1	INFLUENCE OF OMEGA-3 PUFAs ON THE METABOLISM OF
2	PROANTHOCYANIDINS IN RATS
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- 23 **Running title**: ω-3 PUFAs and metabolism of proanthocyanidins
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- 25 bioavailability

26	List of abbreviations
27	EC, (epi)catechin
28	EGC, (epi)gallocatechin
29	Gluc, glucuronyl group
30	GSE, grape seed extract
31	Me, methyl group
32	MRM, multiple reaction monitoring
33	PAs, proanthocyanidins
34	STD, standard diet
35	Sulf, sulfate group
36	SPE, solid-phase extraction

38 Abstract

39 Studies of the bioavailability of proanthocyanidins usually consider them independently 40 of other dietary constituents, while there is a tendency in the field of functional foods 41 towards the combination of different bioactive compounds in a single product. This 42 study examined the long-term effects of ω -3 polyunsaturated fatty acids of marine 43 origin on the metabolic fate of grape proanthocyanidins. For this, female adult Wistar-44 Kyoto rats were fed (18 weeks) with a standard diet supplemented or not with 45 eicosapentaenoic acid/docosahexanoic acid (1:1, 16.6 g/kg feed), proanthocyanidin-rich 46 grape seed extract (0.8 g/kg feed) or both. A total of 39 microbial-derived metabolites 47 and 16 conjugated metabolites were detected by HPLC-MS/MS either in urine or in the 48 aqueous fraction of feces. An unexpected significant increase in many proanthocyanidin 49 metabolites in urine and feces was observed in the group supplemented with ω -3 50 polyunsaturated fatty acids group as compared to the animals fed a standard diet, which 51 contains a small amount of polyphenols. However, proanthocyanidin metabolites in rats 52 given ω-3 polyunsaturated fatty acids and grape seed extract did not significantly differ 53 from those in the group supplemented only with grape seed extract. It was concluded 54 that ω -3 polyunsaturated fatty acids collaborate in the metabolism of polyphenols when 55 present at low doses, while the capacity of ω -3 polyunsaturated fatty acids to induce 56 microbiota transformations when proanthocyanidins are present at high doses is not 57 relevant compared to that of polyphenols themselves.

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61 1. INTRODUCTION

62 Polyphenols are a large group of compounds found in plant foods that have been shown to have health-related effects in relation to several chronic diseases (Scalbert et al., 2005). 63 64 Flavanols, included in the family of flavonoids, are among the most studied polyphenols. They range in complexity from monomers, such as (+)-catechin or (-)-epicatechin, to 65 66 combinations of these structures via different linkages, which gives rise to the corresponding oligomers or polymers- (proanthocyanidins, PAs). Flavanols are found in 67 68 many common foods, such as grapes, nuts or cocoa, and have been shown to have beneficial effects in relation to different markers of cardiovascular disease. Indeed, the 69 70 European Food Safety Agency approved a health claim regarding the effects of cocoa 71 flavanols on endothelium-dependent vasodilatation (EFSA, 2006).

72 A key aspect of the study of PAs is the proper knowledge of their metabolic fate, since they 73 are extensively transformed after ingestion. Dimers and to a lesser extent trimers may be 74 absorbed in the small intestine; the former may be methylated while no post-absorption 75 transformation has been reported for trimers (Monagas et al., 2010). However, most 76 ingested PAs reach the colon, being either extensively depolymerized and absorbed as 77 monomers or metabolized by the gut microbiota (Touriño et al., 2011). Monomers are 78 extensively conjugated in the liver and then circulate in the body before being excreted in 79 urine or accumulated in tissues, or they return to the intestine via enterohepatic circulation. 80 While for those PA transformed by the microbiota, the resulting metabolites are mostly 81 phenolic acids that may be absorbed and follow the same routes as polyphenols absorbed 82 in the small intestine (Urpí-Sardá et al., 2009; Monagas et al., 2010; Mateos-Martín, Pérez-83 Jiménez, Fuguet, & Torres, 2012a). Increasing evidence suggests that circulating 84 polyphenol-derived metabolites, especially those produced during colonic fermentation, 85 may be the compounds responsible for the health-related properties of these food

86 constituents (Williamson, & Clifford, 2010).

87 To elucidate the metabolic fate of polyphenols, they are administered alone and in acute 88 doses (Urpí-Sardá et al., 2009; Monagas et al., 2010; Touriño et al., 2011; Mateos-Martín 89 et al., 2012a). In a common diet, however, polyphenols are consumed in combination with 90 other food components, which may have either synergic or antagonistic effects on their 91 bioavailability. Moreover, there is currently increasing interest in the development of 92 functional foods with combinations of bioactive components (Peluso, Romanelli, & 93 Palmery, 2014), which may affect the bioavailability of polyphenols and the health effects 94 derived from them. Therefore, now that the general process of transformation of these 95 compounds has been reported, there is increasing interest in the effects that other food 96 constituents, such as carbohydrates, proteins or dietary fiber, may have on their 97 bioavailability (Bohn, 2004; Zhang et al., 2014).

98 In relation to dietary fat, studies with animal models (Lesser, Cermak, & Wollfram, 2008) 99 and humans (Tulipani et al., 2002; Guo et al., 2013) have reported that this food constituent 100 increases the bioaccessibility and absorption of certain flavonoids, through different 101 mechanisms. Differential effects of long-chain and medium-chain fatty acids on the 102 bioavailability of polyphenols are probably due to the different metabolic routes that these 103 compounds follow (Lesser, Cermak, & Wollfram, 2006; Murota, Cermak, Terao, & 104 Wollfram, 2013). In contrast, the effects of fatty acids with different degree of unsaturation 105 on the metabolic fate of polyphenols have not been explored. Indeed, studies in this area 106 have only evaluated the differential effects of saturated and monounsaturated fats (Tulipani 107 et al., 2002; Lesser, Cermak, & Wollfram, 2006; Lesser, Cermak, & Wollfram, 2008; Guo 108 et al., 2013; Murota et al., 2013), and to the best of our knowledge, only one *in vitro* study 109 has considered the effects of a polyunsaturated fat: hazelnut oil (Ortega, Macià, Romero, 110 Reguant, & Motilva, 2011).

