Chemical and Biological Technologies in Agriculture

RESEARCH

Variations of elements, pigments, amino acids and secondary metabolites in *Vitis vinifera* (L.) cv Garganega after 501 biodynamic treatment

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Abstract

Background: There is a need for new approaches in agriculture to improve safety of final products as well as to increase environmental acceptability. In this paper, the biodynamic preparation 501 (horn silica) was sprayed on *Vitis vinifera* (L.) cv Garganega plants in two vineyards located in Veneto region, North-East Italy. Leaf samples were collected on the day of 501-treatment and 11 days later, and berries were sampled at harvest time. Leaves and berries samples were analysed combining targeted and untargeted measurements related to primary metabolism (pigment, element and amino acid contents) and to secondary metabolism. Chlorophyll content in leaves, and amino acid and element (C, N, S) analysis in berries were combined with untargeted UPLC-QTOF metabolomics.

Results: The discriminant compounds related to the 501-treatment were annotated on the basis of accurate MS and fragmentation and were identified as secondary metabolites, namely phenolic constituents belonging to the shikimate pathway. The level of most of the identified compounds increased in plants treated with 501 preparation.

Conclusions: Results highlight the prominent value of the metabolomic approach to elucidate the role of the 501 applications on grapevine secondary metabolism.

Keywords: Metabolomics, Horn silica, Secondary grapevine metabolites, OPLS-DA, HR-MS

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Graphical Abstract
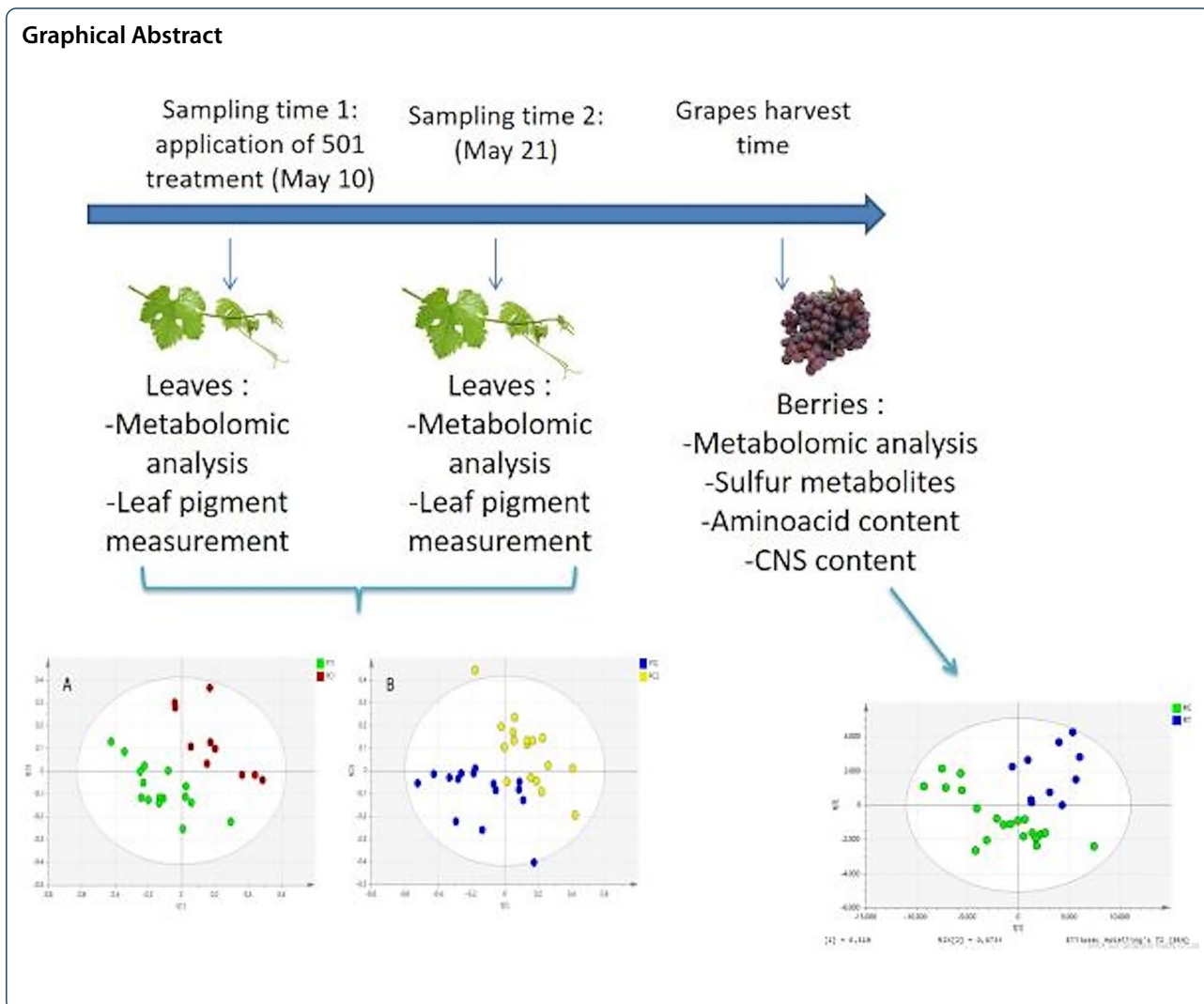
Background

Conventional agriculture relies upon intense utilization of chemical inputs. Visible consequences are the reduction of soil organic matter content, the rise of soil desertification, the chemical contamination of soil and surface and underground water. To counteract this alarming trend, actions for sustainable approaches in agriculture have been implemented in the last years [1]. Organic farming, agro-ecology, permaculture and biodynamic farming are the most diffuse alternative systems to conventional agriculture [2].

Biodynamic agriculture was developed by Rudolf Steiner in 1924 [3], who proposed the use of preparations (numbered from 500 to 508) to be applied on soil, over crops, and in compost pile, with the main aim to improve soil vitality and plant growth and health.

Biodynamic farming emphasizes biodiversity, takes into consideration the influence of celestial bodies and promotes the concept of farm as an organism. Although biodynamics is internationally recognized as a valuable farming system, studies on the effects of the preparations on soil and plants are limited.

Viticulture is an important branch in the agricultural sector of many countries, including Italy. The spread of several chemical compounds to control pathogens, parasites and weeds in vineyards has raised concerns among consumers, producers and policy-makers about the possible negative impacts on the ecosystem and human health [4]. Alternative approaches for a more sustainable grapevine cultivation are then desirable. In the last decades, several winegrowers approached the biodynamic method [5], as a concrete way to encounter the increasing demand of consumers on the quality and sustainability of grape and wine production.

Following Steiner's indications, the biodynamic preparation 500 consists on fresh cow manure placed inside a

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cow horn buried in the top soil during the autumn–winter months, and preparation 501 is pure quartz powder left in spring–summer time in a cow horn buried in the top soil. The preparation 500 is commonly distributed on the soil at a rate of 100 g/ha in Autumn and in Spring, while 501 is spread over the canopy using 3–5 g/ha one or more times during the plant vegetative growth, depending on the seasonal climatic trend. The distribution of the preparations in the vineyards was found to enhance the vegetative–reproductive balance of grape plants [6]. Positive effects on the application of preparations on the soil microbiology and fertility [7, 8], and on the plant resistance to biotic and abiotic stresses, were also evidenced in different grape varieties [9, 10]. Picone et al. found changes in grape berry metabolome due to biodynamic management, likely related to physiological response of the plants treated with preparations [11]. The application of horn silica preparation (501) was noticed to positively affect the quality of grapes and wines [12, 13].

Variations on different biochemical compounds, such as total polyphenols, anthocyanins polymeric pigments and phytocompounds, like catechin, cyanidin-3-glucoside, flavonoid, esters, protocatechuic acid, resveratrol and quercetin were reported in berries and wines after the spreading of preparations [10]. To validate the effect of biodynamic preparations, various approaches have been used, including conventional measurements used in agronomic trials, but also spectral techniques as nuclear magnetic resonance for metabolic confirmation [11, 14].

