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Prados, I. et al., 2020. Evaluation of the relationship between the peptide profiles and the lipid-lowering properties of olive seed hydrolysates as a tool for tuning hypocholesterolemic functionality. *Food & Function*, 2020, 11, 4973-4981

Available at <https://doi.org/10.1039/d0fo00576b>

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Evaluation of the relationship between the peptide profile and the lipid-lowering properties of olive seeds hydrolysates as a tool for tuning hypocholesterolemic functionality

Received 00th January 20xx,
Accepted 00th January 20xx

DOI: 10.1039/x0xx00000x

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Olive processing generates large amounts of stones with high protein content. Previous works demonstrated that olive seed proteins from Manzanilla variety released peptides with lipid-lowering capacity. Nevertheless, no work has demonstrated their roles in the whole hypolipidemic activity. Moreover, further studies using different olive varieties are required to purpose a solid method for the exploitation of olive seeds. Twenty different olive varieties were employed in this work. Proteins were extracted using high-intensity focused ultrasounds and digested with Alcalase. Released peptides were identified using proteomic techniques and their capabilities to reduce the absorption of dietary cholesterol (by inhibiting cholesterol esterase enzyme, binding of bile acids, and reducing micellar cholesterol solubility) or the biosynthesis of endogenous cholesterol were evaluated. Peptides with different lipid lowering capacities were obtained from all varieties although the genotype significantly affected to the hypolipidemic characteristics. Univariate and multivariate statistical analysis showed strong correlations, positive and negative, between the presence of certain peptides in the hydrolysates and their capacity to reduce exogenous cholesterol absorption and endogenous cholesterol synthesis. Therefore, the selection of the olive seed genotype can direct its lipid-lowering properties, e. g. promoting the reduction of dietary cholesterol absorption or the inhibition of cholesterol biosynthesis.

1 Introduction

Olive (*Olea europaea*) stones are a by-product from the olive industry that constitute 16 – 22% of the total olive weight.¹ This olive waste has been used to produce biomass.² However, olive stones are important sources of valuable compounds such as proteins that constitutes a 16-28 % of the olive seed.³ Moreover, proteins can be precursors of peptides with bioactive properties defining a bioactive peptide as a protein fragment that has a positive impact on the functions of our body and that can condition and affect our health.⁴ Exploitation of olive seeds by the recovery of bioactive peptides will enable the valorisation of this underused and sustainable material. On the other hand, the increasing incidence of hypercholesterolemia and related diseases due to non-healthy lifestyles and high-fat diets have risen, especially when levels are moderate, the demand for foods containing smart ingredients with lipid lowering effects. Nevertheless, this rise can be caused by different reasons and, in some cases, can even be due to a genetic predisposition. Indeed, there are different mechanisms involved in the reduction of cholesterol absorption and biosynthesis being very important to characterize the type

of lipid-lowering functionality of a molecule in order to adapt its use to the suitable purpose. Absorption of dietary cholesterol in humans requires its solubilisation in micelles⁵ and the main mechanism to reduce the absorption of exogenous cholesterol is by the disruption of these micelles. On the other hand, bile acids are the main constituents of micelles and are released during cholesterol oxidation in the liver. Molecules with capacity to bind bile acids have a double effect; they can inhibit micelles formation and promote bile acid release by increasing cholesterol oxidation rate.⁶ Other molecules can reduce the absorption of dietary cholesterol by the inhibition of pancreatic cholesterol esterase enzyme, involved in the release of free cholesterol from dietary cholesterol esters.⁷ Regarding the reduction of endogenous cholesterol, molecules with this capability used to be inhibitors of the 3-hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA R) enzyme, since it is the step limiting in the cholesterol biosynthesis mechanism.⁸ Different compounds from natural sources such as plants, microbes, and animals have demonstrated lipid-lowering capacity. Many of them are secondary metabolites, including phenol compounds.⁹ Additionally, some peptides from milk and hempseed have shown *in vitro* and *in vivo* hypocholesterolemic capacity.^{10, 11} Moreover, our research group has proposed a strategy to obtain peptides with capacity to reduce cholesterol from Manzanilla variety olive seeds.¹² Released peptides showed ability to reduce micellar cholesterol solubility and to inhibit bile acids binding and cholesterol esterase enzyme. A more recent work has also demonstrated that peptides from Manzanilla olive seeds exerted *in vitro* capacity to reduce cholesterol biosynthesis by the inhibition of HMG-CoA R enzyme.¹³ These results were confirmed in two *in vivo* assays

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Electronic Supplementary Information (ESI) available: [details of any supplementary information available should be included here]. See DOI: 10.1039/x0xx00000x

53 that showed a significant increase in blood high density lipoproteins (HDL) cholesterol (good cholesterol) when hydrolysate obtained from the Manzanilla olive seeds was administered to mice feeding with a high cholesterol diet¹³. The study of peptides presented in the Manzanilla hydrolysate enabled the identification of up to 33 different peptides. Nevertheless, further researches are required to find out the roles of these peptides in the whole capacity showed by Manzanilla hydrolysate to reduce the micellar cholesterol solubility, to bind bile acids or to inhibit HMG-CoA reductase and cholesterol esterase enzymes. Moreover, preliminary results obtained with the Manzanilla olive seed are promising but additional studies using other olive varieties are required to make a reliable proposal for the valorisation of olive seeds. The aim of this work has been to evaluate the relationship between the peptide profile and the lipid-lowering properties of olive seeds hydrolysates. For that purpose, different olive seed genotypes were employed and hypocholesterolemic properties of their hydrolysates were evaluated through different mechanisms. Proteomic analysis was applied for the identification of peptides in olive seed hydrolysates and the role of peptides in the whole hypocholesterolemic capacity exerted by hydrolysates was studied using univariate and multivariate chemometric tools. The main text of the article should appear here with headings as appropriate.