111 Long-chain ω -3 PUFAs of marine origin are a class of bioactive dietary components that 112 have generated a great deal of interest due to their beneficial effects in both animal and 113 human studies, on parameters related to cardiovascular disease (Aguilera, Díaz, Barcelata, 114 Guerrero, & Ros, 2004; Lorente-Cebrián, Costa, Navas-Carretero, Zabala, Martínez, & 115 Moreno-Aliaga, 2013). In a common diet, and in supplements containing different 116 bioactive compounds, polyphenols may be consumed together with ω -3 PUFAs and 117 different interactions may take place (Peluso et al., 2014), which could also affect their 118 metabolic fate. Therefore, the aim of this study was to evaluate the effect that ω -3 PUFAs 119 had on the metabolic fate of grape PAs after long-term in vivo supplementation. To this 120 end, a pilot study was carried out in Wistar-Kyoto rats, and the profile of polyphenol 121 metabolites was measured by targeted HPLC-ESI-MS/MS analysis of urine and the 122 aqueous fraction of feces.

123 2. MATERIALS AND METHODS

124 **2.1 Chemicals and reagents**

125 The standard diet was Teklad Global 2014 (Harlan Teklad Inc., Indianapolis, IN, USA). Fine Graifnol[®] powder, 98% grape seed, was obtained from JF-Natural Product (Tianjin, 126 127 China), with the following composition: total PAs (UV), $\geq 95\%$; oligometic PAs, $\geq 60\%$; 128 procyanidin dimer B₂ (HPLC), $\geq 1.8\%$; ash, $\leq 1.5\%$; weight loss on drying, $\leq 5.0\%$. 129 Porcine gelatin type A 240/260 was from Juncà (Girona, Spain) and the soybean lecithin 130 Topcithin 50 from Cargill (Barcelona, Spain). Oil with an eicosapentaenoic 131 acid:docosahexanoic acid (EPA:DHA) ratio of 1:1 was obtained by mixing appropriate 132 quantities of the commercial fish oils AFAMPES 121 EPA (A.F.A.M.S.A., Vigo, Spain), 133 EnerZona Omega 3 RX (Milan, Italy) and Oligen liquid DHA 80% (IFIGEN-EQUIP 98, S.L., Barcelona). Soybean oil, obtained from unrefined organic soybean oil (first coldpressing), was from Clearspring Ltd. (London, UK).

136 Ketamine chlorhydrate was purchased from Merial Laboratorios (Barcelona, Spain) and 137 xylazine from Química Farmaceutica (Barcelona, Spain). Standards of (−)-epicatechin (≥ 98%), (-)-epigallocatechin (\geq 95%), 3-hydroxyphenylacetic acid (\geq 99%), 4-138 hydroxyphenylacetic acid (\geq 98%), 3,4-dihydroxyphenylacetic acid (\geq 98%), 3-139 140 hydroxybenzoic acid (\geq 99%), 4-hydroxybenzoic acid (\geq 99%), homovanillic acid (\geq 141 98%), vanillic acid (\geq 97%), caffeic acid (\geq 98%), 3,4-dihydroxyphenylpropionic acid (\geq 98%), 3-hydroxyphenylpropionic acid (\geq 98%), 4-hydroxyphenylpropionic acid (\geq 98%), 142 143 3,4-dihydroxybenzoic acid (\geq 97%), benzoic acid (\geq 99%), hippuric acid (\geq 98%), ferulic 144 acid (\geq 99%), isoferulic acid (\geq 97%), *p*-coumaric acid (\geq 98%), *m*-coumaric acid (\geq 98%), 145 gallic acid (\geq 97%), enterodiol (\geq 95%), phenylacetic acid (\geq 99%), taxifolin (\geq 85%), and 146 tert-butylhydroquinone and formic acid (analytical grade) were obtained from Sigma 147 Chemical (St Louis, MO, USA). Methanol (analytical grade) and hydrochloric acid (≥ 148 85%) were from Panreac (Castellar del Vallès, Barcelona, Spain). Acetonitrile (HPLC 149 grade) was obtained from Merck (Darmstadt, Germany). Water for the assay solutions was 150 obtained using a water Milli-Q purification system (Millipore Corporation, Billerica, MA, 151 USA).

152 **2.2 Diets**

Four diets were prepared: the standard diet; the standard diet supplemented with ω -3 PUFAs; the standard diet supplemented with grape seed extract; and the standard diet supplemented with both ω -3 PUFAs and grape seed extract. The diets without ω -3 PUFAs were enriched with soybean oil in order to make them isocaloric. All the diets were prepared in-house and included tert-butylhydroquinone as an antioxidant, porcine gelatin to promote gelatinization and soybean lecithin as an emulsifier. The mixtures were freeze-

159 dried to obtain pellets that were stored at 4°C to prevent oxidation and fungal 160 contamination. The composition of each diet, including the supplementations with ω -3 161 PUFAs and GSE, as well as both the macronutrient and micronutrient profile, is shown in 162 Supplemental Table 1. A mixture of EPA and DHA in a ratio of 1:1 was used, since it has 163 been suggested that each fatty acid may have different health effects (Lorente-Cebrián et 164 al. 2013). This ratio was previously reported as the most beneficial for cardiometabolic 165 risk factors (Lluís et al., 2013; Méndez et al., 2013). The fatty acid composition of the 166 soybean oil and ω -3 PUFA supplement were ascertained by gas chromatography after 167 methylation (Lepage, & Roy, 1986) and are provided in Supplemental Table 2. Because 168 PUFAs are extremely susceptible to oxidation and due to the potential toxic effects of lipid 169 oxidation byproducts, the lipid oxidation level was checked throughout the dietary 170 interventional experiment (peroxide values < 5 meq. oxygen per kg of oil).