The analyses on sugars, amino acids and some carboxylic acids content in berry juice are routinely performed using enzymatic methods or some high-pressure liquid chromatography approaches [15]. More advanced techniques, combining the ultra performance liquid chromatography with the high-resolution mass spectrometry, offer comprehensive and unbiased approaches of metabolomics. Larger amount of information can be obtained about different groups of compounds in grape tissues, juices and wines than the traditional targeted analysis [15].

The aim of this study was to assess possible metabolic changes induced by the application of preparation 501 in plants of *Vitis vinifera* cv Garganega grown in two separate vineyards. The level of leaf chlorophyll content can be considered a marker of the plant nitrogen status and an indicator of the plant tolerance to various stresses [16]. Berry composition of carbon, nitrogen and sulfur is known to influence the quality of wine, being N and S essential elements for flavours compounds [17]. Some amino acids are precursors of important wine compounds and are nitrogen sources for the growth of yeast

in the grape must [17]. Usually, the most abundant amino acids in grapes are arginine and proline [18].

The targeted analysis of amino acid and element (C, N, S) content in berries, of pigment level in leaves, were combined with untargeted UPLC-QTOF metabolomic analysis performed both in leaves and berries. The data comparison between the 501-treated and control plants was performed with the aim to discover whether or not the spray of preparation 501 over the grapevine plants may have influenced the leaf chlorophyll content, the berries element and amino acid composition and the secondary metabolism of both leaves and berries.
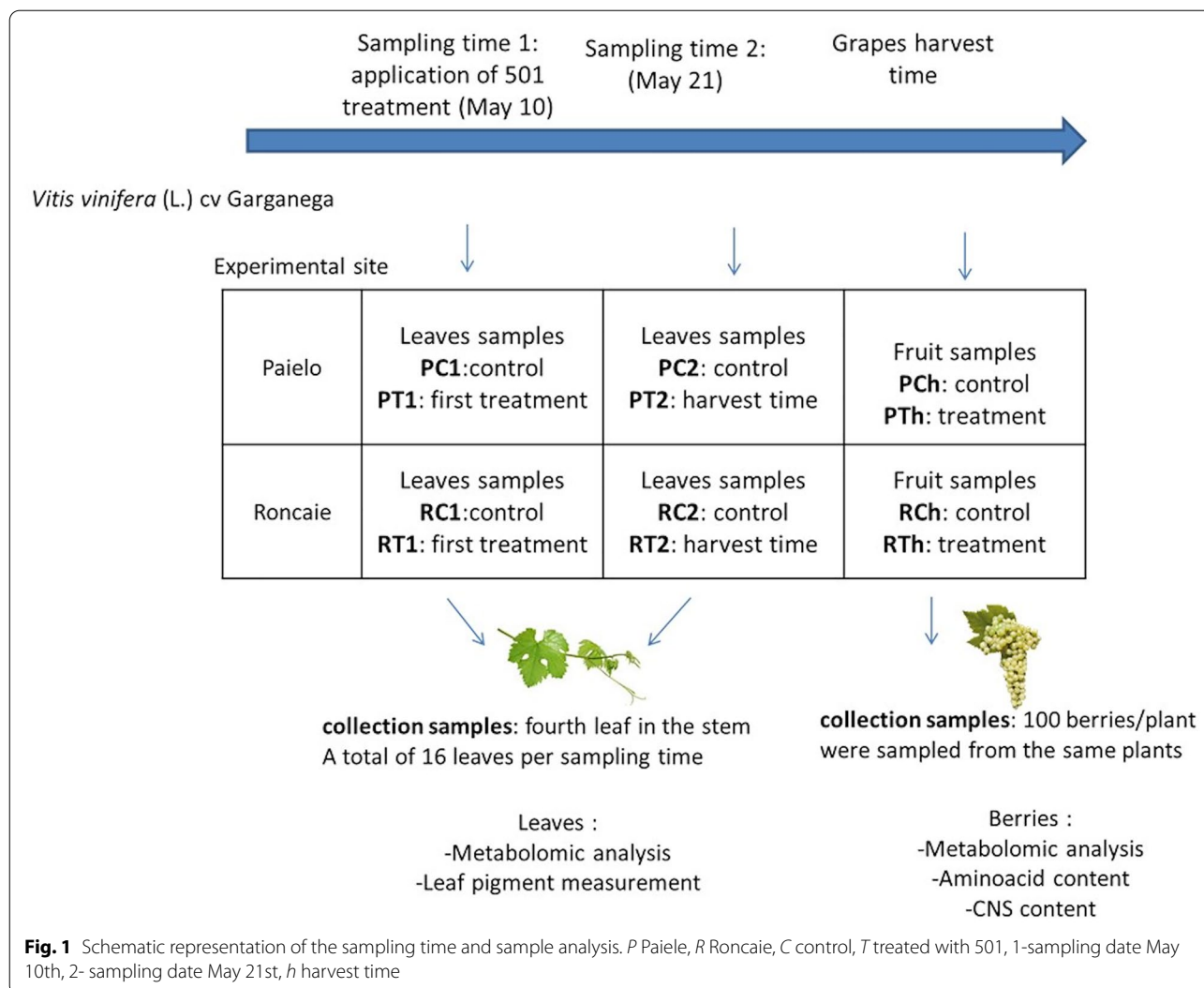
Materials and methods
Experimental site and sampling
The experiment was performed in two vineyards, Roncaie (R) and Paiele (P), located in Gambellara, Vicenza county, North-East of Italy (45°27′44″N 11°20′00″E). The Roncaie vineyard (1 ha) is separated from Paiele (0.5 ha) by a distance of about 500 m. Both vineyards are positioned in East–West direction. In both vineyards, plants of *Vitis vinifera* L. cv Garganega (20–30 years old) are grown with "tendone" as training system and biodynamically managed since 2005 with the use of preparations 500 and 501. The two vineyards, Paiele and Roncaie, were chosen to assess any possible variation due to location.

In each vineyard, a plot of six rows with 25 vines per each row was selected. Three rows were left as control (no 501 treatment) and three rows were spread with 501. The two inner rows (one with and one without 501 treatment) were considered as buffer rows and only the remaining rows were used for sampling and data collection. The preparation 501 was obtained from the certified biodynamic preparations dealer Le madri (Rolo, Italy). In the early morning of May 10th, 3 g of 501 were dissolved in 50 L of rain water and mixed for 1 h, in order to have sufficient solution to treat 1 ha canopy. The solution was manually spread over the grape canopy in both the vineyards. Concomitantly, the control plants were sprayed with the same volume of rain water only.

Leaves samples were collected 6 h after the 501 treatment (sampling 1, May 10th, 2018) and 11 days later (sampling 2, May 21st, 2018) from four randomly chosen plants in each row. The fourth leaf, starting from the base of the shoot, was detached, immediately transferred in a plastic bag and frozen with liquid nitrogen. A total of 16 leaves per sampling time was collected from both control and treated plants in each plot. All the samples were then stored in − 20 freezer until analysis.

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Fig. 1 Schematic representation of the sampling time and sample analysis. *P* Paiele, *R* Roncaie, *C* control, *T* treated with 501, 1-sampling date May 10th, 2- sampling date May 21st, *h* harvest time

At harvest time, the 27th September, 2018, about 100 berries/plant were sampled from the same plants where leaves were collected and transferred in plastic bag and frozen, using the same procedure of the leaf samples.

A schematic description of the sample timing and analyses is reported in Fig. 1.

Leaf pigment measurement

Frozen leaves were cut in small pieces exactly weighted (200 mg), crashed in mortar with 5 mL ethanol 95%(v/v), and then transferred in volumetric flask with the addition of ethanol to the final volume of 10 mL. Flasks were stored at 4 °C in dark condition for 24 h. The surnatant was filtered and used to measure UV absorbance at 665, 649, and 470 nm with Elios α spectrophotometer (Thermo). The concentration of chlorophylls *a* and *b* was then calculated [19].

Metabolomics analysis

Sampled leaves were cut in small pieces exactly weighted (200 mg) and extracted using ultrasound assisted extraction with 10 mL methanol 90% (v/v) for 10 min. Extracts were centrifuged at 13,000 rpm for 10 min and used for analysis. Berries were crushed in a mortar, and the obtained juice (20 mL) was centrifuged, filtered 0.45 μ and used for analysis. Each biological replicate was obtained from three pool samples and analysed in triplicate.