79 2 Materials and Methods

80 2.1 Chemicals and samples

81 All reagents were of analytical grade. Water was obtained with Milli-Q system from Millipore (Bedford, MA, USA). Acetone, methanol, hexane, hydrochloric acid (HCl), acetonitrile (ACN), and acetic acid (AA) were obtained from Scharlau (Barcelona, Spain). Tris(hydroxymethyl)aminomethane (Tris), sodium dodecyl sulfate (SDS), di-sodium tetraborate, and sodium dihydrogen phosphate were from Merck (Darmstadt, Germany). DL-dithiothreitol (DTT), hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA R), bovine pancreatic cholesterol esterase, p-nitrophenyl butyrate (p-NB), sodium taurocholate, taurodeoxycholic acid, oleic acid, phosphatidylcholine, and sodium chloride (NaCl) were all from Sigma-Aldrich (Saint Louis, MO, USA). Cholesterol oxidase kit purchased from BioAssay Systems (Hayward, CA, USA). Total bile kit was from Bio-Quant (San Diego, CA, USA). Alcalase 2.4 L produced by fermentation of a selected strain of *Bacillus licheniformis*, mainly composed by *Subtilisin A*, with catalytic activity on serine, and with an activity of 2.4 Anson units per gram, was kindly donated by Novozymes Spain S.A. (Madrid, Spain).

99 Raw olives of 19 different varieties (Barnea, Bouteillan, Caballero, Cañivano Negro, Cobrancosa, Corbella, Cordobeses de Arroyo de la Luz, Cornicabra, Kalokerida, Khalkali, Lechín de Sevilla, Medjoul, Nevado Azul, Ocal, Picual, Racimal de Jaen, Reixonenca, Safrón, Verdiell) were kindly donated by the World Olive Germplasm Bank of IFAPA (Córdoba, Spain). Manzanilla seed variety was a gift from FAROLIVA S.L. (Murcia, Spain). All olives were collected at same

maturity index (violet). Olives were manually depulped and stones extracted were stored at -20 °C until use.

2.2 Preparation of protein hydrolysates

Olive seeds were extracted from olive stones with a nutcracker. They were next grounded in a domestic mill and defatted with hexane. The powder obtained was dried at room temperature and storage at -20 °C until use. Protein extraction and digestion was carried out following the procedure previously optimized by our research group.¹² Briefly, 5 mL of extraction buffer (0.1 M Tris-HCl, 0.5% (w/v) SDS, and 0.5% (w/v) DTT at pH 7.5) were added to 0.03 g of olive seed powder and the extraction was carried out using a high intensity focused ultrasound (HIFU) probe (model VCX130, Sonic Vibra-Cell, Hartford, CT, USA) at 30% of wave amplitude for 5 min. After centrifugation at 4000g for 10 min, the proteins in the supernatant were collected and precipitated with cold acetone for 24 h at 4 °C. Protein isolate was dissolved in 0.05 M borate buffer (pH 8.5) and hydrolysed with Alcalase (4 h, 50 °C and 0.15 U/g protein). Extraction and digestion of proteins from every variety was performed by duplicate.

2.3 Evaluation of *in vitro* hypocholesterolemic capacity

In vitro hypocholesterolemic capacity was evaluated using four different assays based on three mechanisms to reduce exogenous cholesterol (reduction of micellar cholesterol solubility, binding of bile acids, and inhibition of cholesterol esterase enzyme) and another one to inhibit cholesterol biosynthesis (inhibition of HMG-CoA R enzyme). Reduction of micellar cholesterol solubility, binding of bile acids, and inhibition of cholesterol esterase enzyme assays have been described previously.¹²

2.3.1 HMG-CoA R inhibition

The activity of HMG-CoA R in presence of hydrolysate was measured using the HMG-CoA R assay kit that included the assay buffer, pravastatin, β -nicotinamide adenine dinucleotide 2'-phosphate reduced tetrasodium salt hydrate (NADPH), HMG-CoA, and HMG-CoA R enzyme. Solutions containing 181 μ L of the assay buffer (diluted 5 times), 1 μ L of inhibitor (pravastatin/hydrolysate), 4 μ L of NADPH, 12 μ L of HMGCoA, and 2 μ L of HMGE enzyme were prepared. After mixing, the absorbance of the NADPH was measured every 10 s up to 10 min at a wavelength of 340 nm. The result was expressed as percentage of inhibition of the enzyme.¹³

