# **Multi-platform metabolomic approach to discriminate ripening markers of black truffles (***Tuber melanosporum* **Vittad.)**

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**Running head**: An untargeted metabolomics study for the evaluation of black truffle ripening

### **ABSTRACT**

 Black Périgord truffle (*Tuber melanosporum* Vittad.) is a *Tuber* with a black ascocarp and tiny white veins. This hypogeous fruit body has gained widespread attention among chefs for its aroma. Understanding metabolic variation during ripening of truffles can shed lights on truffle biology. In this work, the comprehensive polar and lipid metabolome along with the volatile organic compounds (VOC) of *T. melanosporum*, were studied at different ripening stages by means of a metabolomic approach using gas chromatography-mass spectrometry (GC-MS). Multivariate statistical data analysis indicated that the polar metabolite profile of truffles changed during ripening and that the metabolites that mostly discriminated truffles in the early ripening stages belonged to the classes of saccharides, while free fatty acids, amino acids, among which precursors of VOC, and others were found at higher levels in the late stages of ripening (December-March). 12 PCA of the volatilome indicated that the modifications of the VOC profile did not have a clear pattern upon ripening. Interestingly, dimethylsulfide and dimethyldisulfide characterized most of the samples collected in December-January, while 1-octen-3-ol was in higher level in samples collected in February-March. No relevant differences were seen in the lipid profile of truffle during ripening. GC-MS based metabolomics can be a powerful tool to study the impact of ripening on polar metabolites and VOC profiles of *T. melanosporum*.



 

Key Words: ascomycete fungus, XCMS, black truffle, OPLS-DA, *Tuber melanosporum*.

## **INTRODUCTION**

28 Truffles are hypogeous ascomycete fungi which live in symbiosis with roots of various angiosperm. and gymnosperm species. The black Perigord truffle or black Spanish truffle *Tuber melanosporum* Vittad.) is a highly prized culinary delicacy widely appreciated because of its unique and characteristic aroma. *Tuber melanosporum* truffles can be found in several regions of southern Europe, especially Spain, Italy and France and are harvested with the aid of dogs, which can smell the ripe truffle volatiles underneath the ground surface. Currently, *T. melanosporum* fruiting bodies are obtained from nature and semi-artificial cultivation and have a limited harvesting season during winter.

 To increase our biological understanding of this organism and to uncover biomarkers of authenticity, freshness, and maturation, several studies have been carried out focusing on different 38 molecular pools. For their peculiar roles in truffles, VOCs have been amply studied and reviewed (Splivallo et al., 2011; Culleré et al., 2010; Vahdatzadeh & Splivallo, 2018; Vita et al., 2018). 40 Volatiles emitted by truffles mediate the interaction with plants, insects, and mammals, and their content greatly varies during ripening (Splivallo et al. 2011). The volatilome of truffles mainly 42 consists of a blend of aldehydes, alcohols, aromatic and sulfur compounds (Vahdatzadeh et al., 2017). Among the most characteristic volatiles, there are dimethyl sulfide (DMS), 1-octen-3-ol, 2- methylbutanal, 3-methylbutanal, 2-methylbutan-1-ol, and 3-methylbutanol. Metabolites, i.e. the low molecular weight hydrosoluble compounds, in truffles were studied by Mannina et al. (2004) using high-field NMR analytical platform. Longo et al. (2017) proposed an untargeted high-resolution 47 mass spectrometry approach to study metabolites involved in the quality modifications over the storage of *T. melanosporum*. Furthermore, Islam and colleagues (Islam et al., 2013) studied, with a proteomic approach, functional characteristics of proteins in black truffle. Studies of changes in the biochemical characteristics of the black truffle associated to maturation (Harki et al., 2006) and freezing processes (Culleré et al., 2013; Campo et al., 2017) were carried out. Tuber melanosporum fruiting is a multigene-mediated process that follows organised differentiation patterns and requires several months (Parguey-Leduc et al. 1984, Martin et al. 2010, Zarivi et al. 54 2015). These patterns can be classified into fruiting induction, typically happening in May-June, sporocarp development (which includes the peridial, veined, ascal and sporal stages), and maturation, typically happening in late autumn and early winter (Montant et al. 1983, Parguey-57 Leduc et al. 1984, Pacioni et al. 2014, Zarivi et al. 2015). After the mating event, the sporocarp starts to develop and its structure becomes gradually complex as the weight rapidly increases. The

sporocarp depends on photosynthetically-derived carbon from the host throughout its development,

with the mycorrhizas also playing a key role in nitrogen acquisition of the sporocarp (Hacquard et al







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83 chromatography coupled to mass spectrometry followed by multivariate statistical data analysis.