To obtain a metabolomic profile of the leaves and berries, a UPLC–HR-MS full-scan method was used. Waters H-Class UPLC system equipped with a Waters Xevo G2 Q-TOF mass spectrometer was employed. The detector was equipped with an electrospray (ESI) ionization source and was operating in negative ion mode. The sampling cone voltage was adjusted at 40 V, the

source offset at 80 V. The capillary voltage was adjusted to 1500 V. The nebulizer gas used was N_2 at a flow rate of 800 L h^{-1}. The desolvation temperature was 450 °C. The mass accuracy and reproducibility were maintained by infusing lockmass (leucine–enkephalin, $[M-H]^-$ *m/z* 554.2620) through Lockspray at a flow rate of 20 µL min^{-1}. Centroided data were collected for each sample in the mass range 50–1200 Da, and the *m/z* value of all acquired spectra was automatically corrected during acquisition based on lockmass. An Agilent XDB C-8 column (2.1 mm × 150 mm, 3.5 µm) was used as stationary phase. The mobile phase was composed of solvent A (acetonitrile with 0.1% formic acid) and solvent B (water with 0.1% formic acid). Linear gradients of solvents A and B were used, as follows: 0 min, 10% A; 10 min, 85% A; 11 min, 100% A; 12 min, 10% A; 12.5 min, 10% A. The flow rate was 300 µL min^{-1} and the injection volume was 1 µL. Pool samples were prepared mixing equal amount of all samples. To control instrument performance during run sequence of samples were randomized and each 6 injection pool samples were injected.

Data extraction and analysis: centroided and integrated chromatographic mass data were processed by MarkerLynx Applications Manager version 4.1 (Waters) to generate a multivariate data matrix. A method for data deconvolution, alignment and peak detection was created and the data were subsequently elaborated by the software. The parameters used were retention-time range 1.00–19.00 min, mass range 100–1200 Da, mass tolerance 0.01 Da, noise elimination level was set to 6.00, minimum intensity was set to 12% of base peak intensity, maximum masses per RT was set to 6 and, finally, RT tolerance was set at 0.01 min. A list of the ion intensities of each peak detected was generated, using retention time and the *m/z* data pairs as the identifier for each ion. The resulting three-dimensional matrix contains arbitrarily assigned peak index (retention time-*m/z* pairs), sample names (observations), and ion intensity information (variables). As first step, the matrix was composed of 11,060 mass × variables and to reduce the number of components, we proceed with the exclusion of the variables having more than 30% of missing data in the different groups under investigation. The obtained matrix was log-transformed and normalized by median fold change normalization and mean centred. The obtained matrix was then elaborated using SIMCA (Umetrics) software and PCA and PLS-DA models were generated. Compounds describing the different groups were selected. For the model validation, N-fold full cross-validation with different values of N ($N=6,7,8$) and permutation test on the responses (150 random permutations) were performed, in order to avoid overfitting. Time × mass variables contributing to group separation were selected on the basis of their variable importance on projection (VIP) value. Only variables bearing VIP values > 11 were considered significant in differentiating the groups. Compounds were putatively identified using accurate mass value, fragmentation pathway generated using MS^e function of the Q-TOF mass spectrometer and by comparison with online available database as Human Metabolome Database (HMDB), Food Metabolome database (FOOBD), and available online chemical database as Chemspider. Particularly, confirmation of the identity of some compounds was obtained by comparison with authentic standards, for rutin, catechin, epicatechin, resveratrol, which were all provided by Sigma Aldrich. The tables in the results section report the variation (%) calculated from the average area of annotated metabolite in the treated samples compared to the average area of the same metabolite in control samples.

CNS content in berries

Berries were dried completely in oven at 80 °C for 48 h, and then crushed to make fine powder. Ten mg of powdered samples were used to measure the carbon, nitrogen and sulfur content by vario micro-cube instrument run at CHNS analyzer (Elementar Vario ELIII).

Analysis of amino acids

Berry juice (0.3 mL) was added to 5 mL HCl (0.5 M) for 10 min at room temperature. Solution were centrifuged and used for analysis. Standard solutions were prepared weighting exact amount of each amino acid in HCl solution (0.5 M) in four different concentrations: 10, 5, 2, 1 µg mL^{-1}. For analysis, an Agilent Z-HILIC Column (3 × 100 mm, 4 micron) was used as stationary phase, and eluents were acetonitrile, (**A**) and water 0.5% formic acid (**B**). A gradient program was used as follows: 0 min, 95% A;1 min, 95% A; 11 min, 70% A; 14 min, 40% A, 14.5 min, 95% A then isocratic for 5 min. Flow rate was 0.450 mL min^{-1}. Each amino acid transition was optimized with corresponding standard solution. MS/MS parameter was as reported in previous work [20].

Statistical analysis

Data on amino acids, chlorophylls, CNS, secondary metabolites were subjected to a one-way analysis of variance (ANOVA). All the experiments were performed in triplicate.

Related to the metabolomics analysis the MS data deriving from the Q-TOF were transformed in matrix that was imported into Simca 12 software (Umetrix, Sweden). Unsupervised principal component (PCA) and supervised orthogonal partial least square discriminant (OPLS-DA) analyses were performed using centering and

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pareto scaling. The unsupervised PCA was carried out to observe homogeneous sample clusters that were used as Y classes in the supervised PLS-DA. As final output, compounds that are related to the cluster separation in OPLS-DA were identified. The statistical analyses were validated by performing permutation test (150 permutations); CV-ANOVA ($p < 0.05$); t-test ($p < 0.05$) for a cluster characterizing molecule.

Results
Changes induced in leaf tissues by 501
The preparation 501 is commonly sprayed over the canopy in the early morning, in absence of rainfall and wind. Consequently, the leaves are the organs of the plants mostly exposed to the treatment. The effect of 501 on leaves was assessed by measuring the content of chlorophyll a and b, as markers of impact on the leaf photosynthetic apparatus, and by an untargeted UPLC-QTOF–MS method followed by multivariate data analysis to estimate metabolite variations.

Leaves pigment measurement
The leaf content of chlorophyll a and chlorophyll b did not significantly change between control and 501-treated plants, although a higher level was measured in 501-treated plants of Paiele vineyard, and the opposite was found in the leaves of plants in Roncaie vineyard (Table 1). No significant differences were also observed comparing the two vineyards.

Untargeted-metabolomic analysis
To assess any possible effect of the 501 distribution, metabolomic analysis was performed in leaves of *Vitis vinifera* L. cv Garganega plants at two different times, 6 h after 501 application (T1), and 11 days later (T2).

UPLC-QTOF–MS metabolomics was performed in negative ion mode and allowed the identification of metabolites on the basis of the retention time, accurate *m/z* value, MS^e fragmentation pattern and by comparison of available online metabolomic database (Human Metabolome Database-HMDB, Food Metabolomic Database-FOODB). The datasets were elaborated first using principal component analysis (PCA) to observe any possible clusterization of the samples. The stability of chromatographic system and MS spectrometer was assessed, as shown by the "pool" samples that are well clusterized in the centre of the plot for the samples of both the vineyards (Additional file 2:Figure SA1, Additional file 3: Figure SA2). No clusterization was observed considering treated and control samples in PCA. To highlight the differences between sampling times 1 and 2, data from control and treated plants were also elaborated using the supervised method by orthogonal partial least square discriminant analysis (OPLS-DA). Each multivariate model will lead to a graphical representation of treated vs control samples for each vineyard. Detailed elaboration and results are described in the following chapters.

Metabolomic analysis of leaves in the Paiele vineyards
The data related to the Paiele leaf samples are illustrated in Additional file 4: Figure SA3. No clusterization of control (C) versus treated (T) samples is observed. This indicates that metabolomic changes can be ascribed to the time of sampling rather than to the 501 treatment. OPLS-DA was performed considering sampling time 1 and 2 separately. The OPLS-DA model for the samples 6 h after the treatment described 93% of the data variance using 3 components, and the variance predicted was 53%. Y-axes intercept after permutation test ($n = 150$) resulted in $R2 = (0.0, 0.99)$, $Q2 = (0.0, 0.673)$. OPLS-DA model for the samples 11 days after the treatment explained 97% of the data variance using 3 components and the variance predicted was 69%. Y intercept after permutation test ($n = 150$) resulted in $R2 = (0.0, 0.711)$, $Q2 = (0.0, 0.012)$.