2.4 Separation and identification of peptides by reversed-phase high-performance liquid chromatography coupled to mass spectrometry (RP-HPLC-MS/MS)

The analysis of peptides in the 20 olive seed hydrolysates was performed using a High Performance Liquid Chromatography (HPLC) system 1100 from Agilent (Agilent Technologies, Santa Clara, CA, USA) coupled to a high sensitive Quadrupole-Time-Of-Flight mass spectrometer (Q-TOF/MS) (Agilent 6530 series, Pittsburgh, PA, USA)

153 equipped with an orthogonal electrospray ionization (ESI) source
 154 (Agilent Jet Stream, AJS). Agilent Mass Hunter Workstation software
 155 B.07.00 from Agilent was used for HPLC and MS control, data
 156 acquisition, and data analysis. Analytical separation was carried out
 157 in an Ascentis Express Peptide ES-C18 column (100 x 2.1 mm, 2.7 μ m
 158 particle size) with an Ascentis Express Peptide ES-C18 guard column
 159 (5 x 2.1 mm, 2.7 μ m particle size), both from Supelco (Bellefonte, PA,
 160 USA). The mobile phases consisted of water with 0.3% acetic acid
 161 (v/v) (phase A) and acetonitrile with 0.3% acetic acid (v/v) (phase B).
 162 The column temperature was 25 °C and the flow rate was 0.3
 163 mL/min. Injection volume was 15 μ L. Elution gradient was: 5% B for
 164 10 min, 5–65% B in 35 min, 65–95% B in 2 min, and 95% B for 3 min.
 165 A reversed gradient from 95 to 5% B in 5 min was used to return
 166 the initial eluting conditions and next injection was carried out after
 167 a 15 min post-time.

168 Mass spectrometry detection was carried out in the positive ion
 169 mode using a mass range from 100 to 1500 m/z. MS conditions were:
 170 fragmentator voltage (cone voltage after capillary), 200 V; nebulizer
 171 pressure, 50 psig; capillary voltage, 3500 V; gas temperature, 350 °C;
 172 drying gas flow, 12 L/min; skimmer voltage, 60 V; and octapole
 173 voltage, 750 V. The Jet Stream sheath gas temperature and flow were
 174 400 °C and 12 L/min, respectively. MS/MS was carried out using the
 175 Auto mode with the following conditions: 5 precursors per cycle and
 176 a collision energy of 4 V for every 100 Da. Internal mass calibration
 177 was performed by infusing throughout the analysis a solution
 178 containing purine and HP-0921 (hexakis(1H,1H,3H,3H-tetrafluoroproxy)phosphazine) (injected in acetonitrile-water,
 179 90:10 (v/v)) yielding ions at m/z 121.0509 and m/z 922.0098,
 180 respectively. All samples were injected by triplicate.

182 Raw data from RP-HPLC-QTOF were exported to PEAKS Studio
 183 Version 7 software from Bioinformatics Solutions Inc. (Waterloo,
 184 Canada) for *de novo* sequencing of peptides. Since it is not possible
 185 to make differences between isoleucine (I) and leucine (L) amino
 186 acids, only isoforms with L were displayed, although peptide
 187 sequences containing I amino acid instead of L are also possible.
 188 Isoelectric points and the water solubility were obtained using
 189 Innovagen's peptide property calculator. Data were also analyzed by
 190 PEAKS DB (database tool) using FASTA database that included
 191 protein sequences from *Olea Europaea* organism obtained from
 192 UniProt database. Peptides sequences were associated to a protein
 193 if the error tolerance was < 10 ppm and the mass tolerance was 0.1
 194 Da for the fragments. Peptides with a -10lgP equal or higher to 15
 195 confirmed the confidence between them. Only peptides appearing in
 196 all injections (six injections, three injections of each extract) were
 197 considered. Moreover, peptides with an ALC (expected percentage
 198 of correct amino acids in the peptide sequence) above 90% in at
 199 least, four injections and above 70% in the rest of injections were
 200 taken into account.

201 2.5 Univariate and multivariate statistical analysis

202 Statistical analysis was performed using Statgraphics Software
 203 5.1 (Statpoint Technologies, Inc., Warranton, VA, USA). Data
 204 comparison was carried out by one-way analysis of variance
 205 (ANOVA). Duncan's Multiple Range test was used to determine
 206 statistically significant differences (p-value < 0.05) between mean
 207 values from different samples at 95% confidence level. Data were

presented as mean \pm standard deviation of, at least, three
 independent experiments.

Pairwise correlations between peptides from the olive seed
 hydrolysates and cholesterol-lowering capacity were calculated by
 Pearson's correlation coefficient test using Stata software (version
 12, StataCorp, Lakeway Drive, College Station, Texas, USA).

Multivariate statistical analysis was performed using SIMCA 14.0
 software (MSK Data Analytics Solutions, Umetrics, Umeå, Sweden).
 The peak areas of peptides correlated with hypocholesterolemic
 capacity in the 20 hydrolysates and their hypocholesterolemic
 capacities were used as variables. Unsupervised multivariate
 principal components analysis (PCA) and hierarchical clustering
 (HCA) was performed. PCA was carried out without transformation
 and Ward distance was the criterion in HCA. Unsupervised
 multivariate PCA models were depicted as score and loading plots.