#### **MATERIALS AND METHODS**

 **Chemicals.** Analytical standard grade methanol, chloroform, hexane, trichloroacetic acid, pyridine, O-methylhydroxylamine hydrochloride, sodium methoxide 25 wt % in methanol, N-methyl-N- (trimethylsilyl)trifluoroacetamide (MSTFA), 2,2,3,3-*d4*-succinic acid, potassium chloride, were purchased from Sigma Aldrich (Milano, Italy). Bi-distilled water was obtained with a MilliQ purification system (Millipore, Milan, Italy).

 **Truffle samples.** A total of 55 samples of fresh and healthy ascocarp samples of *T. melanosporum* were collected from October to March (2017-2018) in cultivated truffle-grounds under holm oak trees (*Quercus ilex* L. subsp. *ballota* (Desf.) Samp) in Sarrion (Teruel, Spain), and taxonomically authenticated by morphological features (Riousset et al., 2001). Fresh truffles were washed to remove contaminants. A sample from the inner part of each gleba was taken, lyophilized and kept at -20 °C. For each sample the following data were collected: month of sampling (one sampling every 30 days was performed), the sporocarp development stage according to Zarivi et al. (2011), and whether the dig was found by the dog (aroma is developed at least in one truffle) or the dog passed over and didn´t mark the place, in these cases we carefully excavated the soil until finding the truffles (Tables 1S and 2S).

 **Sample preparation for GC-MS analysis.** Truffle samples were stored into sterile plastic Falcon 101 tubes at -20 °C before analysis. Truffle samples were thawed on ice and ground to a fine powder. Six hundred µL of a mixture of methanol and chloroform (2:1 *v/v*) were added to 100 mg of sample. Samples were sonicated for 15 min and left for 24 h in the dark at room temperature. Further 500 µL of the same mixture were added and samples were ultrasonicated with a Vibracell cell disruptor (Labotal Scientific Equipment, Abu Ghosh, Israel). The ultrasonication was performed twice with 20 s pulses at 60% amplitude (130 W, 20 kHz). Then, 100 µL of aqueous KCl 0.2M and 200 µL of chloroform were added. Samples were vortexed for 10 sec. Samples were then centrifuged at 15294 g for 10 min. A volume of 200 µL of the methanol/water mixture and the organic layer was extracted from each sample and moved into different 1.5 mL sterile glass vials, and dried under a gentle nitrogen stream. The aqueous layer was derivatized adding 40 µL of MSTFA and samples were vortexed. After 30 min at 70 °C, 600 µL of hexane containing 4.15 mg/L of 2,2,3,3-*d4*- succinic acid were added as the internal standard and homogenized again before GC-MS analysis (Caboni et al. 2016). Fatty acids of the lipid fraction were methylated using sodium methoxide in anhydrous methanol. To each dried chloroform extract was added 500 μl of hexane and 200 μl of sodium methoxide. The sample was placed in an oven at 55 °C for 30 min. Then, 200 μl of HCl 2N were added, and samples were centrifuged for 5 min at 15294 g. The supernatant was placed in a glass vial for the GC-MS analysis.

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 **GC-MS analysis.** The derivatized samples were analyzed with a Hewlett Packard 6850 Gas Chromatograph, 5973 mass selective detector, and 7683B series injector (Agilent Technologies, Palo Alto, CA), using helium as carrier gas at 1.0 mL/min flow. One μL of each sample was 123 injected in the split-less mode and resolved on a 30 m  $\times$  0.25 mm  $\times$  0.25 µm DB-5MS column (Agilent Technologies, Palo Alto, CA). Inlet, interface, and ion source temperatures were 250, 250 125 and 230 °C, respectively. Oven starting temperature was set to 50 °C, final temperature to 230 °C 126 with a heating rate of  $5^{\circ}$ C/min for 36 min and then for 2 min at a constant temperature. Electron impact mass spectra were recorded from m/z 50 to 550 at 70 eV. Chromatograms in the AIA format were then uploaded to the XCMS Online platform (Tautenhahn, Patti, Rinehart, & Siuzdak, 2012). The output pf XCMS consisted of a list of >4000 features for the aqueous fraction and 60 for the lipid fraction. Each feature corresponded to the area value of an *m/z* ion at a specific retention time value.

