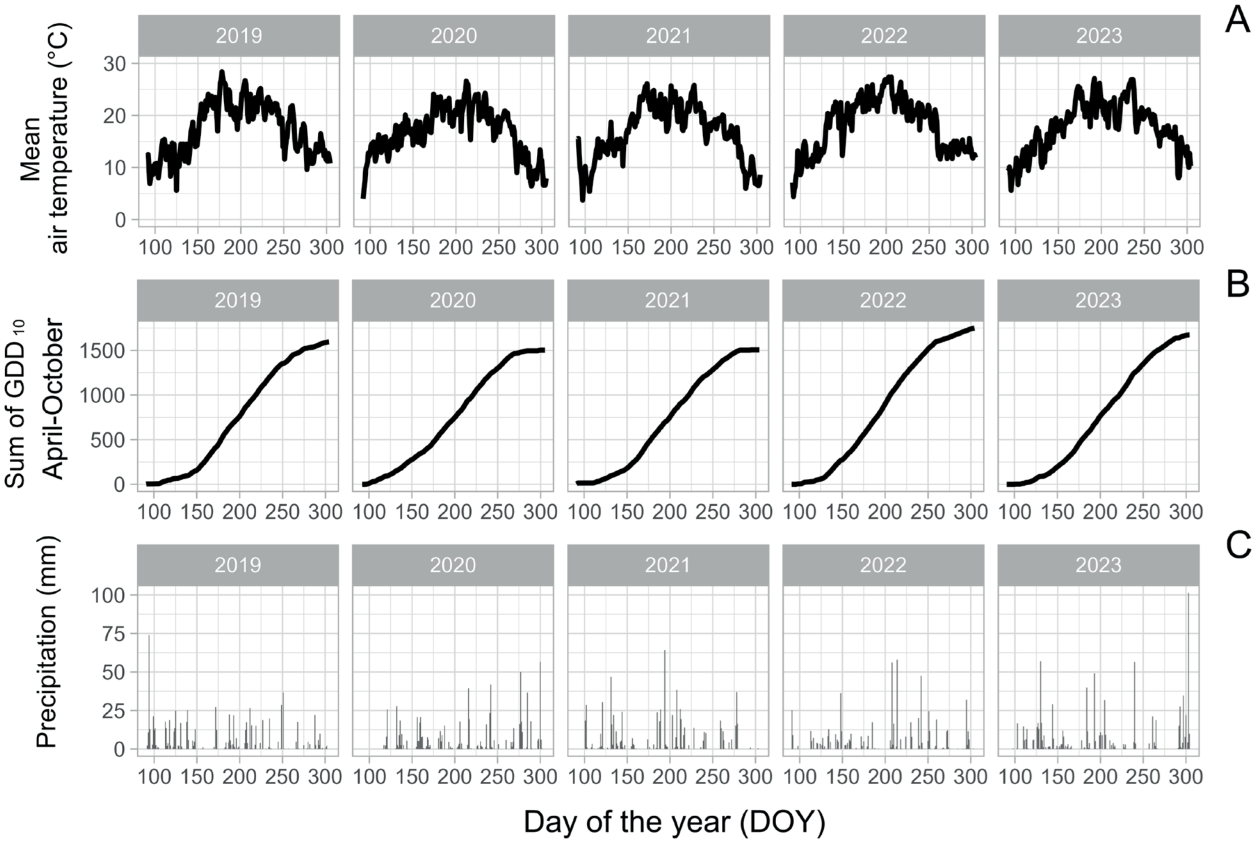

FIGURE 1. Time course of daily mean air temperature (°C; A), cumulative growing degree days on base 10 (GDD10; B), precipitation (mm; C) from 2019 to 2023 vintages. DOY represents the day of the year and covers the period between 1 April and 31 October.

The number of buds per vine was kept relatively constant between clones (p = 0.614), with a total average number between 24 and 18 buds per vine (Figure 2). No significant differences were observed overall for the number of shoots per plant and the percentage of budburst between clones (p = 0.761 and p = 0.611), while some trends were observed for the Year factor (p = 0.057, p = 0.093, respectively). Although no significant differences between clones and years were observed for the number of bunches per vine, there were significant variations for bud and shoot fruitfulness between Clone ($p < 0.05$) and Year ($p < 0.001$). In general, the highest bud and shoot fruitfulness were observed for the clone ersa142 (between 1–1.2 and 1.5–2, respectively), while the lowest was for SMA102 and Lb16.