3 Results and discussion

Previous work using olive seeds from a Manzanilla variety has
 enabled to obtain a hydrolysate with high and multifunctional lipid-
 lowering properties.^{12, 13} In order to find out whether this property is
 common to other olive seeds and to evaluate the role of the different
 peptides in the whole hypocholesterolemic capacity of hydrolysates,
 20 different olive genotypes have been studied in this work. Peptides
 released from olive seeds genotypes were analysed to evaluate their
 capacity to reduce dietary cholesterol absorption and to inhibit
 endogenous cholesterol biosynthesis. After peptide identification,
 univariate and multivariate chemometric tools have been applied to
 find out the role of these peptides in the whole lipid-lowering
 capacity.

3.1 Evaluation of lipid-lowering functionalities in hydrolysates

Figure 1 shows the functionality of the 20 olive seed hydrolysates to
 reduce endogenous and exogenous cholesterol. All hydrolysates
 presented capacity to reduce the micellar cholesterol solubility that
 ranged from 11 to 49 %. This capacity has been related to the
 presence of hydrophobic and amphiphilic peptides. The varieties
 which displayed a significantly higher ability to reduce the micellar
 cholesterol solubility (44 – 49%) were Nevado Azul, Cornicabra,
 Cañivano Negro, Racimal de Jaén, and Picual (p \leq 0.05), while
 Kalokerida, Lechín de Sevilla, and Verdiell showed lower capacity (11
 – 30%). The presence of hydrophobic amino acids in the sequence of
 peptides has also been correlated to their ability to bind bile acids.¹⁴
 Indeed, the olive seed hydrolysates that showed the highest capacity
 for binding bile acids (those obtained from Verdiell, Caballo,
 Reixonenca, Picual, and Khalkali varieties) also exerted high capacity
 to reduce the micellar cholesterol solubility. On the other hand, the
 capacity to inhibit the cholesterol esterase enzyme was not very high
 in any variety (from 15 to 31 % of enzyme inhibition) and more than

Hypocholesterolemic capacity

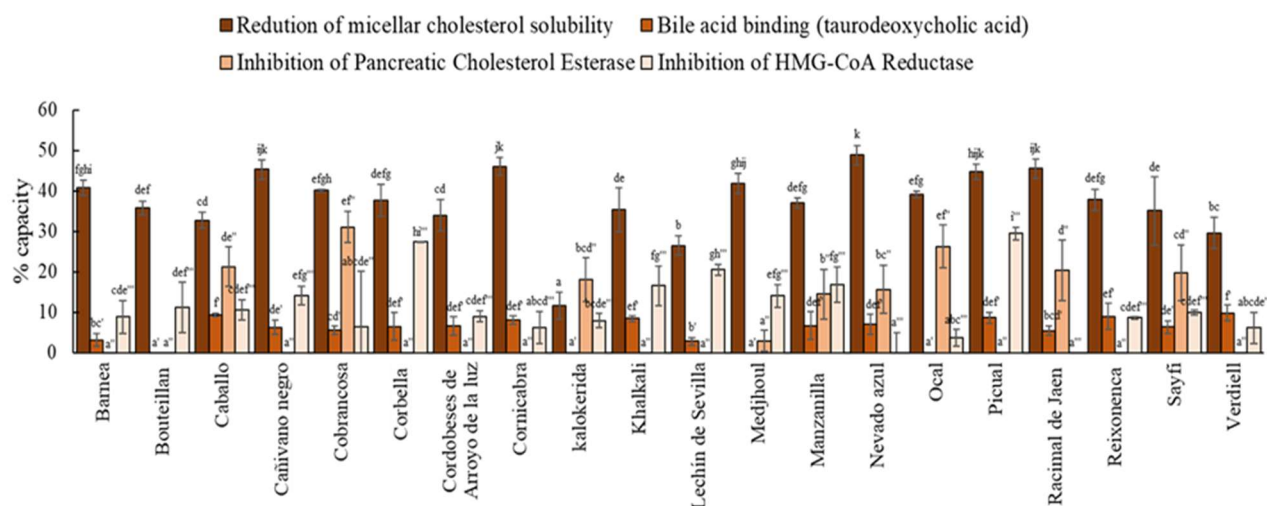


Figure 1. Capacity to reduce cholesterol levels through four different methods exerted by hydrolysates obtained from 20 olive seed varieties. Different letters represent significant differences ($p \leq 0.05$).

254 half did not show any (Barnea, Bouteillan, Cañivano Negro, Corbella, 289
 255 Cordobeses de Arroyo de la Luz, Cornicabra, Khalkali, Lechin de 290
 256 Sevilla, Medjhouh, Picual, Reixonenca, and Verdiell). All varieties 291
 257 except Nevado Azul and Racimal de Jaén, had capacity to inhibit 292
 258 HMG-CoA R enzyme observing the highest value in the hydrolysate 293
 259 obtained from the Lechin de Sevilla olive seed. Hydrolysates 294
 260 obtained from Caballo, Cobrancosa, Manzanilla, and Sayfi seeds 295
 261 exerted capacity to reduce dietary cholesterol absorption by the 296
 262 three employed mechanisms and to inhibit endogenous cholesterol 297
 263 biosynthesis. Hypocholesterolemic capacity of hydrolysates obtained 298
 264 with alcalase from Manzanilla variety have been evaluated by 299
 265 different methods in previous works^{12,13} and the results obtained 300
 266 were similar to the obtained in this work with the Manzanilla variety.