 The identification of metabolites was performed by mass spectra comparison with analytical standards and NIST14 library database of the National Institute of Standards and Technology (Gaithersburg, MD) and Golm library [\(http://gmd.mpimp-golm.mpg.de/\)](http://gmd.mpimp-golm.mpg.de/).

 **HS-GC-MS analysis.** The aromatic profile was analyzed by static headspace (HS) technique by using a Turbomatrix HS16 sampler (PerkinElmer, Massachusetts, USA). Four grams of sliced 137 truffle were placed in 20 mL vials and hermetically closed. Samples were heated at  $120^{\circ}$  for 20 min and 1 min of pressurization time. The injection was carried out over 6 s at 20 psi and an inlet 139 temperature of 220 °C. HS Sampler was connected to a Clarus 500 Gas Chromatography system coupled with a Mass Spectrometer (PerkinElmer, Massachusetts, USA) equipped with a DB-Wax capillary column (60m x 0.25mm i.d.x 0.25 µm film thickness) (Agilent Technologies, California, USA). A flow of 1 mL/min was used with helium as a carrier gas. The oven temperature was 45ºC 143 held for 2 min, 45-110°C at a rate of 7 °C/min, and finally to 225 °C at 10 °C/min, and held for 5 min. The mass spectrometer used the electron impact (EI) mode with an ionization potential of 70 eV and an ion source temperature of 200ºC. The interface temperature was 220ºC. The mass spectrometer scanning was recorded in full scan mode (40-300 m/z). A TurboMass ver. 5.4.2 software was used for controlling the GC-MS system. Peak identification of the volatile components was achieved by comparison of the mass spectra with mass spectral data from the NIST MS Search Program 2.0 library and by comparison of previously reported Retention Index (RI) with those calculated using an n-alkane (C7-C25) series under the same analysis conditions.

- **Multivariate statistical data analysis (MVA).** The GC-MS data were submitted to Multivariate statistical analysis (MVA) as implemented in SIMCA-P+ software (version 14.1, Umetrics, Umeå,
- Sweden). Prior to MVA, GC features were mean centred and scaled to unit variance column-wise.





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- Principal component analysis (PCA) was performed to investigate sample distributions, deviating
- features and prevailing trends. The partial least squares-discriminant analysis (PLS-DA) and its 165 **ha eliminato:** common
- orthogonal variant (OPLS-DA) were performed for classification of samples and identification of
- the most discriminant variables. The variable importance in projection (VIP) scores, that summarize
- 163 the contribution of each variable to the model, were **analyzedand** only those metabolites having VIP
- values > 1 were deemed as discriminant between the classes.



### **RESULTS**

 *Polar metabolites.* At first, GC-MS data of the hydro soluble fraction of truffles were submitted to 170 PCA. Sample distribution in the first 2 PC (score plot Figure 1A) evidenced that samples can be divided into two main classes, one composed by samples harvested in October-November and the other by those harvested from December to March. This sample's behavior suggests that the metabolite levels in truffles mainly depend on the month of harvesting, to note, the influence of other characteristics, such as sporocarp development stage and the ability of dogs to find samples, 175 were unfruitfully explored (see score plots in Figure 1SA and B, supporting information). In the 176 corresponding loading plot (Figure 1B) we highlighted some of the GC-MS features ascribed to the metabolites that mostly influenced sample distribution. The list of detected metabolites is reported 178 in Table 1. An OPLS-DA was carried out comparing the two classes i.e. samples collected in October-November vs those collected from December to March. The metabolites discriminating samples from December to March were mainly organic acids, polyols, free fatty acids, and free amino acids. While the metabolites discriminating samples from October-November were: mono 182 and disaccharides, phenol and a highly discriminant not annotated metabolite at 16.96 min (Table 2). As reported in Tables 1S and 2S, December-March is the best period for harvesting mature truffles (sporocarp developmental stage VI-b,c), probably in these months the polar metabolites reach a well defined profile, different from immature truffles. *VOC analysis***.** VOC data are reported in Table 3. As we can see, different main classes of compounds were identified, in agreement with the fact that black truffles are regarded as those having the most intense aroma of all the truffles (Wang et al., 2011). A PCA was carried out for the VOC data (Figure 2). The score plot of Figure 2A showed a different sample distribution with respect to that reported for the polar metabolites (Figure 1A). In fact, samples did not form well defined groups; however, most of the samples collected in December-January and in February- March differentiated from the others that, instead, tightly clustered. Interestingly, in the score plot 193 when we used the same color for those samples found in the same dig  $(Figure 2S)$ , we observed that samples found in the same dig are next to each other, therefore they have a similar VOC profile.