The doses of ω-3 PUFAs (16.6 g/kg feed) and grape PAs (0.8 g/kg feed) were chosen on
the basis of previous studies where similar doses showed beneficial effects (Masson et al.,
2008; Castell-Auví, Cedó, Pallarés, Blay, Pinent, & Ardévol., 2013) and as realistic doses,
i.e., doses which could easily be incorporated into a typicalcommon diet.

175 **2.3 Animals and sample collection**

Twenty female, 8- to 9-week-old, Wistar-Kyoto rats (Charles River Laboratories, Wilmington, MA, USA) were housed in cages (n = 2-3/cage) under controlled conditions of a 12 h light/12 h dark cycle, temperature of 22°C ± 2°C and relative humidity of 50% ± 10%. They had free access to water and pelleted feed (**Supplemental Table 1**) for 18 weeks after being randomly divided into the four dietary groups: STD group (n = 5), given the standard diet supplemented with soybean oil; ω -3 group (n = 5), given the standard diet supplemented with ω -3 PUFAs; GSE group (n = 5), given the standard diet supplemented

183 with grape seed extract and soybean oil; and ω -3+GSE group (n = 5), given the standard diet supplemented with both ω -3 PUFAs and grape seed extract. For urine and feces 184 185 collection, the rats were individually placed in metabolic cages and deprived of food for 24 186 h. At the end of the experiment, the rats were fasted overnight and anesthetized by an 187 intraperitoneal injection of 80 mg/kg of ketamine (Imalgene 1000, Merial Laboratorios 188 S.A., Barcelona, Spain) and 10 mg/kg of xylazine (Rompun 2%, Química Farmacéutica 189 S.A., Barcelona, Spain). Female rats were chosen because they had previously been 190 demonstrated to be as valid model for studying the metabolic fate of PAs (Mateos-Martín 191 et al., 2012a; Touriño et al., 2011; Molinar-Toribio et al., in press)

The handling and killing of the animals were in full accordance with the European Union guidelines on the care and management of laboratory animals, and the pertinent permission was obtained from the CSIC Subcommittee for Bioethical Issues (ref. AGL2009-12 374-C03-03).

196 **2.4 Sample processing**

197 Urine samples were processed following a previously described solid-phase extraction 198 (SPE) procedure (Touriño, Fuguet, Vinardell, Cascante, & Torres, 2009) for the extraction 199 of phenolic metabolites. Briefly, Oasis HLB (60 mg) cartridges from Waters Corporation 200 (Milford, MA, USA) were activated with 1 mL of methanol and 2 mL of water acidified to 201 pH 3 with formic acid (acid water). The samples (total volume of collected urine) were 202 loaded, interfering components were removed with 9 mL of acid water and then the 203 phenolic compounds were eluted with 1 mL of methanol. Taxifolin (final concentration of 204 5 mg L^{-1}) was used as internal standard.

Fecal samples collected over 24 h were re-suspended in acid water and homogenized on a vortex. Then, after adding the internal standard (taxifolin, 5 mg L⁻¹) the mixtures were centrifuged (10000 g, 10 min at 4°C) to obtain a supernatant containing the aqueous

fraction of the feces. This supernatant was freeze-dried and re-suspended in 1 mL of acid water, homogenized on a vortex, and then subjected to SPE and the work-up process described for the urine samples.

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212 **2.5 HPLC-ESI-MS/MS** analysis of polyphenol metabolites

213 An Applied Biosystems (PE Sciex, Concord, Ontario, Canada) API 3000 triple quadrupole 214 mass spectrometer with a TurboIon spray source was used in negative mode to obtain MS 215 and MS/MS data. HPLC separations were performed on an Agilent 1100 series (Agilent, 216 Waldbronn, Germany) liquid chromatograph equipped with a Phenomenex (Torrance, CA, 217 USA) Luna C18 (50 x 2.0 mm i.d.) 3.0 µm particle size column and a Phenomenex 218 Securityguard C18 (4 x 2.0 mm i.d.) column. Gradient elution was performed with a binary 219 system consisting of [A] 0.1% aqueous formic acid and [B] 0.1% formic acid in CH₃CN. 220 The following increasing linear gradient (v/v) of [B] was used, (t (min), % B): 0.8; 10,23; 221 15,50; 20,50; 21,100 followed by a re-equilibration step. MS conditions were as previously 222 described (Touriño et al., 2009). Each metabolite in the urine samples was first identified 223 by MRM (multiple reaction monitoring) transition of the putative metabolites using a dwell 224 time of 100 ms and then confirmed either by comparison with a standard when available, 225 second MRM, or neutral-loss and product ion scan experiments. Identification details are 226 published elsewhere (Molinar-Toribio et al., in press). The MS conditions for each MRM 227 transition were optimized by direct injection of metabolite standards, when available; for 228 other metabolites, the conditions of the most structurally similar standard were used. 229 Analyst 1.4.2 software from AB Sciex was used for data acquisition and processing. 230 Standard calibrations curves were made for each metabolite using between 4 and 11 231 different concentrations for each of them, between 0.001 and 60 mg L⁻¹, and they were 232 used to determine the concentration of each metabolite in the samples, after correction by the internal standard concentration. When no commercial standard was available, the metabolites were quantified using a structurally related commercial standard. For details of the calibration curves used, see **Supplemental Table 3**. The structurally related commercial standard may still show a different response from that of the metabolite, so this method should be used mainly for comparative purposes.

238 **2.6 Statistics**

239 Results are expressed as mean concentrations + standard error of the mean (SEM), expressed in µmol/L urine or µmol/g dried feces, adjusted in both cases per kg feed/kg 240 241 body weight. Mean body weight and feed consumption data per group were used for this 242 adjustment. Since the data did not follow a normal distribution, the non-parametric 243 Kruskal-Wallis and Mann-Whitney U tests were applied to analyze the significant 244 differences (P < 0.05) comparing the four groups to one another. The Kruskal-Wallis test 245 was applied to determine any significant difference between the treatments and, if any 246 were detected, the Mann-Whitney U test was used to compare all the different pairs of the 247 treatments. The SPSS IBM 19 package for Windows was used throughout.