The OPLS-DA models were used to distinguish the possible changes of leaf metabolites (control vs treated), 6 h after the biodynamic treatment (sampling time 1) (Fig. 2A) and 11 days later (sampling time 2) (Fig. 2B).

Thanks to UPLC–MS data, the changes in leaves composition were identified as phenolic compounds, mostly ascribable to flavonoids, stilbenoids and hydroxycinnamic acid derivatives. Identification of the compounds

Table 1 Leaf content of chlorophyll a (Chla) and chlorophyll b (Chlb) (mg g^{-1} fresh weight)

	Chla	Chlb
PC1	0.84 ± 0.23	0.49 ± 0.23
PT1	0.78 ± 0.27	0.39 ± 0.20
PC2	1.03 ± 0.24	0.46 ± 0.17
PT2	0.78 ± 0.27	0.39 ± 0.24
RC1	0.71 ± 0.25	0.24 ± 0.08
RT1	0.78 ± 0.29	0.24 ± 0.11
RC2	0.51 ± 0.23	0.19 ± 0.02
RT2	0.69 ± 0.11	0.34 ± 0.22

Data are means of $n = 6$ samples $\pm$ standard deviation

P Paiele, *R* Roncaie, *C* control, *T* treated with 501, 1-sampling date May 10th, 2-sampling date May 21st

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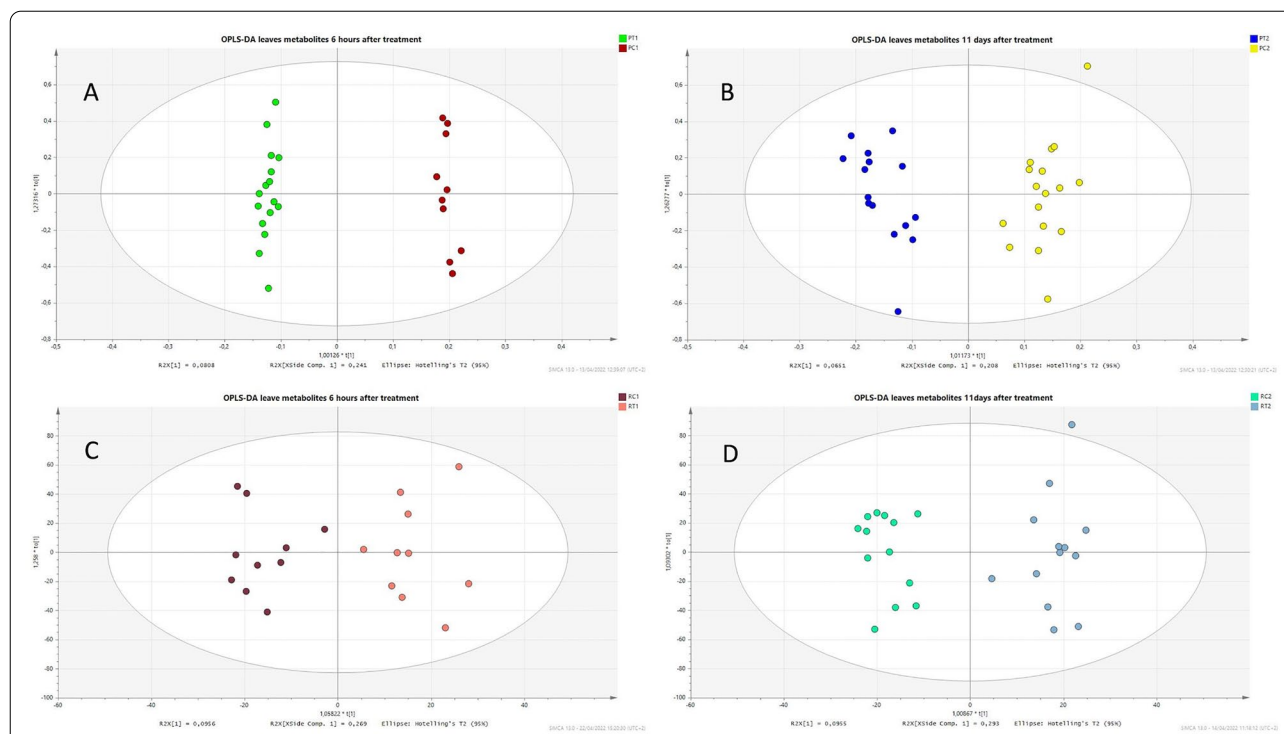
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Fig. 2 OPLS-DA model for metabolites in leaves of plants in Paiele and Roncaie vineyards, comparing control (PC or RC) and 501-treatment (PT or RT) at the sampling time 1 and 2. PC1vsPT1 (**A**), PC2vsPT2 (**B**), RC1vsRT1 (**C**), RC2vsRT2 (**D**). *P* Paiele, *R* Roncaie, *C* control, *T* treated with 501, 1-sampling date May 10th, 2-sampling date May 21st

Table 2 Differential metabolite changes in leaves of Paiele plants treated with preparation 501 (PT) compared to control (PC) at both sampling times

Retention time	Var ID (m/z)	PT1 vs PC1	PT2 vs PC2	Identification
4.05	463.0889	+ 1.0%	+ 1.5%	Quercetin glucoside[a]
4.16	593.1519	+ 0.2%	+ 3.2%[§]	Kaempferol rutinoside
4.12	289.0704	+ 0.7%	+ 2.7%	Epi-Catechin
5.38	227.1283	+ 1.0%	+ 1.5%[§]	Resveratrol[a]
4.56	477.0686	+ 3.0%	+ 16.0% [§]	Quercetin glucuronide
5.62	507.2453	+ 12.0%[§]	+ 0.5%[§]	Dicaffeoyl hexose
4.76	609.1472	+ 1.5%	+ 32.0%[§]	Rutin[a]
4.79	447.0938	+ 5.0%	+ 11.0%[§]	Kaempferol glucoside
4.82	461.0727	+ 3.0%	+ 11.0%[§]	Methoxy kaempferol glucoside
4.86	301.0352	+ 1.5%	+ 1.0%	Quercetin[a]

Compounds presenting VIP > 11 were selected, putative identification was obtained considering HR-MS spectra as well as fragmentation obtained by MS[e] approach

([a])When available, reference compounds were used to confirm findings. §indicates statistical difference $p < 0.05$

that mostly described differences between treated and control samples, and their relative amount are reported in Table 2.

At sampling time 1, 6 h after the 501-treatment, a general increase of the selected phenolic secondary metabolites is observed in leaves of 501-treated plants compared to controls, but only the content of dicaffeoyl hexose augmented significantly. At sampling time 2, 11 days after the 501 distribution, significant variation for seven of the selected phenolic metabolites can be noticed. The results indicate that

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501-treatment mainly induced the increase in the amount of kaempferol and quercetin derivatives, as well as in resveratrol, epicatechin and caffeoyl ester with hexoside.

Metabolomic analysis of leaves in Roncaie vineyards

The data related to the Roncaie leaves samples are shown in Additional file 3: Figure SA4. As for Paiele samples, the PCA revealed a grouping due to time sampling but no clusterization of control (C) versus treated (T) samples was observed. Even in Roncaie vineyard, the most intense changes can be ascribed more to the sampling time than to the 501-treatment. The multivariate data elaboration (OPLS-DA) was then performed considering sampling time 1 and 2 separately. The OPLS-DA model for the samples 6 h after the treatment described 92% of the data variance using 3 components and the variance predicted was 52%, Y intercept after permutation test ($n = 150$) resulted in $R2 = (0.0, 0.947)$, $Q2 = (0.0, 0.0315)$. The OPLS-DA model for the samples 11 days after the treatment described 94% and the variance predicted was 72%, Y intercept after permutation test ($n = 150$) resulted in $R2 = (0.0, 0.948)$, $Q2 = (0.0, 0.554)$.