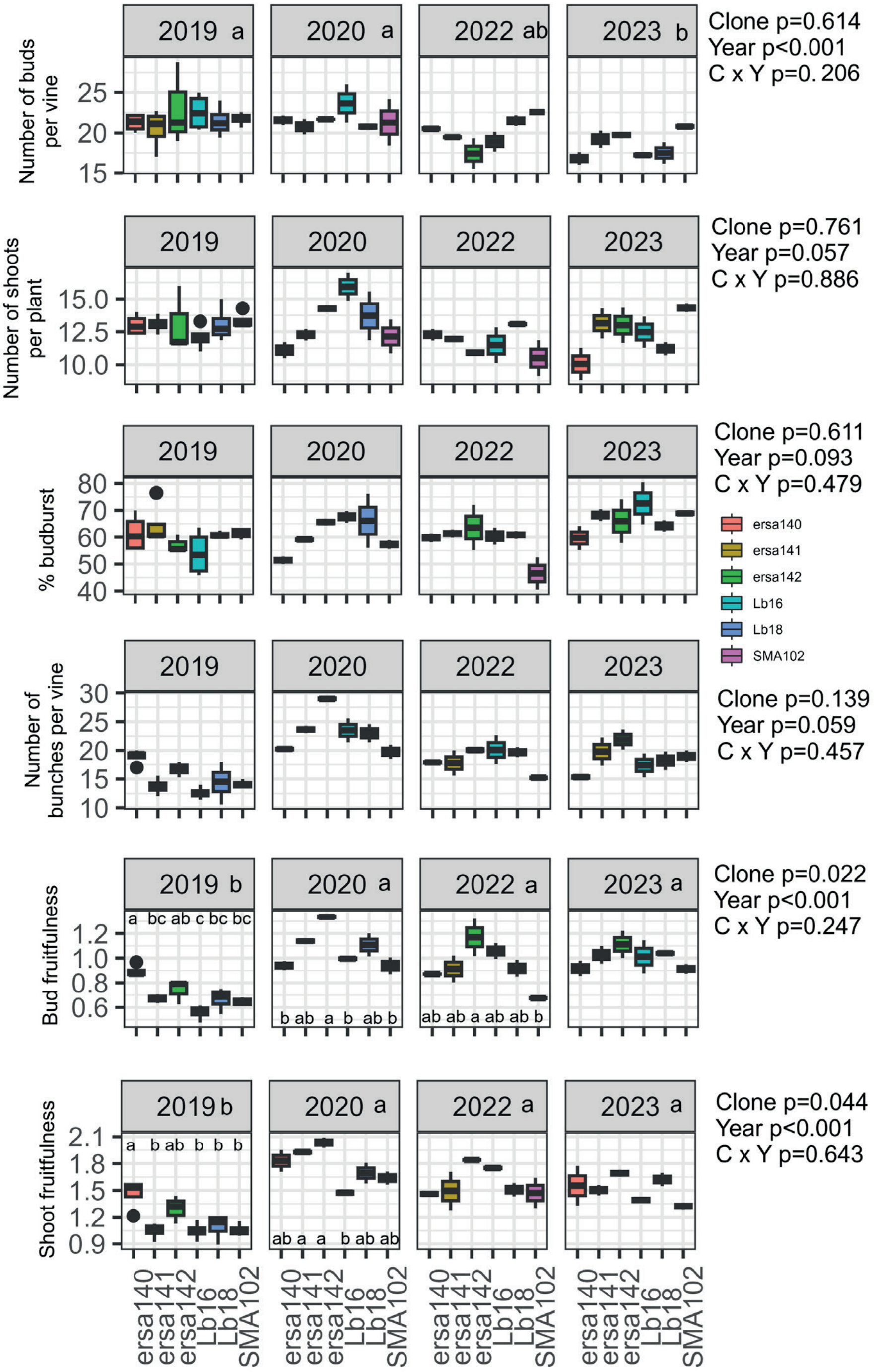

FIGURE 2. Number of buds per vine, number of shoots per vine, percentage of budburst, number of bunches per vine, bud fruitfulness, and shoot fruitfulness over four vintages (2019, 2020, 2022, and 2023) and for six Pinot blanc clones (ersa140, 141, 142; Lb16 and 18, and SMA102). The data represent average values of up to 50 vines. Data were analysed with two-way ANOVA with Clone and Year as factors, while p-values are shown in the graphs. When present, different letters represent significant differences (for either Year—within grey panels or Clone—within the graph) according to Tukey's test ($p < 0.05$).

Mean bunch weight was significantly different between clones, ranging from over 200 g in the Lb16 clone to 100 g for the ersa140 clone ($p < 0.001$; Figure 3). Significant differences were also observed for the Year factor ($p = 0.011$), with 2020 showing the overall lightest mean bunch weight. Productivity was overall variable, with generally ersa142 being the most productive clone (3 to 5 kg per vine), while ersa140 showed the lowest productivity (1.5–2 kg per vine). Lb16, 18, and SMA102 showed an average productivity between 2 and 4 kg per vine. Pruning weight was significant for Clone and Year ($p < 0.001$), with ersa140 showing the highest pruning weight, above all in the vintage 2021 (overall highest pruning weight). Ravaz index fluctuated between 1 and 6 kg/kg ($p < 0.001$) with ersa142 showing the highest values (5 kg/kg on average) and ersa140 the lowest (around 1.5 on average) (Figure 3).

The mean number of berries per bunch exhibited statistically significant variation among clones and across vintages ($p < 0.001$). In general, Lb16 was the clone with the highest number of berries per bunch (150 on average), while lower values were observed for ersa140 and SMA102 (100 on average) (Figure 4). Similarly, significant differences were observed for bunch length (rachis length), ranking from 12 to 16 cm depending on Clone and Year ($p < 0.001$). Lb16 possesses the longest bunch length, while SMA102 and ersa140 possess the shortest. Mean berry weight ranked from 1 to 2 g, with significant differences between clones: ersa140 had the lowest berry weight (1 g on average) while ersa142 showed the heaviest weight (up to 2 g). Lb16, 18 and SMA102 showed in between values (around 1.5–1.6 g on average). The percentage of seedless (stenospermocarpy) berries was higher in 2020 and 2021 (6 and 8 %) than, for

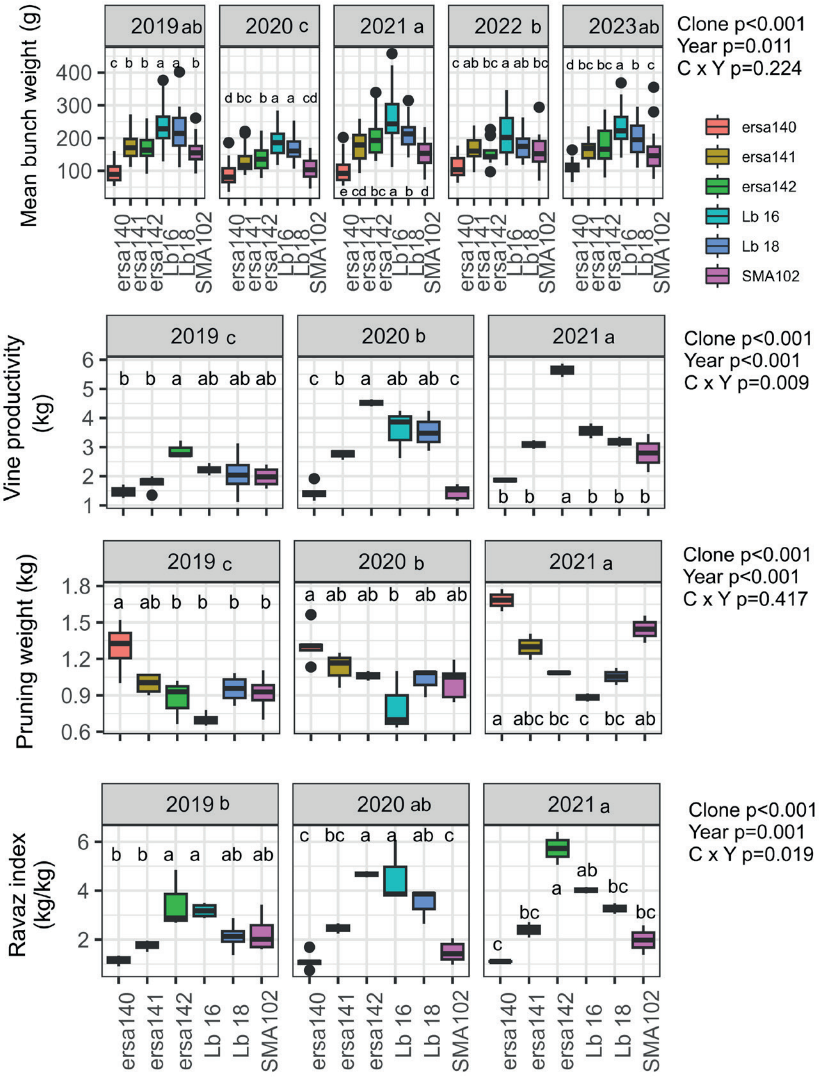

FIGURE 3. Mean bunch weight, vine productivity, pruning weight, and Ravaz index over five (2019, 2020, 2021, 2022, and 2023) or three vintages (2019, 2020, and 2021) and for six Pinot blanc clones (ersa140, 141, 142, Lb16, 18, and SMA102). The data represent average values of up to 50 vines. Data were analysed with two-way ANOVA with Clone and Year as factors, while *p*-values are shown in the graphs. When present, different letters represent significant differences (for either Year—within grey panels or Clone—within the graph) according to Tukey's test ($p < 0.05$).