248 **3. RESULTS**

3.1 Feed intake

Feed intake was monitored throughout the study. Mean values standardized by rat weight (g/kg rat/day) were: STD group, 59.4 (SEM 2.6); ω -3 group, 41.4 (SEM 4.5); GSE group, 56.4 (SEM 4.2); ω -3+GSE group, 40.0 (SEM 3.6). The intakes in ω -3 group and in the ω -3+GSE group were significantly lower than in the STD group (*P* 0.020 and 0.0058, respectively). The mean values of caloric intake (kcal/100 g rat/day) throughout the study were: STD group, 184.0 (SEM 38.9); ω -3 group, 128.4 (SEM 44.5); GSE group, 174.8 (SEM 44.5); ω -3+GSE group, 124.9 (SEM 39.7). Similarly, the energy intakes in ω -3 257 groups were significantly lower than in the STD and in the GSE groups. Due to these
258 differences in the intakes, the results were adjusted per feed intake and body weight.

259 **3.2** Conjugated metabolites of (epi)catechin and (epi)gallocatechin in urine

A total of 39 transitions were searched for in urine, corresponding to mono-, di- and triconjugated metabolites of (epi)catechin (EC) and (epi)gallocatechin (EGC) (derived from the combinations of the methylated or Me, sulfated or Sulf and glucuronidated or Gluc forms). The fragmentation patterns obtained for the different compounds were compared with those reported in the literature for PA-derived conjugated metabolites (Urpí-Sardá et al., 2009; Mateos-Martín et al., 2012a).

266 A total of 8 transitions were detected in the samples, corresponding to 12 metabolites from 267 EC and 2 from EGC. Different metabolites may be identified by the same transition, since 268 a substituent may be attached at different positions of the phenolic structure. This is the 269 case, for example, of Gluc-EC, for which 5 different positional isomers were separated and 270 identified by HPLC-MS/MS. The identification spectra for Gluc-EC is shown in 271 Supplemental Figure 1. Characteristic fragments of this metabolite were detected at m/z272 289, indicating the loss of the glucuronide moiety, as well as at m/z 175 and 113, 273 corresponding to the degradation of this moiety.

The concentrations of the conjugated metabolites detected in urine are provided in **Table 1**. For the individual metabolites identified, urine concentrations of Gluc-EC-1, Me-Gluc-EC-1, Me-Gluc-EC-2 and Me-Gluc-EC-3 were significantly increased in both the GSE and ω -3+GSE groups, compared to the STD and ω -3 groups (Me-Gluc-EC-2, **Supplemental Figure 2**). Gluc-EC-2 was also significantly increased in the GSE group but not in the ω -3+GSE group, compared to the STD group. In the ω -3 group, the urinary excretion of three glucuronidated EC forms was significantly higher than in the STD group.

281 Overall, the levels of conjugated metabolites of the monomers of PAs excreted in urine

were increased in both the GSE and the ω -3+GSE groups as compared to the STD group.

283 **3.3 Microbial-derived metabolites in urine**

We searched for 48 transitions, corresponding to the microbial metabolites formed in the 8 different steps of the microbial fermentation of PAs (valerolactones, lignans, phenylvaleric acids, phenylpropionic acids, phenylacetic acids, benzoic acids, cinnamic acids and glycinated benzoic acids) in the samples.

A total of 31 transitions were detected in the samples, corresponding to 39 metabolites, since it is known that the microbial metabolites of some PAs may present structural isomers—e.g., 3- or 4-hydroxybenzoic acid—and some of them may later be conjugated at different positions (Redeuil et al., 2011). For instance, the identification of *m*-coumaric and p-coumaric acid was based on standard retention times (**Supplemental Figure 3**). Metabolite concentrations are shown in **Table 2**.

In the GSE group, 24 metabolites occurred at concentrations significantly greater than in the STD group. In the case of the ω -3+GSE group, this affected 19 metabolites. No significant differences were observed between the two groups supplemented with GSE. In the ω -3 group, the concentration of 18 metabolites significantly increased with respect to the STD group- in most of the cases, the concentrations found in this group were lower than those found in the GSE and in the ω -3+GSE group.

300 **3.4 Microbial-derived metabolites in feces**

None of the EC or EGC conjugated metabolites found in urine were detected in feces. However, 11 microbial-derived metabolites were identified in the fecal samples (**Table 3**). In the GSE and ω -3+GSE groups, 7 metabolites were significantly greater than in the STD group. 4-Hydroxyphenylpropionic acid was also significantly higher in the ω -3+GSE group as compared to the STD group. In the ω -3 group, 5 metabolites were at significantly 306 greater concentrations than in the STD group. The concentrations in the ω -3 and the ω -307 3+GSE groups were within the same range for some compounds, while 4-308 hydroxyphenylpropionic acid showed the highest concentration in the ω -3+GSE group, 309 and 3-hydroxyphenylpropinic acid, Me-hippuric acid-1 and Me-hippuric acid-2 showed the 310 highest concentrations in the GSE group, although for Me-hippuric acid-1 the increment 311 was not statistically significant.