The OPLS-DA models related to the leaf metabolites (control vs treated) 6 h after the biodynamic treatment (sampling time 1) and 11 days later (sampling time 2) are described in Fig. 2C, D.

The UPLC–MS data revealed changes in the level of some phenolic compounds. Identification of the compounds that mostly highlight the differences between treated and control group and their relative amount are reported in Table 3.

The leaves of 501-treated plants displayed a variation of phenolic compounds compared to controls at both sampling dates. Epicatechin, resveratrol and catechin, significantly decreased compared to control at both sampling times. The application of 501 boosted the level of caftaric acid ($+301.6$) and caffeic acid ($+298.2$) at sampling time 2, and significant increase was recorded for kaempferol glucoside, S-furanopetasitin and rutin. The augmented level of the two metabolites, ethyl 7-epi-12-hydroxyjasmonate glucoside and S-furanopetasitin, not belonging to the class of polyphenols, was also recorded.

Assessing changes induced by 501-treatment in berries

Limited information is available up to now to the possible influence of biodynamic treatment with 501 on berries of grapevine. Some targeted measurements, namely the elemental composition (C, N, S) and the amino acid content, and untargeted UPLC-QTOF–MS metabolomics analysis were performed on berries to assess the effects of the 501 application.

C, N, S and amino acid content

The treatment with preparation 501 did not vary significantly the content of sulfur, carbon and nitrogen in the berries (Additional file 1: Table S1), although a slight increase of sulfur ($+7.4\%$ in PT and 15.6% in RT) and nitrogen ($+16.0\%$ in PT and $+9.4\%$ in RT) was recorded in 501-treated berries.

The berry content of free amino acids was also investigated. Aspartic acid and proline were the two most abundant in berries of both vineyards. Significant increased levels of cysteine ($+49.9\%$), methionine ($+100\%$), phenyl alanine ($+24.9\%$), and decreased amounts of proline (-21.1%), arginine (-26.2%) and serine (-21.0%) were

Table 3 Differential metabolite changes in the leaves of Roncaie plants treated with preparation 501 (RT) compared to controls (RC), at both sampling times

Retention time	Var ID (m/z)	RT1 vs RC1	RT2 vs RC2	Identification
2.40	311.0395	+ 2,6%	+ 301.6%[§]	Caftaric acid[a]
2.40	179.0335	+ 2.2%	+ 298.2%[§]	Caffeic acid[a]
4.83	415.1960	+ 5.7%	+ 29.7%	Ethyl 7-epi-12-hydroxyjasmonate glucoside
4.02	431.1911	+ 3.0%	+ 25.0%[§]	S-Furanopetasitin
4.12	289.0704	− 1.5%[§]	− 12.7%[§]	Epi-Catechin[a]
5.38	227.0717	− 2.5%[§]	− 60.2%[§]	Resveratrol[a]
4.79	447.0924	+ 1.1%	+ 1.1%[§]	Kaempferol glucoside
4.76	609.1460	+ 2.0%	+ 3.2%[§]	Rutin[a]
3.61	289.0705	− 5.0%[§]	− 12.0%[§]	Catechin[a]

Metabolites presenting VIP > 11 were selected, putative identification was obtained considering HR-MS spectra as well as fragmentation obtained by MS[e] approach

([a])When available, reference compounds were used to confirm findings. [§]indicates statistical difference $p < 0.05$

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Table 4 Free amino acid contents (mg kg^{-1}) in berries of Paiele and Roncaie plants

Compound	m/z	PCh	PTh	RCh	RTh
Alanine	90	30.8 ± 1.5	26.3 ± 1.5	40.6 ± 2.1	39.1 ± 2.6
Cysteine	122	21.7 ± 1.5	32.5 ± 2§	15.0 ± 1.0	35.2 ± 1.0§
Aspartic acid	134	323.2 ± 8.8	390.1 ± 10	310.3 ± 11	315.5 ± 15
Glutamic acid	148	61.5 ± 6.5	72.4 ± 5	50.05 ± 9	56.9 ± 10
Phenyl alanine	165	45.7 ± 3.7	57.1 ± 5.6§	64.31 ± 3.5	65.1 ± 3.1
Glycine	76	14.7 ± 1.2	13.5 ± 0.4	12.28 ± 2.8	14.5 ± 0.9
Histidine	155	11.3 ± 1.1	11.0 ± 1.5	13.3 ± 1.2	15.5 ± 1.9
Isoleucine	132	25.5 ± 2.0	22.3 ± 1.6	25.6 ± 1.5	19.5 ± 2.3
Leucine	147	12.8 ± 1.1	10.9 ± 1.5	12.8 ± 1	14.8 ± 1.3
Lysine	132	15.3 ± 1.2	16.0 ± 1.5	13.8 ± 2	13.5 ± 1.2
Methionine	150	1.5 ± 0.2	3.3 ± 0.2§	2.6 ± 0.5	2.9 ± 0.5
Asparagine	133	28.6 ± 2.5	28.5 ± 1.4	24.1 ± 1.7	23.7 ± 1.5
Proline	116	266.2 ± 18.3	209.9 ± 8§	247.8 ± 18	236.8 ± 23
Glutamine	147	6.4 ± 1.5	5.8 ± 1.2	5.8 ± 1	7.3 ± 0.5
Arginine	175	38.2 ± 1.8	28.2 ± 1.5§	34.5 ± 1.5	46.8 ± 0.9§
Serine	106	4.2 ± 0.8	3.3 ± 0.5§	4.1 ± 1.7	4.7 ± 1
Threonine	120	15.6 ± 1.2	14.5 ± 1.1	17.2 ± 3.5	15.7 ± 1.5§
Valine	118	30.8 ± 1.5	25.4 ± 1.5	22.7 ± 1.3	26.5 ± 3.5
Tryptophan	205	47.2 ± 1.5	53.6 ± 1.5	32.6 ± 1.1	54.7 ± 4.1§
Tyrosine	182.1	14.5 ± 1.5	16.3 ± 1.5	18.1 ± 1.2	16.4 ± 1.2§

P Paiele, *R* Roncaie, *C* control, *T* treated with 501, *h* harvest

§ indicates $p < 0.05$ treated vs control

observed in 501-treated fruits compared to control, in Paiele vineyard (Table 4).

Significant higher amount of cysteine (+ 133.3%), arginine (+ 36.0%), tryptophan (+ 67.8%) and lower concentration of isoleucine (− 23.8%) threonine (− 8.4%) tyrosine (− 9.3%) were measured in Roncaie berries of treated plants compared to control (Table 4). Overall, the distribution of 501 induced distinct, although limited, variations in the berry free amino acid composition in the two vineyards.

Metabolomic analysis of berries
To observe any possible change in berries composition related to 501-treatment, metabolomic UPLC-QTOF–MS analysis was performed.

PCA analysis did not evidence clear grouping for both the vineyards (Additional file 4: Figure SA5, Additional file 5: Figure SA6). Paiele and Roncaie datasets were elaborated separately, using the OPLS-DA to detect any variation between the control and 501-treated berries.

The OPLS_DA models related to control and treated samples of Paiele and Roncaie berries are reported in Fig. 3. In the OPLS-DA model for the samples 6 h after

the treatment, the *R2* was 0.751 and prediction ability was Q2Y 0.213. Permutation test ($n = 150$) resulted in $R2 = (0.0, 0.62)$, $Q2 = (0.0, 0.0145)$. The significance of the model was also proved for the samples 11 days after the treatment, with *R2* 0.729 and prediction ability Q2Y 0.393. Permutation test ($n = 150$) resulted in $R2 = (0.0, 0.991)$, $Q2 = (0.0, 0.624)$.