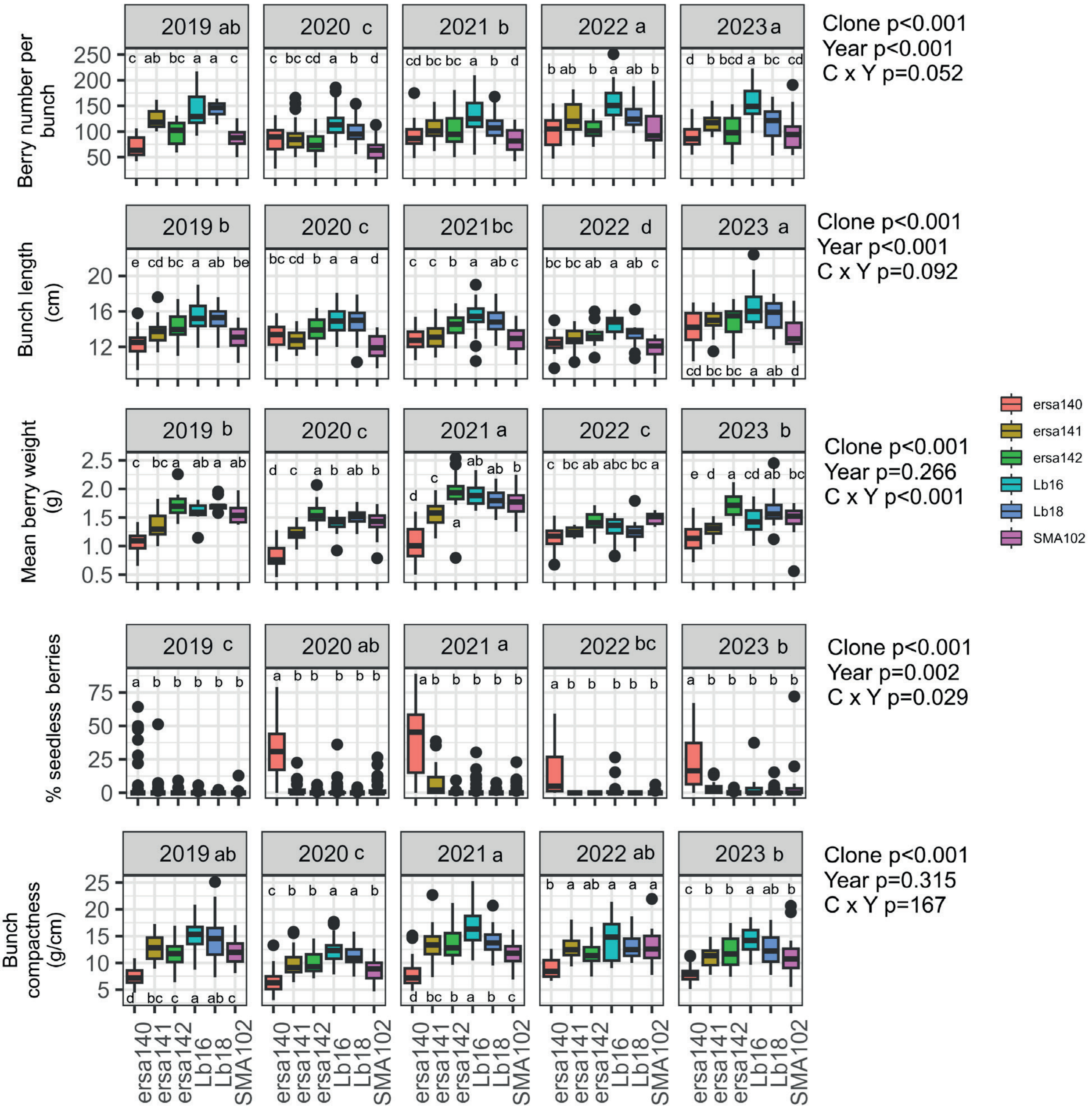

FIGURE 4. Average berry number per bunch, bunch length, mean berry weight, percentage of seedless berries, and bunch compactness over five vintages (2019, 2020, 2021, 2022, and 2023) and for six Pinot blanc clones (ersa140, 141, 142, Lb16, 18, and SMA102). The data represent average values of up to 50 vines. Data were analysed with two-way ANOVA with Clone and Year as factors, while *p*-values are shown in the graphs. When present, different letters represent significant differences (for either Year—within grey panels or Clone—within the graph) according to Tukey's test ($p < 0.05$).

example, 2019 (1.6 %) (p = 0.002). The highest rate of stenospermocarpy (up to 23 %) was shown by ersa140, followed by ersa141 (4 %).

Total soluble solutes at harvest were significantly different between clones, with ersa140 (20.4 °Brix) and ersa141 (20.0 °Brix) showing the highest values at harvest compared to ersa142 and Lb18 (18.4 °Brix) (p = 0.004, Figure 5). Significant variation for total acidity was also observed (p = 0.038, 7.86 g/L on average), and pH was significantly different between clones, although ersa140 and ersa141 showed the highest values (p < 0.001, 3.29 and 3.27, respectively). This was associated with an indeed higher concentration of tartaric acid (p < 0.001) for the abovementioned clones (up to 7.04 g/L) and associated with a non-significant difference for malic acid (p = 0.147, 4.72 g/L on average) yet a higher potassium concentration for ersa140 and ersa141 (p < 0.001, 1.6 g/L for both clones). Overall, yeast available nitrogen was statistically different between clones, with ersa140 and ersa141 showing higher values than all the other clones (p < 0.001, 323.67 and 296.33 g/L, respectively).