312 4. DISCUSSION

313 Here, we carried out a pilot study on the effects of ω -3 PUFAs on the metabolic fate of 314 PAs; an aspect that had not previously been explored. To mimic a human dietary situation, 315 this was evaluated in rats after long-term exposure to diets that incorporated both 316 components. PA-derived conjugated EC and microbially generated metabolites were 317 measured in urine; the biological fluid considered the most appropriate for evaluating the 318 bioavailability of polyphenols (Pérez-Jiménez et al., 2010), given the short half-life in 319 plasma of their metabolites. These metabolites were also measured in fecal water, i.e., the 320 fraction of the feces closest to the colonic epithelium (Gill et al., 2010) that could 321 potentially be involved in the reported effects of PAs on colonic health (Rossi, Bossetti, 322 Negri, Lagiou, & La Vecchia, 2010; Sánchez-Tena et al., 2013). Since intakes were 323 significantly different between the groups- i-e., the lowest intakes were found in the ω -3 324 groups- metabolite concentrations were adjusted per feed intake. Nevertheless, metabolite 325 concentrations in the GSE groups were in the same range as those reported in studies with 326 similar supplementations for shorter periods (Tsang et al., 2005; Choy et al., 2014). Also, 327 the nature of the metabolites found was the same as that of those previously reported in 328 studies of the metabolic fate of PAs, a process described in detail elsewhere (Mosele, 329 Macià, & Motilva, 2015). This shows that the same tendencies are maintained for long-330 term supplementation.

331 We obtained an unexpected result, in that microbial-derived PA metabolites increased (in 332 urine and in feces), as did some EC conjugates, in the ω -3 group (without GSE 333 supplementation). Since these metabolites are not present in the metabolic routes of ω -3 334 PUFAs, it seems that ω -3 PUFAs collaborated in the transformation of polyphenols already 335 present in the basic STD diet (and responsible for the values obtained in the STD group). 336 The STD diet contained wheat middlings, ground wheat and ground corn; cereals that 337 include PAs among their phenolic compounds (McCallum, & Walker, 1990; Hichem, 338 Mounir, & Naceur, 2009; Arranz, & Saura-Calixto, 2010). Indeed, the STD diet contains 339 not only the PAs that occur free in the food matrix (known as extractable PAs), but also the 340 fraction associated with the dietary matrix, the so-called non-extractable PAs (Arranz, & 341 Saura-Calixto, 2010) which are also extensively metabolized by the colonic microbiota 342 after being released from the food matrix (Mateos-Martín, Pérez-Jiménez, Fuguet, & 343 Torres, 2012b). Our results suggest that ω -3 PUFAs may promote PA metabolism through 344 interactions with the gut microbiota. This point needs to be addressed further, as the 345 information available to date is quite limited. It seems that fish oil supplementation 346 increases the proportion of Lacotobacilliales, as observed in rats with chronic intestinal 347 rejection (Li, Zhang, Wang, Tang, Zhang, & Li, 2011), in a murine model of colorectal 348 cancer (Piazzi et al., 2014) and in gnotobiotic piglets, in this last case with an increase in 349 Lactobacillus paracasei adhesion to the jejunal mucosa (Bomba, Nemcová, Gankarciková, 350 Herich, Guba, & Mudronová, 2002). In contrast, PUFA supplementation of animal models 351 resulted in a decrease in Escherichia coli, Bacteroides spp. and Clostidriales spp., among 352 others (Li et al., 2011; Yu, Zhu, Pan, Shen, Shan, & Das, 2014). Interestingly, 353 Lactobacillus plantarum has been reported to stimulate the colonic fermentation of red 354 wine polyphenols (Barroso et al., 2014), which are quite similar to the PAs included in the 355 GSE tested here.

356 In the present study, the STD diet had a soybean oil content similar to that of PUFAs in the 357 ω -3 diet, in order to make them isocaloric. Since the main constituents of soybean oil are 358 monounsaturated fatty acids (followed by PUFAs), the changes observed in the microbial 359 metabolism of PAs also indicate differences in the microbiota profile when consuming 360 monounsaturated or polyunsaturated fats. Indeed, when comparing the effects on the 361 human gut microbiome of three kinds of monounsaturated fats with those of two kinds of 362 polyunsaturated fats, the modifications in the bacteria profile that resulted from the 363 consumption of monounsaturated fats were observed to be consistent with those derived 364 from PUFA consumption (Pu, Khazenehei, Jones, & Khapifaur, 2016).

Additionally, since cereals contain phenolic acids as major phenolic compounds, and these generate several metabolites in common with those of PAs (Rodríguez-Mateos et al., 2014), it seems plausible that ω -3 PUFAs would also stimulate the release and transformation of such compounds. Additionally, some metabolites, such as hippuric or valerolactones, may originate from other food components (Pero, 2010; Molinar-Toribio et al., *in press*), so their increase in the ω -3 group might be due to an effect on other metabolic routes, becoming particularly evident in a long-term study such as this one.

Another interesting result of this study was that, while GSE contained mostly (95%) oligomeric PAs, in the groups supplemented with it there was an increase in the monomeric conjugated metabolites of EC. This agrees with our previous suggestion (Pérez-Jiménez et al., 2010) of a depolymerization of PAs by bacteria, releasing free EC which would then be subjected to further absorption and conjugation. ω -3 PUFAs also seem to affect the activity of the bacteria responsible for this, since in the ω -3 groups there was also a tendency towards an increase in these compounds, as compared to the STD group.

379 When GSE and ω -3 PUFAs were administered together, the concentrations of the detected 380 metabolites were in the same range than those found in the GSE group, without significant

381 differences. Therefore, ω -3 PUFAs did not have either an enhancing or inhibitory effect on 382 a diet supplemented with grape PA, despite the enhancing effects they showed towards the 383 transformation of polyphenols already present in the basal diet. It is known that polyphenol 384 supplementation causes a shift in microbial communities towards those species indeed able 385 to transform them, e.g. the Eubacterium rectale group (Selma, Espín, & Tomás-Barberán, 386 2009; Queipo-Ortuño et al., 2012). We hypothesize that the changes that ω -3 PUFAs may 387 cause in the microbiota, and that had an effect in the transformation of polyphenols already 388 present in the basal diet, may not be relevant against the modifications that polyphenols 389 themselves cause in the microbiota when provided at high doses.

Anyway, the concentration values for the pool of putatively beneficial circulating PAderived metabolites in the ω -3+GSE group were in the same range than in the GSE group. So, PA metabolites from GSE are bioavailable for possible collaborative functional effects with ω -3 PUFAs. Indeed, when evaluating the effects of ω -3 PUFAs and GSE on the metabolic alterations induced by a high-fat high-sucrose diet, it was observed that the combination was more efficient than the separate supplements at averting metabolic alterations (Ramos-Romero et al., 2016).