 This observation supports the theory of a symbiotic relationship between truffle, soil and microbiome, representing the dig as a small ecosystem.

197 The analysis of the loading plot (Figure 2B) indicated that the December-January samples were characterized, among others, by more dimethyl sulfide (DMS) and dimethyl disulfide (DMDS), key-compounds evoking the aroma typically associated with fresh truffle, while samples collected in February-March by higher levels of 1-octen-3-ol. This eight carbons volatile compound is

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 considered a key odorant in mature truffles (Splivallo et al., 2011) and regulates the interactions with the environment during growth (Holighaus & Rohlfs, 2019).

 **Lipid fraction.** The lipid fraction was also investigated by GC-MS. The multivariate statistical analysis did not show any clear sample grouping; therefore, we can state that under our analytical conditions, the profile of the methoxide derivative fatty acids did not consistently changed upon 207 ripening (see supporting information Figure 3S).

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## **Discussion**

 The discriminant analysis of the polar metabolites indicated that truffles harvested in December-March have higher levels of the free fatty acids: palmitic acid, linoleic acid, oleic acid, and stearic acid. Unsaturated fatty acids in their free form are the preferential targets of lipid oxidation mechanisms. The enzymatic and non-enzymatic oxidation of linoleic acid produces a number of C8 volatile compounds which are important hormone-like factors that regulate the phenotypic *status* of a fungus, i.e. growth, morphological differentiation and secondary metabolite production (Holighaus & Rohlfs, 2019). It has been postulated that in many filamentous fungi these VOC diffuse in the environment and interact with plants, generally exerting at high concentrations toxic effects (Splivallo et al., 2011), and with invertebrates, regulating the response of the ecological communities (Holighaus & Rohlfs, 2019). One of the products of linoleic acid breakdown is the 1-octen-3-ol, which is amongst the most characteristic C8 volatiles found in truffles (Splivallo et al., 2011), in agreement, this VOC was found in higher levels in our samples collected in February-March. Other C8 VOC can be produced by lipid oxidation, some of them were found in our samples.

 Mature truffles (December-March) have higher levels of free amino acids, among which, in agreement with Harki et al. (2006), alanine, serine and glutamine. Other amino acids, precursors of VOC through the Ehrlich pathway, were found upregulated in truffles collected in the last stages, among these, isoleucine and valine. Isoleucine is the precursor of 2-methylbutanal, found upregulated among the VOC of samples collected in December-January. This volatile aldehyde has been found to increase during the maturity of truffles (Harki et al., 2006). Valine is involved in the formation of the VOC diacetyl (2,3-butandione) and 2-methyl-1-propanol, found in higher levels in more mature samples.

 Cysteine, cystathionine, and homocysteine were found upregulated in the truffles of late harvesting (December-March). These compounds are key steps of sulphur metabolism in *T. melanosporum* fruiting body and are precursors of sulfur-containing volatile compounds, such as dimethylsulfide (DMS) and dimethyldisulfide (DMDS), powerful key odorants characteristic of

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 truffles, main attractants of dogs and pigs (Martin et al., 2010; Splivallo et al., 2011). Many sulphur-containing compounds have very low olfactory detection limits and are thus major contributors to the final aroma of truffle fruitbodies (Splivallo et al., 2011). It has been reported that, during fruit body development, the number of sulfur-containing volatile compounds increases, indeed, no sulfur compounds have been identified in completely immature fruit bodies (Zeppa et al., 2004). In agreement, higher levels of DMS and DMDS were found in our samples collected in December-January.

 Among VOC we found furfural, this aldehyde probably derived from the soil fungi (Leff et al., 2008). Among GC-MS polar metabolites, we found ergosta-5,7,22-triene. Ergosterol is the primary sterol of mushrooms and is one of the most important mycochemicals in *T. melanosporum* (Harki et al., 1996). Ergosterol has antioxidant, anti-inflammatory and antitumor properties. According to other authors, ergosterol seems to exhibit hypocholesterolemic effects, like the bioactive phytosterols (Longo et al., 2017).