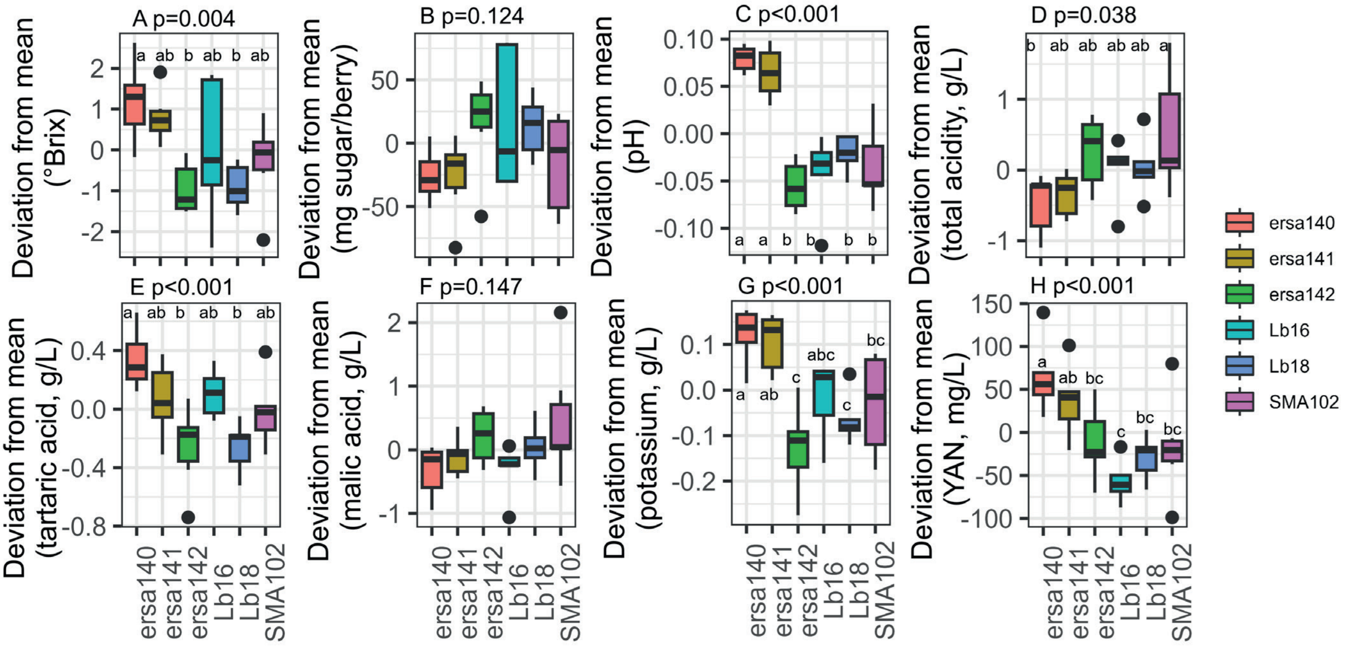

FIGURE 5. Deviation from the mean for total soluble solutes (°Brix), sugar content (mg of sugar per berry), total acidity (g/L), pH, tartaric acid (g/L), malic acid (g/L), potassium (g/L) and yeast available nitrogen (YAN, mg/L) over five vintages (2019, 2020, 2021, 2022 and 2023) and six Pinot blanc clones (ersa140, 141, 142, Lb16, 18 and SMA102) ($n = 5$). Data were analysed with one-way ANOVA with Clone as a factor, while *p*-values are shown in the graphs. When present, different letters represent significant differences according to Tukey's test ($p < 0.05$).

When sampled bunches were evaluated for incidence of bunch rot (divided into seven classes of damage, 120 to 147 bunches per clone depending on the year), significant variation was observed between clones (Figure 6). In particular, the lowest degrees of damage for the 2–5 %, 6–10 % and 11–25 % classes were observed for ersa140 and SMA102 when compared to ersa142 and, to some extent, ersa141, Lb16, and Lb18. This was overall accompanied by a total lower number of bunches with rot damage ($p = 0.041$) and lower frequency of rot damage ($p = 0.022$) for ersa140 and SMA102.

Rain Forest analysis highlighted seven major traits with high discriminative weight between clones, with a mean decrease Gini value up to 60 (Figure 7A). In the PCA analysis carried out on these seven variables (Figure 7B), PC1 and PC2 explained 63.2 % and 19.7 % of the variation, respectively, and a total variance of 82.9 %. PC1 loaded positively with bunch compactness, bunch weight, and length and berry number per bunch. PC2 loaded positively with the mean berry weight and negatively with the percentage of seedless berries. Clusters with a significant overlap between most of the clones were observed, while a distinct cluster was observed for the ersa140 clone. Indeed, trends were observed between average values of bunch compactness and frequency of rot damages ($p = 0.080$) (Figure 7C), while a linear and significant correlation was observed between the number of berries with seeds and bunch compactness ($p = 0.002$).

DISCUSSION

Substantial variation was observed for several traits over five vintages between Pinot blanc clones, including productivity, bunch morphology, rot incidence, and berry composition. Our data complements a previous study on clonal variation for Pinot blanc clones (Regner *et al.*, 2021) in which significant variability for vine yield and sugar accumulation, as well as aroma compounds, was observed. In our work, however, the Year factor often showed significance, suggesting a strong environmental influence for many traits, as expected and already reported in other grapevine varieties (Molitor *et al.*, 2018; Belfiore *et al.*, 2024). For instance, while for vine yield and other yield components (bunch weight, bud fruitfulness, number of bunches per vine), Year as a factor was frequently significant, only vine productivity had a significant Clone × Year interaction, suggesting divergences in vintage-driven response between clones. The ersa142 maintained a steady and high productivity compared to SMA102 or Lb18, for example, which reduced yield in 2020 and 2021, respectively. This may be attributed to differences in sensitivity to specific environmental conditions, in particular, low temperature during the growing season, which specifically hampered the mean berry weight for the two clones over the two distinct vintages (Srinivasan & Mullins, 1981). Part of this effect on the mean berry weight component was accompanied by an increase in the number of stenospermocarpic berries, suggesting a potential role of low ambient temperature in reproductive success and, in particular, in a reduction of pollen tube capacity for ovule