397 The main limitations of this study are intrinsic to experiments on the metabolic fate of 398 polyphenols. First, there is a lack of commercial standards for many metabolites (Kay, 399 2010), which forced us to express the results as equivalents of the most closely related 400 compound, with an associated error. Secondly, we had to deal with the high inter-401 individual variability of results; an aspect widely reported for the metabolic fate of 402 polyphenols in both animals and humans (Choy et al., 2014; Muñoz-González et al., 2014). 403 This latter aspect may have been exaggerated in this study, given that it involved long-term 404 supplementation, where the measured concentrations for each metabolite did not 405 correspond to the maxima and it is not known when each animal received the last dose of 406 polyphenols before fasting, since they were fed *ad libitum*. Also, more animals would have 407 increased the statistical power of the test thereby increasing the likelihood of detecting 408 statistically significant differences in the metabolites. Be that as it may, this did not 409 preclude us from observing the emergence of some general tendencies, as discussed above; 410 while at the same time, it has the advantage of reflecting a situation closer to a genuine 411 human dietary situation.

412 **5. CONCLUSIONS**

413 This study shows that combined long-term supplementation with ω -3 PUFAs and PAs from 414 GSE to healthy rats did not significantly affect the levels of urinary and fecal PA 415 metabolites, compared to supplementation with GSE alone. Meanwhile, ω -3 fatty acids 416 seem to enhance the metabolism of the polyphenols present in the STD feed. ω -3 PUFAs 417 appear to collaborate in the release and metabolism of polyphenols when they are present 418 at low doses in the feed matrix, while their capacity to induce transformations when 419 polyphenols are added at high doses does not seem to be relevant.

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429 AUTHORS' CONTRIBUTIONS

430	I.M., J.L.T. and J.PJ. designed the research. E.MT., S.RR., N.T., M.R., L.M., and J. P
431	J. conducted the research. E.MT., S.RR., E.F. and J.PJ. analyzed the data. J.PJ. and
432	J.L.T. wrote the first draft of the manuscript. All the authors contributed to writing the
433	manuscript and approved the final version. J.PJ. and J.L.T. had primary responsibility for
434	final content.

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436 **CONFLICT OF INTEREST**

437 None of the authors declare any conflict of interest.

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TABLES

Table 1. (Epi)catechin and (epi)gallocatechin conjugated metabolites in urine from rats fed a standard diet without supplementation (STD) or supplemented with ω -3 PUFAs (ω -3), grape seed extract (GSE) or ω -3 PUFAs and grape seed extract (ω -3 + GSE)¹. Results expressed as μ M, adjusted per kg feed intake/kg body weight, after quantification with structurally similar commercial standards (see Table S3).

Metabolite	STD^2			ω-3			GSE	2	ω -3 + GSE			
	Mean	SEM	Mean	SEM	Р	Mean	SEM	Р	Mean	SEM	Р	
EC monoconjugated												
Gluc-EC-1	n.d.		n.d.			5.68	2.87	0.0081 ^{a, b}	6.04	5.21	0.0081 ^{a, b}	
Gluc-EC-2	n.d.		n.d.			3.84	1.93	0.0321 ^{a, b}	3.29	3.18		
Gluc-EC-3	0.64	0.32	8.00	1.40	0.0081ª	3.09	1.21		15.55	5.37	0.0081ª	
											0.0321 ^b	
Gluc-EC-4	0.32	0.09	2.83	0.75	0.0081ª	0.95	0.47		4.49	1.60	0.0081 ^a	
											0.0321°	
Gluc-EC-5	0.88	0.44	3.67	0.80	0.0321 ^a	1.96	1.03		6.34	1.86	0.0161 ^a	

Total	1.84	0.61	14.50	2.86	0.0081ª	15.52	6.24	0.0161ª	35.72	16.64	0.0081ª
EC diconjugated											
Gluc-Sulf-EC	0.97	0.40	1.05	0.20		3.54	1.62	0.0321 ^b	2.99	1.17	
Me-Gluc-EC-1	n.d.		n.d.			0.85	0.28	0.0081 ^{a,b}	1.39	0.98	0.0081 ^{a,b}
Me-Gluc-EC-2	n.d.		n.d.			14.79	4.88	0.0081 ^{a,b}	13.61	9.21	0.0081 ^{a,b}
Me-Gluc-EC-3	n.d.		n.d.			5.26	1.68	0.0081 ^{a,b}	5.79	4.10	0.0081 ^{a,b}
Me-Sulf-EC	2.46	0.84	2.00	0.32		3.03	0.58	0.0081 ^{a,b}	3.85	1.27	0.0161ª
											0.0081 ^b
Total	3.43	1.23	3.05	0.47		27.47	8.09	0.0081 ^{a,b}	27.64	16.33	0.0161ª
											0.0081 ^b
EC triconjugated											
3Me-EC	1.09	0.27	0.94	0.17		1.07	0.30		1.65	0.48	
2Me-Gluc-EC	0.63	0.23	0.86	0.29		1.51	0.37		1.73	0.75	
Total	1.72	0.47	1.80	0.46		2.58	0.58		3.38	1.17	

EGC diconjugated								
2Sulf-EGC	14.16	2.81	15.55	2.71	21.69	4.18	27.72	8.75
EGC triconjugated								
Me-Gluc-Sulf-EGC	3.95	1.23	8.71	1.29	8.17	0.98	16.17	5.95

n.d., non-detected; Gluc, glucuronide; Me, methyl; Sulf, sulfated

¹ Values are mean \pm SEM , n=5

² Molinar-Toribio et al., *in press*.

^a differences with respect to STD group; ^b differences with respect to ω-3 group; ^c differences with respect to GSE group. Comparisons were performed using the Kruskal-

Wallis and Mann-Whitney U tests; pairs comparisons were performed between all the groups.