The same pattern of metabolites for the berries of both the vineyards was observable from the UPLC–MS results (Table 5). In general, the level of phenolic constituents in the berries of treated plant increased. The amount of epigallocatechin significantly augmented in berries of Roncaie plants after 501 applications, and the pigment violaxanthin boosted in treated berries of both vineyards. Two sulphur-containing organic compounds, whose identity was not elucidated, increased in treated berries, but with no statistical significance.
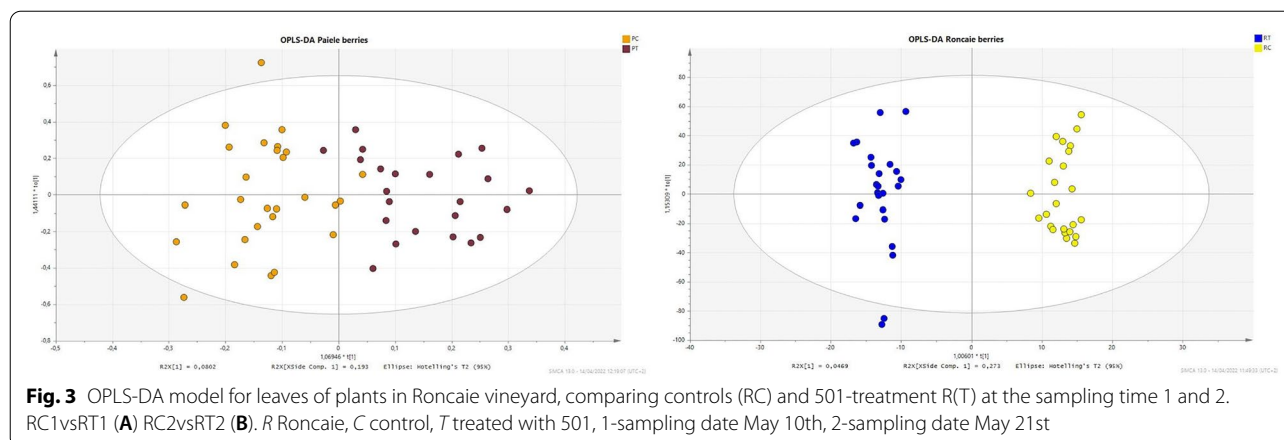
Discussion
Biodynamic agriculture differs from organic management in the use of specific preparations, applied on crops or soil in very small amounts. These preparations are claimed to stimulate soil nutrient cycle, photosynthesis in plants and optimal evolution of compost, enhancing both soil and crop quality [21]. Research on biodynamic viticulture revealed similarity with the organic system concerning soil characteristics, plant growth and yield, resource utilization and biodiversity [22]. The use of preparations had minor influences on growth and yield and did not affect the final quality of the grape berries [23].

The application of horn silica, preparation 501, to the aerial part of the plants is one of the guidelines given by Steiner to accomplish the biodynamic farming. This work was aimed to discover evidences on the effects of 501 distributions in *Vitis vinifera cv* Garganega plants.

Samples of leaves and berries were collected from plants grown in two separate vineyards closely located. The leaves samples were collected at two times, 6 h after the 501-treatment (sampling 1, May 10th) and 11 days later (sampling 2, May 21st) to elucidate whether 501-treatment could induce immediate change in leaves contents or a long-lasting effect could be detectable 11 days after the application. Also, analysis was performed in berries sampled at harvest time.

To assess the variations induced by the application of 501, we first examined the leaf chlorophyll content, commonly regarded as a marker of the nutritional status of the plants. The lack of difference on the level of pigments observed between the leaves of control and 501-treated plants confirms the findings of a previous study on biodynamic treated grapevine [9].

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Fig. 3 OPLS-DA model for leaves of plants in Roncaie vineyard, comparing controls (RC) and 501-treatment R(T) at the sampling time 1 and 2. RC1vsRT1 (**A**) RC2vsRT2 (**B**). *R* Roncaie, *C* control, *T* treated with 501, 1-sampling date May 10th, 2-sampling date May 21st

Metabolomics is successfully applied in plant science [24, 25], and the technical advances and the possibility to acquire large number of raw data, due to high-resolution mass spectrometry coupled with liquid chromatography, allow to achieve inclusive phytochemical profile in plants, opening new research opportunities [26–28]. Multivariate statistical analysis approach is a tool to investigate metabolic alteration in complex samples as plant tissues. Principal component analysis (PCA) is one of the most used techniques in multivariate analysis, aimed at reducing a dataset to its main components and visualizing similarities. PCA has been used in several studies to distinguish varietal and/or geographical origin of grape juice and wines [29]. Other type of data elaboration, as PLS-DA and its implemented version OPLS-DA, may give the advantage of

an easier interpretation of the models. Most "omics" experimental setups aim at the comparison of samples between a control and a case group (e.g. disease or treatment). The goal of such differential analysis is therefore to build up a model able to distinguish the classes of observations and to provide a meaningful interpretation of the observed differences [30].

We studied the metabolite profiles in leaves and berries by UPLC-QTOF–MS analysis using an untargeted metabolomics approach. Unlike the targeted methods, where most of the metabolites in the matrix are ignored, in untargeted metabolomics the aim is to achieve the widest possible metabolic coverage in an unsupervised manner, including unknown compounds. Consequently, the measured metabolites are not pre-defined and method development and validation follow a workflow different from the targeted analysis [31].

The PCA for leaf metabolites of both the vineyards showed clusterization only due to sampling time, suggesting limited variation in the leaves composition caused by the 501-treatment compared to time-induced changes. However, further elaboration by supervised methods allowed to detect changes due to treatment, avoiding any bias related to sampling time and location. Our results are, up to our knowledge, the first demonstration of metabolomic changes related to biodynamic 501 applications on grape leaves.

The metabolites changes in leaves of Paiele and Roncaie plants indicated that secondary metabolism was mostly influenced 11 days after the 501 biodynamic treatment, allowing to exclude a short time (after 6 h) effect. The pathway of shikimate leading to the formation of phenylpropanoids, stilbenoids and flavonoids appears to be triggered in leaves of 501-treated Paiele plants, while the boost of caftaric and caffeic acid in Roncaie plants indicates that mostly the phenylpropanoid biosynthesis is influenced in the treated plants. The great increase in

Table 5 Differential metabolite changes in berries after application of preparation 501 (PT and RT) compared to controls (PC and RT)

Retention time	Var ID (m/z)	PTh vs PCh	RTh vs RCh	Identification
9.37	524.9291	+6.0%	+5.3%	$C_{23}H_{11}NO_4S_5$
10.36	577.8214	+44.8%	+40.0%	Procyanidin B type
3.58	163.4913	+9.0%	+6.6%	*p*-Coumaric acid[a]
6.93	191.1633	+43.9%	+21.2%	Quinic acid[a]
8.56	601.8307	+146.9%[§]	+189.6%[§]	Violaxanthin
8.31	726.0222	+128.3%	+74.8%	$C_{24}H_{22}O_{24}S$
2.22	305.4691	+69.1%	+69.8%[§]	Epigallocatechin[a]
9.52	601.8098	+45.3%	− 23.7%	Luteoxanthin
3.61	290.3107	+20.2%	+14.5%	Catechin[a]

Metabolites presenting VIP > 11 were selected, putative identification was obtained considering HR-MS spectra as well as fragmentation obtained by MSe approach

[a] When available, reference compounds were used to confirm findings.
[§] indicates statistical difference *p* < 0.05

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caffeic and caftaric acids could be counterbalanced by the drop of the level of resveratrol and epicatechin in Roncaie leaves. Resveratrol production in grapevine is related to external stimuli, as microbial infection, light irradiation, water stress, elicitors or signalling compounds [32]. It is known that higher plant tolerance to abiotic stresses is related to increased synthesis of polyphenols, such as phenolic acids and flavonoids [33]. Our results can suggest that the application of preparation 501 may trigger the biosynthesis of antioxidants beneficial to enhance stress tolerance in grapevine plants, although the different variations in the leaf metabolite levels recorded in the plants of the two vineyards may be attributable to a site effect.

Recently, the total amino acid content was found to increase in healthy grape berries during maturation under biodynamic management compared to integrated treatment [23]. In our study, the total amount of free amino acids in berries did not vary, although 501 induced significant variations in some amino acids. However, the lack of consistency in changes between the berries of the two vineyards leads to exclude a common effect of 501 on amino acids biosynthesis, with the exception of the increased level of cysteine. It is known that the amount of individual amino acids in berries could vary with variety, location, age, cultural practices, and method of analysis [34]. In a previous study, 1H-NMR analyses of *Vitis vinifera* L. cv. Sangiovese berries evidenced a higher accumulation of proline, valine and isoleucine in biodynamic than in organic berries [11]. Laghi et al. [14] compared the red wine obtained from biodynamic and organic grapes and concluded that the vineyard management caused limited modifications on the wine composition. Effects on proline, aspartic acid and valine, alcohols and some polyphenols were reported.