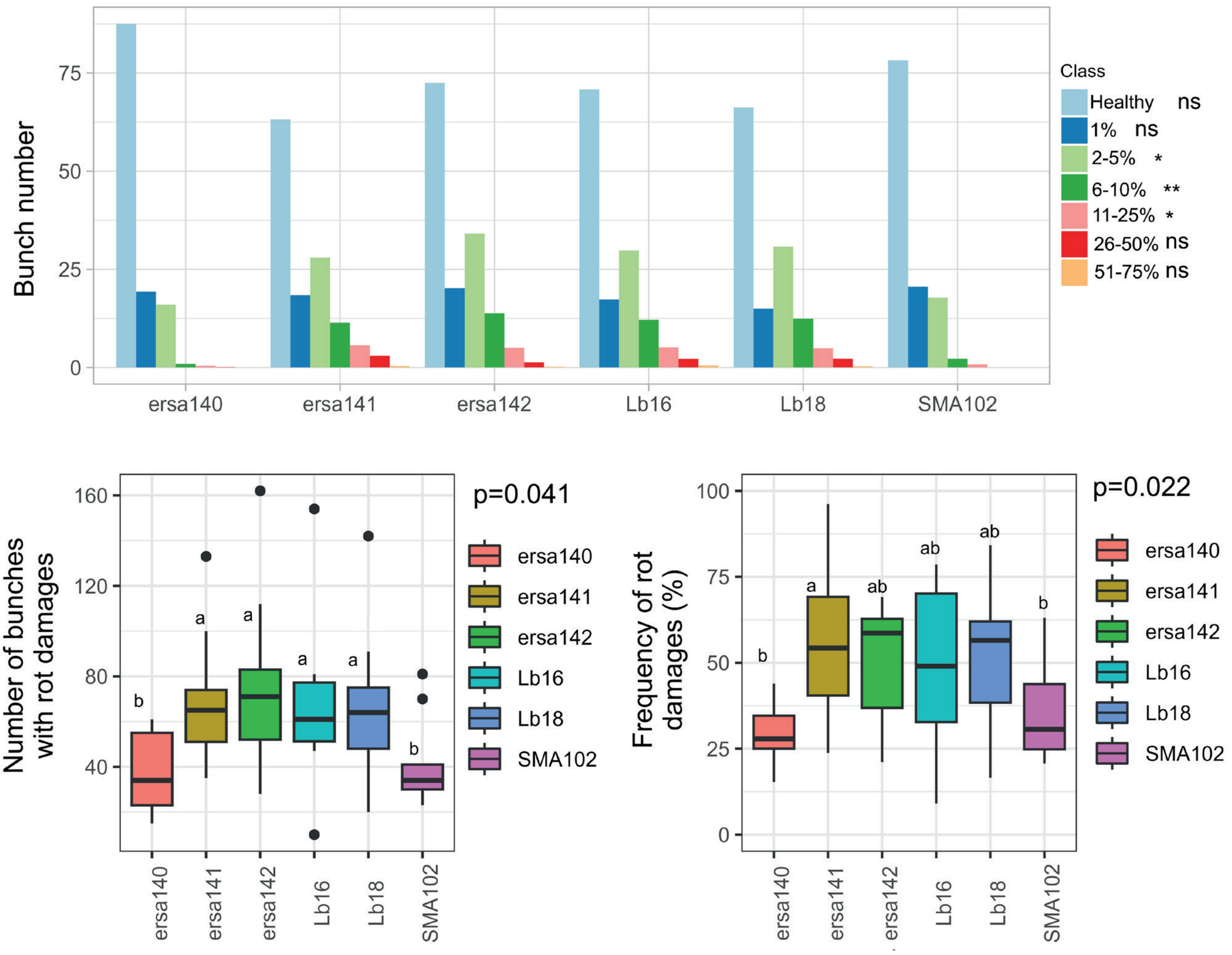

FIGURE 6. Distribution of bunch classes (seven classes, as shown in "Materials and methods") was assessed at harvest for all clones over five vintages. Number of bunches with rot damage and frequency of rot damage assessed at harvest over five vintages (2019, 2020, 2021, 2022, and 2023) and for six Pinot blanc clones (ersa140, 141, 142, Lb16, 18, and SMA102). Data were analysed with one-way ANOVA while *p*-values are shown in the graphs. When present, different letters represent significant differences according to Tukey's test ($p < 0.05$).

fertilisation (Ebadi *et al.*, 1995). Therefore, the significant Clone × Year interaction observed for productivity in these clones highlights the importance of considering their potentially unstable performance under varying climatic conditions. In particular, early events of low temperatures, considerably increasing owing to the advancements in budburst following climate change (Faralli *et al.*, 2024), may impact SMA102 and Lb18 more than others. Interestingly, no Clone × Year interaction was observed for fruitfulness (bud and shoot) traits, suggesting a more conserved behaviour between clones for these traits over years and, in particular, for mechanisms associated with primordia differentiation (Monteiro *et al.*, 2021). Vine yield per clone was indeed mainly driven by the number of bunches per vine and, to a lesser extent, by the number and weight of berries. The ersa142 clone had a consistently higher yield (up to 4.5 kg per vine) compared to the less productive ersa140 (1.7 kg per vine) and SMA102 (2.4 kg per vine). The difference in yield somehow reflected chemical composition at harvest, with the low-yielding clone (ersa140) showing higher total soluble solids and lower total acidity than the highly productive ones, for example, ersa142. This indicates that, assuming a relatively similar phenology (Umberto Malossini, personal communication), the lower crop load led to a faster ripening (Previtali *et al.*, 2021). To confirm this, while malic acid concentration was comparable between clones, tartaric acid concentration was higher in the ersa140 compared to the high-productive clones. Assuming a similar biosynthetic capacity for tartaric acid between clones (hence a similar pool at veraison) (Cholet *et al.*, 2016), the higher values for ersa140 can only be associated with berry water outflow (*i.e.*, tartaric acid concentration) and therefore a more advanced ripening. This was indeed confirmed by a lower sugar content per berry (yet not significant) for both ersa140 and ersa141 clones, suggesting that a concentration effect was occurring. The higher acidity in some clones (ersa140 and ersa141) was also accompanied by higher pH, mainly due to higher potassium concentration. Since potassium uptake in the berry is typically through the xylem (Villette *et al.*, 2020), which seems to stop in post-veraison after xylem disconnection (Mpelasoka *et al.*, 2003), this may be an intrinsic behaviour of specific clones.