3.2. Identification of peptides by RP-HPLC-MS/MS

268 Peptides present in the hydrolysates corresponding to the 20 olive 305
 269 varieties were identified by RP-HPLC-ESI-QTOF-MS/MS. Table S1 306
 270 shows the sequence of the 103 peptides identified using the de novo 307
 271 tool along with their retention time range, experimental m/z, 308
 272 theoretical molecular mass, error/accuracy (ppm), ALC range, 309
 273 isoelectric point, water solubility, and the names of the olive varieties 310
 274 in which they appeared. These 103 peptides could not be identified 311
 275 by database searching using UNIPROT database since olive seed 312
 276 genome is not sequenced yet and proteins in this database refer to 313
 277 the *Olea Europaea* pulp or leaf. Nevertheless, the use of this 314
 278 database enabled the identification of 27 additional peptides, not 315
 279 identified by *de novo*. These peptides, that are present in the olive 316
 280 pulp and leaf, seem to be also in the olive seed. The sequence of 317
 281 these peptides along with their retention time range, experimental 318
 282 m/z, theoretical molecular mass, error/accuracy (ppm), isoelectric 319
 283 point, water solubility, proteins in which the peptides were found 320
 284 and the names of the olive varieties in which they appeared are 321
 285 grouped in Table S2. A total of 130 different peptides were found 322
 286 within all hydrolysates. All peptides had between 4-12 amino acids 323
 287 Every variety showed between 24 – 50 peptides within a mass range 324
 288 from 349-1351 Da. Almost all peptides presented the molecular ion

[M+H]⁺, except the peptides MKLADVPLCLVN and PNYQTPR that 325
 showed the molecular ion [M+2H]²⁺. Figure 2 shows the based peak 326
 chromatogram (BPC) corresponding to the hydrolysate obtained 327
 from the Verdiell variety and the tandem mass spectra of peptides 328
 WNVN ($t_R = 14.4$ min) and VFDGE ($t_R = 6.9$ min). They were the only 329
 peptides observed in all hydrolysates.

More than 50% of peptides had poor solubility in water and more 330
 than 66% presented an isoelectric point lower than 4.0. The peptides 331
 mainly contained hydrophobic (> 57%) (alanine, A (7%); 332
 leucine/isoleucine, L/I (21%); phenylalanine, F (6%); proline, P (8%); 333
 methionine, M (2%); valine, V (12%); and tryptophan, W (1%)), acidic 334
 (~10%) (glutamic, E (5%) and aspartic, D (5%) acids), and basic amino 335
 acids (8%) (lysine, K (4%); histidine, H (2%) and asparagine, R (2%)) 336
 (see Tables S1 and S2). The presence of high amounts of hydrophobic 337
 amino acids has been related to the capacity to reduce cholesterol 338
 by bile acid binding and by micellar cholesterol solubility inhibition 339
 and could justify the results previously observed.¹⁴ Other common 340
 feature within hypocholesterolemic peptides is their amphiphilic 341
 character. Indeed, different hypocholesterolemic peptides from 342
 marine, animal, and plant sources showing a hydrophobic N-terminal 343
 and a hydrophilic C-terminal have been described.^{10,11,15} In the case 344
 of the olive seed hydrolysates, around 33% of identified peptides 345
 showed this amphiphilic character, which could also contribute to 346
 explain their lipid-lowering capacity (Table S1 and S2).

Sequenced peptides were checked against BIOPEP database.¹⁶ 347
 FDGEVK, VPLSPT, and VVVVPH were previously identified as 348
 antioxidant peptides in olive seed hydrolysates. Moreover, the 349
 peptides LPLL and LVVD were part of the N-terminal and C-terminal 350
 parts, respectively, of hypotensive peptides. In addition, some 351
 peptides were found within longer peptides with different 352
 bioactivities. KALM, LLDA, NLLN, and SVLY are part of peptides with 353
 antibacterial capacity. KGAL is also part of antibacterial peptides and 354
 even antioxidative and alpha-amylase inhibitor peptides. SSPL is part 355
 of antibacterial and haemolytic peptides. Moreover, EAKLA, LELL, 356