The berries of the 501-treated plants in both the vineyards showed superimposable pattern of metabolic changes, mostly being identified as phenolics and carotenoids. Observed metabolic changes in berries varied from those found in leaf tissues, and this can be related to the metabolic specificity of the two plant organs. Phenolic compounds are important in grapes due to their protective function against environmental stress and fungal infection [35]. In 501-treated plants of both sites the level of berry phenolic constituents raised, but only violaxanthin increased significantly. Carotenoids are well known photo-protectors in plant tissues and may interfere during the ripening process in grape [36]. Berries metabolically respond to the light by augmenting the level of compounds like polyphenols that have direct antioxidant and "sun-screening" abilities [37]. The rise of epigallocatechin, although only in Roncaie berries, and violaxanthin can be seen as a beneficial effect of the

biodynamic treatment in terms of enhanced response to oxidative stress. The grape berry polyphenols are extracted during wine-making and could influence colour as well as the sensory perception of wine [38]. Additionally, grape carotenoids can play a significant role as potential precursors of aroma compounds, as for example the C13-norisoprenoids, that are responsible for significant sensorial impact in wines [39].

Previous paper investigated the phenolics composition in grape berry of cv Pignoletto and cv Sangiovese, comparing conventional, organic and biodynamic management [40]. Catechin and epigallocatechin had comparable content and rutin decreased in biodynamic treatment compared to conventional and organic management in Pignoletto berries. Even Parpinello et al. (2019) evidenced no significant differences between organic and biodynamic Sangiovese wines, although the latter presented higher concentrations of malvidin-3-glucoside and catechin [10].

Our results revealed that catechin and epigallocatechin increased in berries of Paiele and Roncaie plants (Table 5), suggesting a homogeneous trend under biodynamic treatment, independent from the location. The 501 treatment promoted a general increase of phenolic compounds, except for kaempferol glucoside, in berries of both the vineyards. These results are in agreement with Reeve et al. (2005) who reported increased polyphenols in wine obtained from grapes under biodynamic management [21]. The increment of polyphenols in berries of biodynamically grown plants can confirm the hypothesis of an upregulation of metabolites assumed to induce stress resistance [21, 22]. Higher levels of flavonoids and anthocyanins, with the consequent higher antioxidant potential, were associated to a lower plant vigour, a feature often reported under biodynamic management [41].

Overall, our data indicate a stimulation of the biosynthetic pathways of phenolics in leaves and berries due to the application of 501.

Conclusions

The present study demonstrates that complementary approaches, combining targeted and untargeted data related to primary metabolism and to secondary metabolism, may offer a new opportunity in the evaluation of the complex and multifactorial effects of biodynamic treatment in viticulture.

The application of 501 to plants of *Vitis vinifera* cv Garganega stimulated modifications on the content of phenolic metabolites in leaves and berries. The level of most of the identified compounds by metabolomic approaches increased in plants treated with the biodynamic preparation 501. A common response to 501-treatment was evidenced in the phenolic

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constituents of berries, while in leaves the effect was detectable after 11 days and was dependent on the site of cultivation. The secondary metabolism contributes to the plant adaptation to the environment. The comparison with the results obtained by other studies does not allow to suggest a general influence of 501 application to grapevine leaves and berries. The number of grapevine growers approaching the biodynamic management is increasing worldwide, given the effective success in the cultivation and in the wine-making. The present study could be considered a starting effort to better understand the actual effects of the biodynamic preparation and to support farmers about the scientific knowledge related to the biodynamic method. More research is surely needed to further explore the role of the 501 biodynamic treatment on grapevine secondary metabolism.

Abbreviations
ICP-OES: Inductively coupled plasma-optical emission spectroscopy; UPLC–HR-MS: Ultra performance liquid chromatography–high-resolution mass spectrometry; Q-TOF: Quadrupole time-of-flight; PCA: Principal component analysis; OPLS-DA: Orthogonal partial least square discriminant analysis; Chla: Chlorophyll a; Chlb: Chlorophyll b; VIP: Variable importance on projection.

Supplementary Information
The online version contains supplementary material available at https://doi.org/10.1186/s40538-022-00299-y.

Additional file 1: Table SA1. Sulfur (S), Carbon (C) and Nitrogen (N) content in berries. P-Paiele; R-Roncaie; C-control; T-treated with 501. Data in percent dry weight.

Additional file 2: Figure SA1. PCA analysis of the dataset related to Paiele leaves samples. P-Paiele; Pool-created mixing equal aliquots of all the samples. C-control; T-treated with 501; 1-sampling date May 10th; 2-sampling date May 21st.

Additional file 3: Figure SA2. PCA analysis of the dataset related to Roncaie leaves samples. R-Roncaie Pool-created mixing equal aliquots of all the samples. C-control; T-treated with 501; 1-sampling date May 10th; 2-sampling date May 21st.

Additional file 4: Figure SA3. PCA of 501-treated leaves compared to control in Paiele vineyard. P-Paiele; C-control; T-treated with 501; 1-sampling date May 10th; 2-sampling date May 21st. Red ellipsoid groups samples at sampling time 1 and blue ellipsoid samples at sampling time 2. Green and Blue colours indicate treated samples at time 1 and 2, respectively, while red and yellow colours represent control samples at time 1 and 2, respectively. The samples can be grouped on the basis of time sampling, as highlighted by the red and blue ellipsoid.

Additional file 5: Figure SA4. PCA of 501-treated leaves compared to control in Roncaie vineyard. R- Roncaie; C-control; T-treated with 501; 1-sampling date May 10th; 2-sampling date May 21st. Light green and light blue colours are associated to treated samples at time 1 and 2, respectively, while brown and orange colours represent control samples at time 1 and 2, respectively. Red ellipsoid groups samples at time sampling 1 and blue ellipsoid groups samples at time sampling 2.

Additional file 6: Figure SA5. PCA analysis of the whole dataset related to Roncaie berries. C- Control; T- treated with 501.

Additional file 7: Figure SA6. PCA analysis of the whole dataset related to Paiele berries. C- Control; T- treated with 501.

Declarations

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References
1. Rockström J, Williams J, Daily G, Noble A, Matthews N, Gordon L, et al. Sustainable intensification of agriculture for human prosperity and global sustainability. Ambio. 2017;46(1):4–17.
2. Ponzio C. Organic and biodynamic agriculture: a review in relation to sustainability. Int J Plant Soil Sci. 2013;2(1):95–110.
3. Chalker-Scott L. The science behind biodynamic preparations: a literature review. HortTechnology. 2013;23(6):814–9.
4. Pertot I, Caffi T, Rossi V, Mugnai L, Hoffmann C, Grando MS, et al. 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.
5. Castellini A, Mauracher C, Troiano S. An overview of the biodynamic wine sector. Int J Wine Res. 2017;9(1):1–11.
6. Reeve JR, Carpenter-Boggs L, Sehmsdorf H. Sustainable agriculture: a case study of a small Lopez Island farm. Agric Syst. 2011;104(7):572–9. https://doi.org/10.1016/j.agsy.2011.04.006.
7. Di Giacinto S, Friedel M, Poll C, Döring J, Kunz R, Kauer R. Vineyard management system affects soil microbiological properties. OENO One. 2020;54(1 SE-Original research articles):131–43. https://oeno-one.eu/article/view/2578
8. Meissner G, Athmann ME, Fritz J, Kauer R, Stoll M, Schultz HR. Conversion to organic and biodynamic viticultural practices: impact on soil, grapevine development and grape quality. OENO One. 2019;53(4 SE-Original research articles):639–59. https://doi.org/10.20870/oeno-one.2020.54.1.2578
9. Botelho RV, Roberti R, Tessarin P, Garcia-Mina JM, Rombolà AD. Physiological responses of grapevines to biodynamic management. Renew Agric Food Syst. 2016;31(5):402–13.
10. Parpinello GP, Ricci A, Rombolà AD, Nigro G, Versari A. Comparison of Sangiovese wines obtained from stabilized organic and biodynamic vineyard

management systems. Food Chem. 2019;283:499–507. https://doi.org/10.1016/j.foodchem.2019.01.073.