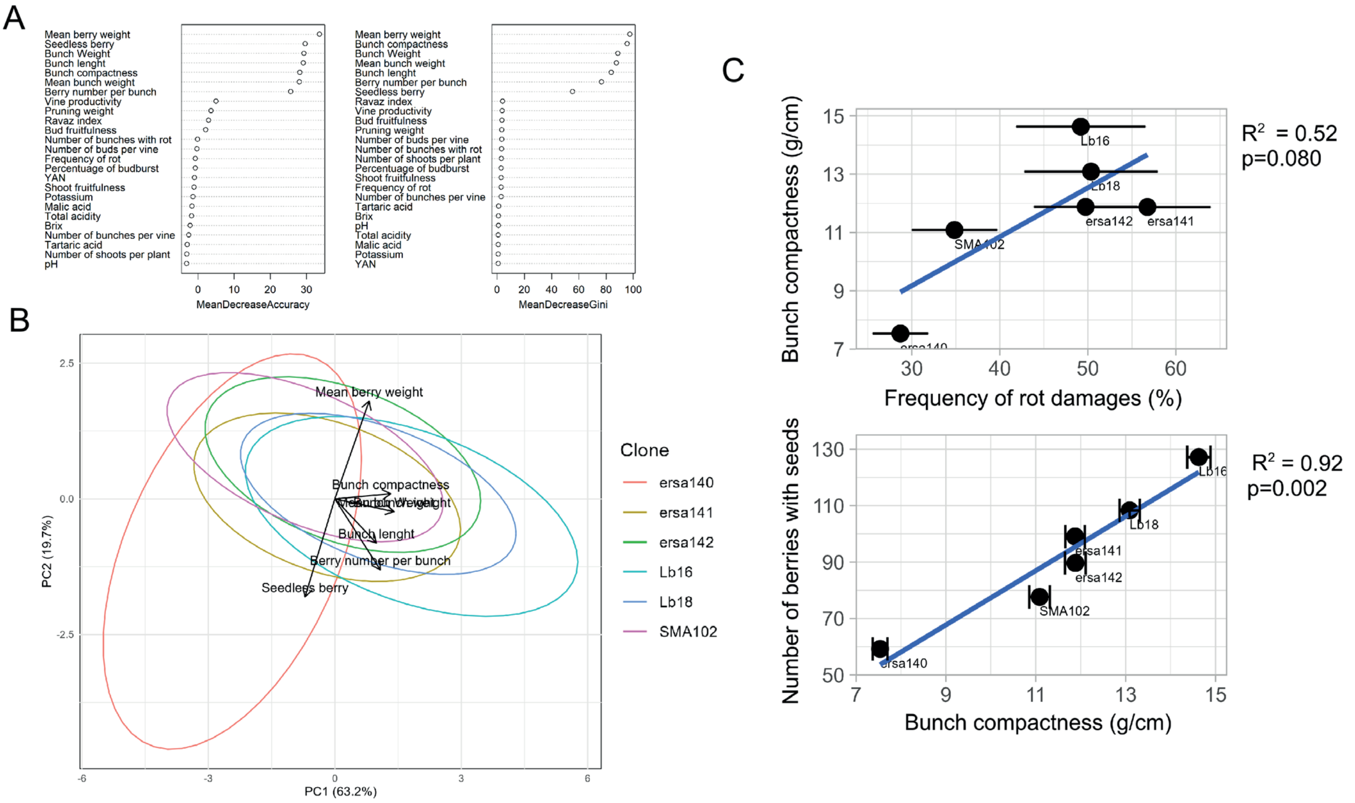

FIGURE 7. (A) Assessment of the traits' hierarchical importance via Random Forest analysis and (B) Principal component analysis for the seven most important traits assessed in (A). In (C) the association between traits of interest related to bunch compactness and bunch architecture. Analysis was carried out via linear regression, and error bars represent the standard error of the means (SEM). Goodness of fit and significance (*p*-value) of the regression are shown in the graphs.

The higher potassium accumulation in grapes causes the hydrogen ions from organic acids to be exchanged with potassium ions, thereby resulting in lower concentrations of free acids (especially tartaric acid; Wang *et al.*, 2024) and therefore explains the observed increase in juice pH. Although YAN levels were overall satisfactory for a problem-free fermentation (266.1 mg/L on average), the observed higher YAN levels for some clones may indeed be associated with solute concentration, although at this stage, only speculatively. Potential clonal effect may still be attributed to YAN variation, and further experiments may help define the observed trends.

Significant clonal variation for fruit set has been previously reported in Malbec (Calderón *et al.*, 2025) and Tempranillo (Tello *et al.*, 2021). This variation was attributed to atypical floral morphologies, reduced pollen viability and/or quantity, and impaired gamete viability—factors that, however, may contribute to increased susceptibility to environment-dependent fruit set disorders, such as millerandage. These reproductive abnormalities, consistently associated with reduced bunch compactness, may potentially explain our observed phenotype in Pinot blanc, in which, in addition, looser bunch architecture correlates with decreased bunch rot incidence (Tello & Ibáñez, 2018; Wegher *et al.*, 2022). Indeed, the analysis of seedless berries provides evidence of a significant relationship between bunch compactness and stenospermocarpy. While this is somehow expected due to the reduction in berry mass per unit of rachis length, and although a trend was observed (p = 0.080), there was no significant linear relationship between the frequency of rot damage and bunch compactness. Although speculative, one explanation for this may be due to the fact that loose bunches had a high degree of unfertilised flowers due to pollination failure: senescing anthers and ovaries are the source of inoculum for the infection of healthy berries (Tello & Ibanez, 2018). Therefore, loose bunches, although they resulted in better airflow and less contact between berries, resulted in a certain degree of infection (Grimplet *et al.*, 2019). In addition, other factors may determine tolerance to rot, mainly mechanical-physical properties of the skin and the grape in general (endo-mesocarp), resulting in compactness as only part of the tolerance mechanism: in fact, higher values of skin thickness may represent a physiological protection against rot, above all after stress conditions. We speculate that in our work, a combination of loose bunch traits and potential mechanical properties of the berries contributed to the reduction in rot incidence in some clones. Considering the increase in extreme events such as high precipitation, sustained humidity, and elevated temperatures—all critical environmental variables for rot incidence—this work highlights potential clones with sustained tolerance to bunch rot, likely supported by multiple bunch-related traits.

The expected relationship between bunch compactness and yield was evident in this work, suggesting how loose and therefore lighter bunches can dramatically reduce grapevine productivity. Some clones, in particular SMA102, resulted in an intermediate interaction between productivity and bunch rot frequency. Under mesoclimatic conditions in which bunch rot has a limited yet significant pressure, these clones may be suitable for high-quality wines, considering also the similar juice chemical composition compared to highly productive clones. Further work should focus on understanding the underlying physiological processes associated with a high rate of stenospermocarpy in some clones, but also on berry skin traits to better define the mechanisms associated with bunch rot tolerance in Pinot blanc.

CONCLUSIONS

Our work provides evidence of a broad variation for several agronomical and technological traits in six Pinot blanc clones grown under cool environmental conditions in northern Italy. The broad variation was associated with several traits, while specific trade-offs between yield and bunch compactness were detected, as well as yield and juice chemical parameters. While some clones with extremely loose bunches (6 g/cm) (*e.g.*, ersa140) may be suitable under cool-humid areas, at the expense of productivity, the highly productive ersa142 and Lb16 should be exploited under more temperate basins in which bunch rot pressure is low. The intermediate clones may be considered good in-between materials with partial tolerance to bunch rot, particularly SMA102 that is also balanced by an adequate productivity per vine. Further research will aim to elucidate the mechanisms underlying clonal variation, with the goal of identifying the physiological and morphological traits associated with enhanced bunch rot tolerance under high bunch rot pressure in Pinot blanc.