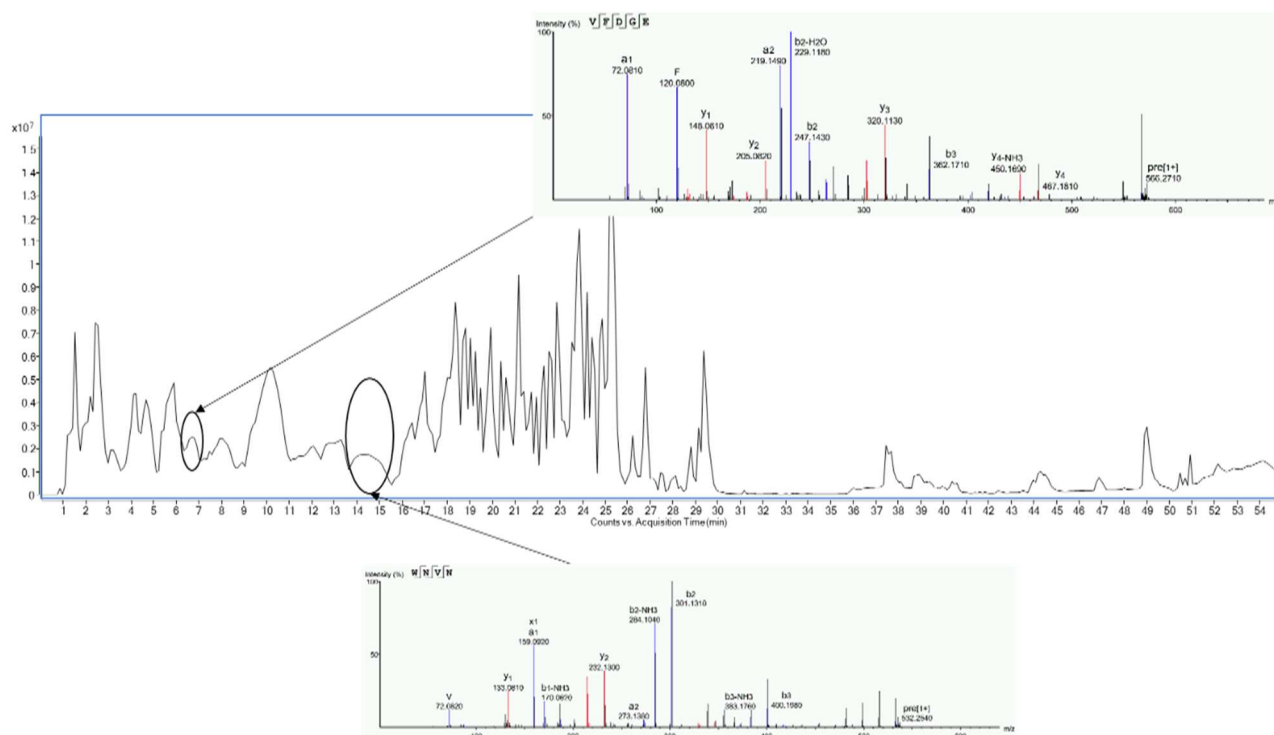


Figure 2. Base Peak chromatogram (TIC) corresponding to the separation of peptides from the olive seed hydrolysate obtained from Verdiell variety and the fragmentation spectra of peptides WNVN and NDGE (present in all varieties with ALC \geq 90%).

323 and VVLQ are part of two membrane-active peptides and a celiac
324 toxic peptide, respectively.

325 Proteins in olive seed were identified in a previous work of our
326 research group.¹⁷ The comparison of peptides in Table S1 with
327 proteins identified in that work, enabled to associate 7 peptides with
328 olive seed proteins: **ADIY** (in protein Triticin OS = *Triticum aestivum*),
329 PE = 2 SV = 1 (tr|B2CGM5|B2CGM5_WHEAT), **ELLI** (in five histones
330 H3 (tr|B9GVX4|B9GVX4_POPTR, sp|P06353|H33_HORVU,
331 tr|Q4JKA5|Q4JKA5_RHEAU, tr|D8QUA3|D8QUA3_SELML, and
332 tr|E9MZ24|E9MZ24_9CHLO)), **IILPQ** (in transposon protein,
333 putative, CACTA, En/Spm sub-class OS=*Oryza sativa* subsp. *japonica*),
334 GN=LOC_Os10g04760 PE=4 SV=1 (tr|Q7XH13|Q7XH13_ORYZA),
335 **ISPL** (in two predicted protein OS=*Populus trichocarpa*),
336 GN=POPTRDRAFT_818720 PE=3 SV=1 (tr|B9H8M5|B9H8M5_POPTR) and
337 GN=POPTRDRAFT_830076 PE=3 SV=1 (tr|B9GS11|B9GS11_POPTR)), **TLPIL** (in 11S globulin isoform
338 OS=*Sesamum indicum* PE=2 SV=1 (tr|Q2XSW6|Q2XSW6_SESAMI)),
339 **VLAL** (in three histones H3 (tr|E9MZ24|E9MZ24_9CHLO,
340 sp|P06353|H33_HORVU, and tr|B6UH77|B6UH77_MAIZE)), and
341 **VYIE** (in 11S globulin seed storage protein 2 OS = *Sesamum indicum*),
342 PE = 2 SV = 1 (sp|Q9XHP0|11S2_SESIN)).¹⁷

344 Despite the identification of peptides has been important to justify
345 hypocholesterolemic properties of hydrolysates observed in Section
346 3.1, further studies are needed to find out their roles in the whole
347 bioactivity.