 These overall results suggest that at the first stage of ripening lipolytic and proteolytic enzymes acted on the macromolecular classes yielding primary metabolite products (i.e. fatty acids and amino acids), that in turn are broken-down to a plethora of VOC. These bottom down products of the maturation process regulate the interactions with the environment, plants and animals, and also give the peculiar aroma that elevates Black Périgord truffle to one of the most prized and appreciated food delicacy.

 

## **ACKNOWLEDGMENTS**

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 Figure 1. PCA of hydrophilic metabolites. A) score plot, explained variance 35%; B) loading plot: light blue circles = unk1; dark green circles = disaccharides; dark blue circles = *scyll*o-inositol; dark yellow circles = serine, cystathione and cysteine; violet circles = alanine; red circles = valine; grey

circles = polyols. Red 4 point star = phytosterols. Brown boxes = glutamine; light green boxes =

linoleic acid. Light blue triangles = erythrose; brown triangles = palmitic acid.

Figure 2. PCA of volatile metabolites. A) score plot, explained variance 48 %; B) loading plot, only

- discussed metabolites are reported.
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352 Table 1. GC-MS characteristics of truffle metabolites.

Metabolite	$RT^a$	Mass $(m/z)$		
Unk $1b$	14.29	72	87	69
Unk2	15.05	147	73	174
2,3-butanediol	15.10	117	147	73
Unk3	15.35	174	130	75
Lactic acid	15.62	117	147	191
Glycolic acid	15.88	147	66	205
Alanine	16.45	116	73	147
Glycine	16.78	102	73	103
Unk4	16.96	130	188	144
β-lactic acid	17.24	147	219	177
β-hydroxybutyric acid	17.54	147	117	191
Unk5	17.71	73	188	144
2-aminobutyric acid	17.76	130	147	204
Unk <sub>6</sub>	18.12	147	221	117
Unk7	18.47	130	202	174
Valine	18.51	144	218	147
Urea	18.86	147	189	171
Leucine	19.39	158	147	232
Phosphate	19.45	299	73	314
Unk8	19.60	180	136	299
Isoleucine	19.71	158	218	45
Proline	19.75	142	147	102
Succinic acid	19.95	147	75	247
Glyceric acid	20.29	189	292	205
Fumaric acid	20.41	245	147	75
Serine	20.71	204	218	100
Threonine	21.09	218	117	291
Unk9	21.2	261	158	129
3,4-dihydroxybutanoic acid	21.66	233	189	117
Unk10	21.83	57	117	147
Unk11	21.86	273	147	175
Homoserine	21.9	218	128	103
Aminomalonic acid	22.18	179	105	147
Malic acid	22.40	233	245	133
Erythrose	22.72	170	147	217
Unk12	22.73	147	217	205
Pyroglutamic acid	22.76	156	147	258
Aspartic acid	22.81	232	100	218
Unk13	22.84	174	84	75
2,3,4-trihydroxybutyric acid	23.17	292	220	205
Cysteina	23.22	218	220	243
5,2-dihydroxy-4-pyran-4-one	23.46	271	147	45
Unk14	23.82	244	219	103
Glutamine	23.97	246	73	128



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353 a) retention time; b) unk = not identified; c) saccharide = compounds with fragmentation pattern ascribable to mono- or disaccharides.

fragmentation pattern ascribable to mono- or disaccharides.

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# 360 metabolites.





# 363 Table 3. VOC profile by HS-GC/MS of truffle samples. Area?







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Figure 1A and B

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# Figure 2A and B

## **Supporting information**



Table 2S. Truffle sample characteristics.



Figure 1S: GC-MS polar metabolites: PCA score plot, samples colored by A) detected (1) or not detected (0) by dogs; B) sporocarp development stages: IV (4), V (5), VI-a (6), VI-b,c (7). See Table 1 for details.





Figure 2S: GC-MS volatile metabolites: PCA score plot, truffle samples found in the same dig have same colors. bottom DMS



Figure 3S: GC-MS lipid fraction: PCA score plot, samples colored by A) month of harvesting; B) detected (1) or not detected (0) by dogs; C) sporocarp development stages: IV (4), V (5), VI-a (6), VI-b,c (7), see Table 1 for details.