Table 2. Microbial-derived proanthocyanidin metabolites in urine from rats fed a standard diet without supplementation (STD) or supplemented with ω -3 PUFAs (ω -3), grape seed extract (GSE) or ω -3 PUFAs and grape seed extract (ω -3 + GSE)¹. Results expressed as μ M, adjusted per kg feed intake/kg body weight, after quantification with structurally similar commercial standards (see Table S3).

Metabolite	STD^2			ω-3			GSE ²		ω -3 + GSE		
	Mean	SEM	Mean	SEM	Р	Mean	SEM	Р	Mean	SEM	Р
Valerolactones											
3- or 4-Hydroxyphenylvalerolactone	24.17	7.33	205.81	15.67	0.0081ª	379.24	129.69	0.0081 ^a	604.60	268.55	0.0081ª
3,4-Dihydroxyphenylvalerolactone	5.97	4.09	89.81	26.91	0.0081ª	219.53	73.37	0.0081ª	595.09	281.69	0.0081ª
Gluc-3,4-dihydroxyphenylvalerolactone	51.48	15.61	133.16	41.14		164.87	29.47	0.0081ª	318.25	115.12	0.0321ª
Sulf-3,4-dihydroxyphenylvalerolactone	15.92	9.76	535.46	98.76	0.0081ª	1373.86	117.59	0.0081 ^{a,b}	1638.69	604.44	0.0081ª
3-Hydroxyphenylmethylvalerolactone	24.17	7.20	32.31	4.5		93.35	26.46	0.0081 ^a	56.64	16.46	
								0.0321 ^b			
4-Hydroxyphenylmethylvalerolactone	214.92	73.50	341.12	59.26		628.27	174.41	0.0321 ^a	481.06	125.84	
Gluc-3-hydroxymethylphenylvalerolactone	112.73	42.56	128.90	58.41		171.21	23.38	0.0321 ^b	170.88	57.94	
Sulf-3- or 4-hydroxymethylphenylvalerolactone	69.40	23.06	37.77	7.81		91.63	16.42		77.34	22.49	
Total	517.06	103.86	1504.34	305.22	0.0081ª	3121.97	446.61	0.0081ª	3987.54	1393.77	0.0081ª
								0.0321 ^b			

Lignans											
Enterolactone	>60		>60			>60			>60		
Sulf-enterolactone	>60		>60			>60			>60		
Phenylvaleric acids											
3-Hydroxyphenylvaleric acid	31.10	13.42	20.63	5.25		102.08	15.47	0.0161ª	157.89	73.49	0.0321 ^b
								0.0081 ^b			
4-Hydroxyphenylvaleric acid	4.63	1.71	17.37	3.74	0.0321ª	47.35	15.97	0.0081ª	28.53	4.43	0.0081ª
3,4-Dihydroxyphenylvaleric acid	8.74	2.49	70.33	18.25	0.0081 ^a	47.14	12.24	0.0161ª	86.66	22.09	0.0081 ^a
Sulf-3,4-dihydroxyphenylvaleric acid	28.02	11.34	530.70	160.71	0.0081ª	1053.66	220.98	0.0081ª	1061.01	403.49	0.0081ª
Total	72.49	23.05	639.03	182.16	0.0081 ^a	1250.23	223.86	0.0081 ^a	1334.09	482.74	0.0081 ^a
Phenylpropionic acids											
3-Hydroxyphenylpropionic acid	6638.51	2746.72	4097.84	597.18		14257.84	9274.35		8957.36	2307.88	
4-Hydroxyphenylpropionic acid	>60		>60			>60			>60		
Gluc-3- or- 4hydroxyphenylpropionic acid	21.34	12.93	13.93	6.64		17.10	2.09		28.36	11.52	
Dihydrocaffeic acid (3,4-	3.65	1.60	10.49	2.65		56.85	45.95	0.0321ª	20.82	5.86	
Dihydroxyphenylpropionic acid)											
Sulf-3,4-dihydrocaffeic acid	39.65	15.31	41.14	10.75		120.60	76.86		60.74	15.85	
Total ²	670.47	2751.81	4163.41	610.83		14452.40	9397.29		9067.28	2334.52	

Phenylacetic acids											
	(2.1.4	26.56	224.12	(7.52	0.00013	407.07	(7.20)	0.00018	020.02	294.14	0.02218
3-Hydroxyphenylacetic acid	63.14	26.56	324.13	67.53	0.0081"	427.27	67.29	0.0081"	838.83	284.14	0.0321"
4-Hydroxyphenylacetic acid	60.97	23.56	532.53	142.90	0.0081ª	1816.39	312.24	0.0081ª	1859.17	585.26	0.0081ª
								0.0321 ^b			
3,4-Dihydroxyphenylacetic acid	0.86	0.36	3.09	0.61	0.0161ª	10.27	5.04	0.0081ª	16.65	4.87	0.0161ª
Sulf-3,4-dihydroxyphenylacetic acid	7.79	4.41	8.91	1.48		8.41	1.90		14.19	4.19	
Total	132.77	46.12	868.66	170.81	0.0081ª	2262.34	292.60	0.0081ª	2728.84	745.56	0.0081ª
								0.0161 ^b			
Benzoic acids											
4-Hydroxybenzoic acid	13.88	5.56	78.01	23.75	0.0081 ^a	63.86	20.04	0.0321ª	52.31	13.40	
3,4-Dihydroxybenzoic acid	0.36	0.22	7.16	2.72	0.0161 ^a	21.35	9.80	0.0081 ^a	19.36	11.58	0.0081 ^a
Gluc-3-hydroxybenzoic acid	0.24	0.13	1.04	0.34		2.73	1.17	0.0081ª	1.77	0.50	0.0321ª
Gluc-4-hydroxybenzoic acid	0.02	0.01	0.14	0.03	0.0321ª	0.31	0.09	0.0081 ^a	0.26	0.17	0.0321ª
Sulf-3,4-dihydroxybenzoic acid	6.52	2.08	20.11	3.45	0.0081ª	69.10	37.61	0.0081ª	34.97	9.90	0.0321ª
Sulf-vanillic-acid	327.72	64.53	681.32	200.67		459.50	78.29		1432.01	507.86	
Total	348.74	60.23	787.78	228.73		616.85	129.27	0.0161 ^a	1540.69	539.51	
Cinnamic acids											
Caffeic acid	0.95	0.44	1.18	0.74		3.07	1.85		1.39	0.45	