3.3 Evaluation of the role of peptides in the hypocholesterolemic activity of hydrolysates

350 In order to determine which peptides are more significant in the
351 reduction of the exogenous and endogenous cholesterol, different
352 chemometric tools were next applied.

3.3.1 Univariate analysis

354 The relationship between the presence of peptides in the olive seeds
355 hydrolysates and their capacity to reduce cholesterol micellar
356 solubility, to bind bile acids, and to inhibit cholesterol esterase and
357 HMG-CoA R enzymes was studied using correlation analysis. For that
358 purpose, peptides appearing in, at least, three different varieties
359 were considered. Thus, the correlation analysis was carried out with
360 78 peptides from the 130 peptides identified within varieties (see
361 Table S1 and S2). Those peptides that showed a strong correlation
362 (positive or negative) with, at least, one mechanism to reduce
363 cholesterol were represented in Figure 3. Only 40 peptides were
364 correlated ($r > 0.5$) with, at least, one of the capacities. Peptide
365 NFVVLK displayed the strongest correlation with the capacity to
366 reduce the micellar cholesterol solubility and the highest area was

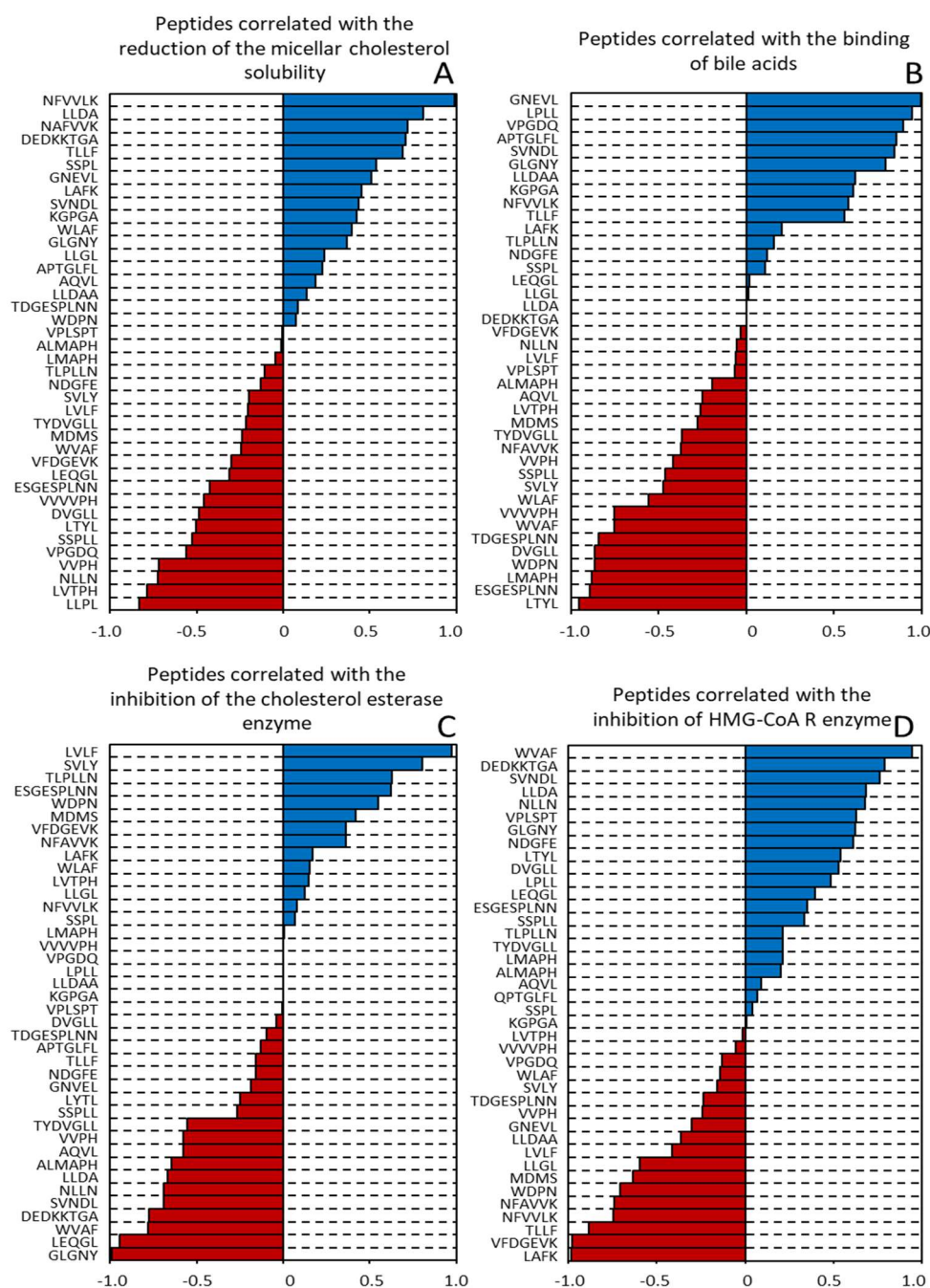


Figure 3. Pearson's correlation (r) between 40 peptides identified in olive seed hydrolysates and the capacity to (A) reduce the micellar cholesterol solubility, (B) bind bile acids, (C) inhibit the pancreatic cholesterol esterase, and (D) inhibit the HMG R. Peptides showing strong correlation presented bigger area.