11. Picone G, Trimigno A, Tessarin P, Donnini S, Rombolà AD, Capozzi F. 1H NMR foodomics reveals that the biodynamic and the organic cultivation managements produce different grape berries (*Vitis vinifera* L. cv. Sangiovese). Food Chem. 2016;213:187–95. https://doi.org/10.1016/j.foodchem.2016.06.077.

12. Fritz J, Athmann M, Meissner G, Kauer R, Köpke U. Quality characterisation via image forming methods differentiates grape juice produced from integrated, organic or biodynamic vineyards in the first year after conversion. Biol Agric Hortic. 2017;33(3):195–213. https://doi.org/10.1080/01448765.2017.1322003.

13. Fritz J, Döring J, Athmann M, Meissner G, Kauer R, Schultz HR. Wine quality under integrated, organic and biodynamic management using image-forming methods and sensory analysis. Chem Biol Technol Agric. 2021;8(1):1–15. https://doi.org/10.1186/s40538-021-00261-4.

14. Laghi L, Versari A, Marcolini E, Parpinello GP. Metabonomic investigation by 1H-NMR to discriminate between red wines from organic and biodynamic grapes. Food Nutr Sci. 2014;05(01):52–9.

15. Pinu FR. Grape and wine metabolomics to develop new insights using untargeted and targeted approaches. Fermentation. 2018;4(4):92.

16. Luo YY, Li RX, Jiang QS, Bai R, Duan D. Changes in the chlorophyll content of grape leaves could provide a physiological index for responses and adaptation to UV-C radiation. Nordic J Bot. 2019;37(4):e02314. https://doi.org/10.1111/njb.02314.

17. Bell SJ, Henschke PA. Implications of nitrogen nutrition for grapes, fermentation and wine. Aust J Grape Wine Res. 2005;11:242–95.

18. Gutiérrez-Gamboa G, Portu J, López R, Santamaria P, Garde-Cerdán T. Elicitor and nitrogen applications to Garnacha, Graciano and Tempranillo vines: effect on grape amino acid composition. J Sci Food Agric. 2018;98:2341–9.

19. Wellburn AR, Lichtenthaler H. Formulae and program to determine total carotenoids and chlorophylls A and B of leaf extracts in different solvents. Sybesma C. Dordrecht: Springer; 1984.

20. Ravazzolo L, Trevisan S, Forestan C, Varotto S, Sut S, Dallacqua S, et al. Nitrate and ammonium affect the overall maize response to nitrogen availability by triggering specific and common transcriptional signatures in roots. Int J Mol Sci. 2020;21(2):686.

21. Reeve JR, Carpenter-Boggs L, Reganold JP, York AL, McGourty G, McCloskey LP. Soil and winegrape quality in biodynamically and organically managed vineyards. Am J Enol Vitic. 2005;56(4):367–76.

22. Döring J, Collins C, Frisch M, Kauer R. Organic and biodynamic viticulture affect biodiversity and properties of vine and wine: a systematic quantitative review. Am J Enol Vitic. 2019;70(3):221–42.

23. Döring J, Frisch M, Tittmann S, Stoll M, Kauer R. Growth, yield and fruit quality of grapevines under organic and biodynamic management. PLoS ONE. 2015;10(10):1–28.

24. Habran A, Commisso M, Helwi P, Hilbert G, Negri S, Ollat N, et al. Rootstocks/scion/nitrogen interactions affect secondary metabolism in the grape berry. Front Plant Sci. 2016;7(AUG 2016):1–11.

25. Paul K, Sorrentino M, Lucini L, Rouphael Y, Cardarelli M, Bonini P, et al. Understanding the biostimulant action of vegetal-derived protein hydrolysates by high-throughput plant phenotyping and metabolomics: a case study on tomato. Front Plant Sci. 2019;10(February):1–17.

26. Jorge TF, Rodrigues JA, Caldana C, Schmidt R, van Dongen JT, Thomas-Oates J, et al. Mass spectrometry-based plant metabolomics: metabolite responses to abiotic stress. Mass Spectrom Rev. 2016;35(5):620–49.

27. Lamichhane S, Sen P, Dickens AM, Hyötyläinen T, Orešič M. Chapter fourteen—an overview of metabolomics data analysis: current tools and future perspectives. In: Jaumot J, Bedia C, Tauler R, editors. Data analysis for omic sciences: methods and applications. Amsterdam: Elsevier; 2018. p. 387–413.

28. Piasecka A, Kachlicki P, Stobiecki M. Analytical methods for detection of plant metabolomes changes in response to biotic and abiotic stresses. Int J Mol Sci. 2019;20(2):379.

29. Coelho EM, da Silva Padilha CV, Miskinis GA, de Sá AGB, Pereira GE, de Azevêdo LC, et al. Simultaneous analysis of sugars and organic acids in wine and grape juices by HPLC: method validation and characterization of products from northeast Brazil. J Food Compos Anal. 2018;66:160–7. https://doi.org/10.1016/j.jfca.2017.12.017.

30. Boccard J, Rutledge DN. A consensus orthogonal partial least squares discriminant analysis (OPLS-DA) strategy for multiblock Omics data fusion. Anal Chim Acta. 2013;769:30–9.

31. Arapitsas P, Ugliano M, Marangon M, Piombino P, Rolle L, Gerbi V, et al. Use of untargeted liquid chromatography-mass spectrometry metabolome to discriminate Italian monovarietal red wines, produced in their different terroirs. J Agric Food Chem. 2020;68(47):13353–66.

32. Hasan MM, Bae H. An overview of stress-induced resveratrol synthesis in grapes: perspectives for resveratrol-enriched grape products. Molecules. 2017;22:294.

33. Sharma A, Shahzad B, Rehman A, Bhardwaj R, Landi M, Zheng B. Response of phenylpropanoid pathway and the role of polyphenols in plants under abiotic stress. Molecules. 2019;24(13):1–22.

34. Lamikanra O, Kassa AK. Changes in the free amino acid composition with maturity of the noble cultivar of *Vitis rotundifolia* Michx. grape. J Agric Food Chem. 1999;47(12):4837–41.

35. Rusjan D, Veberič R, Mikulič-Petkovšek M. The response of phenolic compounds in grapes of the variety "Chardonnay" (*Vitis vinifera* L.) to the infection by phytoplasma Bois noir. Eur J Plant Pathol. 2012;133(4):965–74.

36. Havaux M, Niyogi KK. The violaxanthin cycle protects plants from photooxidative damage by more than one mechanism. Proc Natl Acad Sci USA. 1999;96(15):8762–7.

37. Joubert C, Young PR, Eyéghé-Bickong HA, Vivier MA. Field-grown grapevine berries use carotenoids and the associated xanthophyll cycles to acclimate to UV exposure differentially in high and low light (Shade) conditions. Front Plant Sci. 2016;7(June2016):1–17.

38. Niculescu V-C, Paun N, Ionete R-E. The Evolution of polyphenols from grapes to wines. In: Jordao AM, Cosem F, editors. Grapes and wines-advances in production processing, analysys and valorization. Intech open; 2018. p. 119–41.

39. Crupi P, Santamaria M, Vallejo F, Tomás-Barberán FA, Masi G, Caputo AR, Battista F, Tarricone L. How pre-harvest inactivated yeast treatment may influence the norisoprenoid aroma potential in wine grapes. Appl Sci. 2020;10(10):3369. https://doi.org/10.3390/app10103369.

40. Tassoni A, Tango N, Ferri M. Comparison of biogenic amine and polyphenol profiles of grape berries and wines obtained following conventional, organic and biodynamic agricultural and oenological practices. Food Chem. 2013;139(1–4):405–13. https://doi.org/10.1016/j.foodchem.2013.01.041.

41. Cortell JM, Halbleib M, Gallagher AV, Righetti TL, Kennedy JA. Influence of vine vigor on grape (*Vitis vinifera* L Cv Pinot noir) and wine proanthocyanidins. J Agric Food Chem. 2005;53(14):5798–808.

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