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REFERENCES

Becker, T. & Knoche, M. (2012). Water induces microcracks in the grape berry cuticle. *Vitis-Journal of Grapevine Research* 51, Nr. 3, 51(3), 141-142.

Belfiore, N., Lovat, L., Zanchin, A., Mian, G., Gaiotti, F., Franceschi, D., Marcuzzo, P., & Tomasi, D. (2024). Agronomic evaluation and adaptability of *Pinot gris* to an environment with high grey mould disease pressure: a comparative analysis on 17 clones. *OENO One*, 58(2). https://doi.org/10.20870/oeno-one.2024.58.2.7681

Bertamini, M., Faralli, M., Varotto, C., Grando, M. S., & Cappellin, L. (2021). Leaf monoterpene emission limits photosynthetic downregulation under heat stress in field-grown grapevine. *Plants*, 10(1), 181. https://doi.org/10.3390/plants10010181

Calderón, L., van Houten, S., Muñoz, C., Oroño, T., Bree, L., Bergamin, D., ... & Lijavetzky, D. (2025). Natural genetic variation for fruit set rate within Malbec grapevine (Vitis vinifera L.) clones. *BMC Plant Biology*, *25*(1), 606. https://doi.org/10.1186/s12870-025-06660-1

Cholet, C., Claverol, S., Claisse, O., Rabot, A., Osowsky, A., Dumot, V., ... & Gény, L. (2016). Tartaric acid pathways in *Vitis vinifera* L.(cv. Ugni blanc): a comparative study of two vintages with contrasted climatic conditions. *BMC plant biology*, 16, 1-18. https://doi.org/10.1186/s12870-016-0833-1

Díez-Méndez, A., García-Izquierdo, I., & Poveda, J. (2024). Microbial biological control of *Botrytis* bunch rot (*Botrytis cinerea*) of grapevine (*Vitis vinifera*) crops: a meta-analysis. *Crop Protection*, 107085. https://doi.org/10.1016/j.cropro.2024.107085

Ebadi, A., May, P., Sedgley, M., & Coombe, B. G. (1995). Effect of low temperature near flowering time on ovule development and pollen tube growth in the grapevine (*Vitis vinifera* L.), cvs Chardonnay and Shiraz. *Australian Journal of Grape and Wine Research*, 1(1), 11-18. https://doi.org/10.1111/j.1755-0238.1995.tb00072.x

Emanuelli, F., Battilana, J., Costantini, L., Le Cunff, L., Boursiquot, J. M., This, P., & Grando, M. S. (2010). A candidate gene association study on muscat flavor in grapevine (*Vitis vinifera* L.). *BMC plant biology*, 10, 1-17. https://doi.org/10.1186/1471-2229-10-241

Faggioli, F., Anaclerio, F., Angelini, E., Antonelli, M. G., Bertazzon, N., Bianchi, G., Bianchedi, P., Bianco, P. A., Botti, S., Bragagna, P., Cardoni, M., Casati, P., Credi, R., De Luca, E., Durante, G., Gianinazzi, C., Gambino, G., Gualandri, V., Luison, D., Luvisi, A., Malossini, U., Mannini, F., Saldarelli, P., Terlizzi, F., Triolo, E., Trisciuzzi, N., & Barba, M. (2013). Harmonization and validation of diagnostic protocols for the detection of grapevine viruses covered by phytosanitary rules. *Advances in Horticultural Science*, 27 (3), pp. 107-108. https://doi.org/10.36253/ahsc-18433

Faralli, M., Mallucci, S., Bignardi, A., Varner, M., & Bertamini, M. (2024). Four decades in the vineyard: the impact of climate change on grapevine phenology and wine quality in northern Italy. *OENO One*, 58(3). https://doi.org/10.20870/oeno-one.2024.58.3.8083

Gabler, F. M., Smilanick, J. L., Mansour, M., Ramming, D. W., & Mackey, B. E. (2003). Correlations of morphological, anatomical, and chemical features of grape berries with resistance to *Botrytis cinerea. Phytopathology*, 93(10), 1263-1273. https://doi.org/10.1094/PHYTO.2003.93.10.1263

Grimplet, J., Ibáñez, S., Baroja, E., Tello, J., & Ibáñez, J. (2019). Phenotypic, hormonal, and genomic variation among *Vitis vinifera* clones with different cluster compactness and reproductive performance. *Frontiers in plant science*, 9, 1917. https://doi.org/10.3389/fpls.2018.01917

Hed, B., Ngugi, H. K., & Travis, J. W. (2009). Relationship between cluster compactness and bunch rot in Vignoles grapes. *Plant disease*, 93(11), 1195-1201. https://doi.org/10.1094/PDIS-93-11-1195

Kretschmer, M., Kassemeyer, H. H., & Hahn, M. (2007). Age-dependent grey mould susceptibility and tissue-specific defence gene activation of grapevine berry skins after infection by *Botrytis cinerea. Journal of Phytopathology*, 155(5), 258-263. https://doi.org/10.1111/j.1439-0434.2007.01216.x

Lorenz, D. H., Eichhorn, K. W., Bleiholder, H., Klose, R., Meier, U., & Weber, E. (1995). Growth Stages of the Grapevine: Phenological growth stages of the grapevine (*Vitis vinifera* L. ssp. *vinifera*)—Codes and descriptions according to the extended BBCH scale. *Australian Journal of Grape and Wine Research*, 1(2), 100-103. https://doi.org/10.1111/j.1755-0238.1995.tb00085.x

Malossini, U., Zulini, L., Moser, S., Versini, G., Carlin, S., Nicolini, G., Bianchedi, P., Dalla Serra, A. (2006). Agronomical and enological performances of heat-treated vs. GFLV-infected Gewürztraminer clones in Trentino (N-East Italy). In: 15th Meeting of the international council for the study of virus and virus-like diseases of the grapevine (ICVG). Stellenbosch: *South African society for enology and viticulture*: 226-227. ISBN: 1868493180.

Molitor, D., Baus, O., Hoffmann, L., & Beyer, M. (2016). Meteorological conditions determine the thermal-temporal position of the annual Botrytis bunch rot epidemic on *Vitis vinifera* L. cv. Riesling grapes. *Oeno One*, 50(4). https://doi.org/10.20870/oeno-one.2016.50.3.36

Molitor, D., Biewers, B., Junglen, M., Schultz, M., Clementi, P., Permesang, G., ... & Berkelmann-Löhnertz, B. (2018). Multi-annual comparisons demonstrate differences in the bunch rot susceptibility of nine *Vitis vinifera* L.'Riesling'clones. *Vitis*, 57(1).