<i>m</i> -Coumaric acid	116.69	54.97	102.91	29.16		247.53	30.90		140.64	47.78	
<i>p</i> -Coumaric acid	24.03	8.90	20.41	10.93		32.90	9.37		46.87	31.48	
Sulf-coumaric acid-1	n.d.		6.53	4.78	0.0081ª	14.05	4.77	0.0081ª	7.67	5.87	0.0081ª
Sulf-coumaric acid-2	0.04	0.01	7.00	5.09	0.0321ª	13.37	4.17	0.0081ª	7.53	5.76	0.0081ª
Ferulic acid	15.31	6.21	18.23	15.20		20.30	7.54		29.46	14.32	
Total	157.02	65.75	156.26	65.01		331.22	44.11		235.56	101.24	
Glycinated benzoic acids											
Hippuric acid	48.02	17.74	1385.71	396.40	0.0081 ^a	2219.53	1311.56	0.0081ª	1494.77	317.90	0.0081 ^a
Hydroxyhippuric acid	0.29	0.26	14.31	5.03	0.0081ª	16.99	3.57	0.0081ª	18.23	5.35	0.0081ª
Me-hippuric acid-1	0.15	0.15	67.03	54.54	0.0081ª	94.37	35.88	0.0081 ^a	73.06	57.30	0.0081ª
Me-hippuric acid-2	2.91	1.22	5.49	4.84		14.05	7.41		16.62	13.76	
Total	51.37	18.50	1472.53	443.46	0.0081ª	2344.94	1313.91	0.0081ª	1602.68	328.88	0.0081ª

n.d., non-detected; Gluc, glucuronide; Me, methyl; Sulf, sulfated

Compounds detected in all the groups above the highest concentration of the calibration: Enterolactone, Sulf-Enterolactone and 4-Hydroxyphenylpropionic acid

¹ Values are mean \pm SEM , n=5

² Molinar-Toribio et al., *in press*.

^a differences with respect to STD group^{; b} differences with respect to ω-3 group. Comparisons were performed using the Kruskal-Wallis and Mann-Whitney U tests; pairs

comparisons were performed between all the groups.

Table 3. Microbial-derived proanthocyanidin metabolites in feces from rats fed a standard diet without supplementation (STD) or supplemented with ω -3 PUFAs (ω -3), grape seed extract (GSE) or ω -3 PUFAs and grape seed extract (ω -3 + GSE)¹. Results expressed as μ mol/g dried feces, adjusted per kg feed intake/kg body weight, after quantification with structurally similar commercial standards (see Table S3).

Metabolite	ST	D^2		ω-3			GSE ²		ω -3 + GSE		
	Mean	SEM	Mean	SEM	Р	Mean	SEM	Р	Mean	SEM	Р
Lignans											
Enterolactone	> 60		> 60			> 60			> 60		
Phenylvaleric acids											
3-Hydroxyphenylvaleric acid	3.14	1.47	78.48	36.55	0.0161ª	985.26	872.17	0.0081ª	975.65	485.91	0.0081ª
Phenylpropionic acids											
3-Hydroxyphenylpropionic acid	45.05	3.84	35.68	23.50	0.0161ª	101.96	93.02	0.0081ª	12.60	0.00	0.0081ª
4-Hydroxyphenylpropionic acid	10.91	2.77	381.06	242.99	0.0321ª	41.15	32.21		2033.79	1653.65	0.0321ª
Total	55.96	41.61	416.73	246.22		143.10	90.51		2046.39	1653.65	
Benzoic acids											

4-hydroxybenzoic acid	n.d.		0.15	0.10		1.06	0.75	0.0081 ^a	3.94	1.68	0.0081ª
3,4-Dihydroxybenzoic acid	n.d.		n.d.			0.22	0.16	0.0081 ^{a,b}	0.26	0.14	0.0321 ^{a, b}
Total	n.d.		0.15	0.10		1.27	0.91	0.0081ª	4.20	1.72	0.0081ª
Cinnamic acids											
Caffeic acid	0.01	0.01	0.51	0.29	0.0081ª	0.53	0.41	0.0081ª	1.55	0.67	0.0081ª
<i>p</i> -coumaric acid	0.04	0.02	1.66	1.02		2.72	2.06	0.0321ª	4.83	1.76	0.0321ª
Total	0.05	0.03	2.16	1.31	0.0321ª	3.25	2.47	0.0321ª	6.38	2.41	0.0161 ^a
Glycinated benzoic acids											
Hippuric acid	0.05	0.03	0.75	0.75		0.04	0.03		1.50	0.76	
Me-hippuric acid-1	6.54	5.23	486.95	453.35		12279.53	11463.14		1023.35	584.48	
Me-hippuric acid-2	n.d.		269.32	165.44	0.0081ª	6283.37	5735.59	0.0081 ^a	137.49	119.35	0.0081 ^a

Total	6.59	5.24	757.01	567.91	18562.94	17211.60	0.0081 ^a	1162.33	554.38	0.0081ª	
n.d., non-detected; Gluc, glucuronide; Me, methyl; Sulf, sulfated											
¹ Values are mean \pm SEM , $n=5$											
² Molinar-Toribio et al., <i>in press</i> .											
^a differences with respect to STD group ^{; b} differences with respect to ω-3 group. Comparisons were performed using the Kruskal-Wallis and Mann-Whitney U tests; pairs											
comparisons were performed between all	l the group	5.									