Monteiro, A. I., Malheiro, A. C., & Bacelar, E. A. (2021). Morphology, physiology and analysis techniques of grapevine bud fruitfulness: A review. *Agriculture*, 11(2), 127. https://doi.org/10.3390/agriculture11020127

Mpelasoka, B. S., Schachtman, D. P., Treeby, M. T., Thomas, M. R. (2003). A review of potassium nutrition in grapevines with special emphasis on berry accumulation. *Australian Journal of Grape and Wine Research*. 9 (3), 154–168. https://doi.org/10.1111/j.1755-0238.2003.tb00265.x

OIV. (2023). International Organization of Vine and Wine.

Palliotti, A., Gardi, T., Berrios, J. G., Civardi, S., & Poni, S. (2012). Early source limitation as a tool for yield control and wine quality improvement in a high-yielding red *Vitis vinifera* L. cultivar. *Scientia Horticulturae*, 145, 10-16. https://doi.org/10.1016/j.scienta.2012.07.019

Portu, J., Baroja, E., Rivacoba, L., Martínez, J., Ibáñez, S., & Tello, J. (2024). Evaluation of the intra-varietal diversity of 'Tempranillo Tinto'clones prospected in the demarcated winemaking region of Rioja (Spain). *Scientia Horticulturae*, *329*, 113015. https://doi.org/10.1016/j.scienta.2024.113015

Previtali, P., Dokoozlian, N. K., Pan, B. S., Wilkinson, K. L., & Ford, C. M. (2021). Crop load and plant water status influence the ripening rate and aroma development in berries of grapevine (*Vitis vinifera* L.) cv. Cabernet Sauvignon. *Journal of Agricultural and Food Chemistry*, 69(27), 7709-7724. https://doi.org/10.1021/acs.jafc.1c01229

Regner, F., Philipp, C., Reichl, M., Hack, R., Eder, P., Rockenbauer, A., ... & Endler, A. (2021). Comparison of clones of the grapevine variety 'Pinot blanc'.

Regner, F., Philipp, C., Reichl, M., Zöch, B., Hack, R., Prammer, N., & Rockenbauer, A. (2018). Investigating variability of the cultivar 'Pinot blanc' under different aspects. In *XII International Conference on Grapevine Breeding and Genetics 1248* (pp. 445-456). https://doi.org/10.17660/ActaHortic.2019.1248.62

Regner, F., Stadlbauer, A., Eisenheld, C., & Kaserer, H. (2000). Genetic relationships among Pinots and related cultivars. *American Journal of Enology and Viticulture*, 51(1), 7-14. https://doi.org/10.5344/ajev.2000.51.1.7

Richter, R., Rossmann, S., Gabriel, D., Töpfer, R., Theres, K., & Zyprian, E. (2020). Differential expression of transcription factor- and further growth-related genes correlates with contrasting cluster architecture in *Vitis vinifera* 'Pinot Noir'and *Vitis* spp. genotypes. *Theoretical and Applied Genetics*, 133(12), 3249-3272. https://doi.org/10.1007/s00122-020-03667-0

Robinson, J., Harding, J., & Vouillamoz, J. (2012). Wine grapes: a complete guide to 1,368 vine varieties, including their origins and flavours. Penguin UK.

Sapkota, S., Chen, L. L., Yang, S., Hyma, K. E., Cadle-Davidson, L., & Hwang, C. F. (2019). Construction of a high-density linkage map and QTL detection of downy mildew resistance in *Vitis aestivalis*-derived 'Norton'. *Theoretical and applied genetics*, 132, 137-147. https://doi.org/10.1007/s00122-018-3203-6

Srinivasan, C., & Mullins, M. G. (1981). Physiology of flowering in the grapevine—a review. *American Journal of Enology and Viticulture*, 32(1), 47-63. https://doi.org/10.5344/ajev.1981.32.1.47

Steel, C. C., Blackman, J. W., & Schmidtke, L. M. (2013). Grapevine bunch rots: impacts on wine composition, quality, and potential procedures for the removal of wine faults. *Journal of agricultural and food chemistry*, 61(22), 5189-5206. https://doi.org/10.1021/jf400641r

Tello, J., & Ibáñez, J. (2018). What do we know about grapevine bunch compactness? A state-of-the-art review. *Australian Journal of Grape and Wine research*, 24(1), 6-23. https://doi.org/10.1111/ajgw.12310

Tello, J., Aguirrezábal, R., Hernáiz, S., Larreina, B., Montemayor, M. I., Vaquero, E., & Ibáñez, J. (2015). Multicultivar and multivariate study of the natural variation for grapevine bunch compactness. *Australian Journal of Grape and Wine research*, 21(2), 277-289. https://doi.org/10.1111/ajgw.12121

Tello, J., Royo, C., Baroja, E., García-Escudero, E., Martínez-Zapater, J. M., & Carbonell-Bejerano, P. (2021). Reduced gamete viability associated to somatic genome rearrangements increases fruit set sensitivity to the environment in Tempranillo Blanco grapevine cultivar. *Scientia Horticulturae*, *290*, 110497. https://doi.org/10.1016/j.scienta.2021.110497

Townsend, G. R., & Heubergeb, J. W. (1943). Methods for estimating losses caused by diseases in fungicide experiments, *Plant Disease Reporter*, *27*, 340–343.

Vezzulli, S., Leonardelli, L., Malossini, U., Stefanini, M., Velasco, R., & Moser, C. (2012). Pinot blanc and Pinot gris arose as independent somatic mutations of Pinot noir. *Journal of Experimental Botany*, 63(18), 6359-6369. https://doi.org/10.1093/jxb/ers290

Villette, J., Cuéllar, T., Verdeil, J.-L., Delrot, S., & Gaillard, I. (2020). Grapevine Potassium Nutrition and Fruit Quality in the Context of Climate Change. *Frontiers in Plant Science* 11, 123. https://doi.org/10.3389/fpls.2020.00123

Wang, J., Lu, Y., Zhang, X., Hu, W., Lin, L., Deng, Q., ... & Lv, X. (2024). Effects of potassium-containing fertilizers on sugar and organic acid metabolism in grape fruits. *International Journal of Molecular Sciences*, 25(5), 2828. https://doi.org/10.3390/ijms25052828

Wegher, M., Faralli, M., & Bertamini, M. (2022). Cluster-zone leaf removal and GA3 application at early flowering reduce bunch compactness and yield per vine in *Vitis vinifera* cv. Pinot Gris. *Horticulturae*, 8(1), 81. https://doi.org/10.3390/horticulturae8010081

Wilcox, W. F. (2016). Botrytis Bunch Rot: A Disease Requiring Integrated Control.

Wilcox, W. F., Gubler, W. D., & Uyemoto, J. K. (Eds.). (2015). Compendium of grape diseases, disorders, and pests (pp. 39-45). St. Paul, MN, USA: APS Press, *The American Phytopathological Society.* https://doi.org/10.1094/9780890544815