367 observed in the Nevado Azul variety (data not shown). Indeed, 378
 368 variety had demonstrated a high capacity to reduce the micellar 379
 369 cholesterol solubility in Section 3.1. There was not any peptide 380
 370 showing a strong correlation with the four measured capacities 381
 371 (Figures 3 and S3). Only SSPL peptide showed positive correlation 382
 372 all hypocholesterolemic capacities (see Figure S3) whereas VVPH 383
 373 VVVVPH peptides had negative or zero correlation coefficients with 384
 374 all capacities. It was remarkable the fact that the 30% of peptides 385
 375 showed an opposite correlation between the capacities to reduce 386
 376 the endogenous and exogenous cholesterol (Figure S3). For instance,
 377 the peptides ALMAPH, LMAPH, LTYL, NLLN, SSPL, TYDVGLL, VPLSPT,

and WVAF displayed a positive correlation with the mechanism to
 inhibit cholesterol biosynthesis and a negative or zero correlation
 with the capacity to reduce dietary cholesterol absorption. The
 opposite behaviour was shown by LAFK, LLDA, LLGL, and NFVVLK
 peptides; they presented a positive correlation with the capacity to
 reduce the dietary cholesterol and a negative correlation with the
 capacity to reduce the cholesterol biosynthesis. The best peptide for
 reducing exogenous cholesterol absorption was NFVVLK while WVAF
 exhibited the highest capacity to reduce endogenous cholesterol.

387 Additionally, 73% of the 40 peptides showed simultaneously capacity
 388 to reduce micellar cholesterol solubility and to bind bile acids (see
 389 Figures 3 and S3). This seems to be related to the hydrophobic
 390 character of peptides¹⁸ and had been observed in Section 3.1. Unlike
 391 this behaviour, most peptides (around 80%) displayed opposite
 392 correlation coefficients (correlation coefficients < - 0.5) in
 393 capacities to inhibit the cholesterol esterase and the HMG-CoA
 394 enzymes. Thus, those peptides with high capacity to inhibit the HMG-
 395 CoA R enzyme had low capacity to inhibit the cholesterol esterase
 396 enzyme.

397 3.3.2 Multivariate Analysis

398 Multivariate analysis was carried out using the 40 peptides that
 399 correlated with, at least, one of the hypocholesterolemic capacities.
 400 Cluster analysis (HCA) using the Ward method was able to form 4
 401 clusters among peptides (see Figure 4). On the other hand, HCA
 402 enables to select most important variables (principal components)
 403 and to separate samples (hydrolysates from different olive varieties)
 404 according to their peptides profiles and their capacity to reduce
 405 blood cholesterol.¹⁹ A total of 4 components explained the 77.6% of
 406 the total data variability (Figure 5A). PCA grouped the varieties in a
 407 similar way to the HCA (same colours were employed in the HCA and
 408 PCA). All groups in HCA were clearly observed in the score plot of
 409 PCA. Principal Component 1 was able to differentiate groups 1 and 2
 410 from groups 3 and 4 while Component 2 almost separated groups 2

and 4 from groups 1 and 3. The loading plot of PCA is presented in
 Figure 5B in order to clarify why the hydrolysates from the different
 olive seed varieties have been grouped in that way. Peptides close to
 one capacity in the PCA loading plot are positively correlated with
 this capacity and vice versa. The varieties belonging to every group
 showed similar capacities to reduce cholesterol. For example, group
 4 displayed the lowest capacity to inhibit the HMG-CoA R enzyme
 and the varieties pertaining to this group were opposite to this
 capacity in the PCA loading plot (observed by overlapping Figures 4B
 and 4C). Similarly, group 2 exhibited low capacity to reduce the
 micellar cholesterol solubility and to bind bile acids; whereas all
 varieties from group 1 presented high capacity to inhibit the HMG-
 CoA R enzyme and low or any capacity to inhibit the cholesterol
 esterase enzyme. Additionally, group 4, which is opposite to group 2
 in the PCA score plot (Figure 5A), showed a high capacity to reduce
 the micellar cholesterol solubility and to bind bile acids, just in the
 other way around that group 4 (Figures 5A and 5B). In the same way,
 Ocal, Cobrancosa, and Racimal de Jaén varieties, which are part of
 group 4, showed the highest capacities to inhibit cholesterol esterase
 (observed by overlapping Figures 5A and 5B). They were even better
 than the rest of varieties in group 4 since they were closer to this
 capacity in the loading plot. However, varieties of group 1 (Lechín de
 Sevilla, Corbella, Picual, Khalkali, and Cañivano Negro), located at
 the opposite side, had the lowest capacity to inhibit cholesterol
 esterase. Therefore, the varieties with the highest capacities in all
 assays to reduce cholesterol were Manzanilla, Cobrancosa, Caballo,
 and Sayfi, which were placed in the middle of the PCA (Figure 5A).
 These results are in agreement with the observed in the Section 3.3.1.

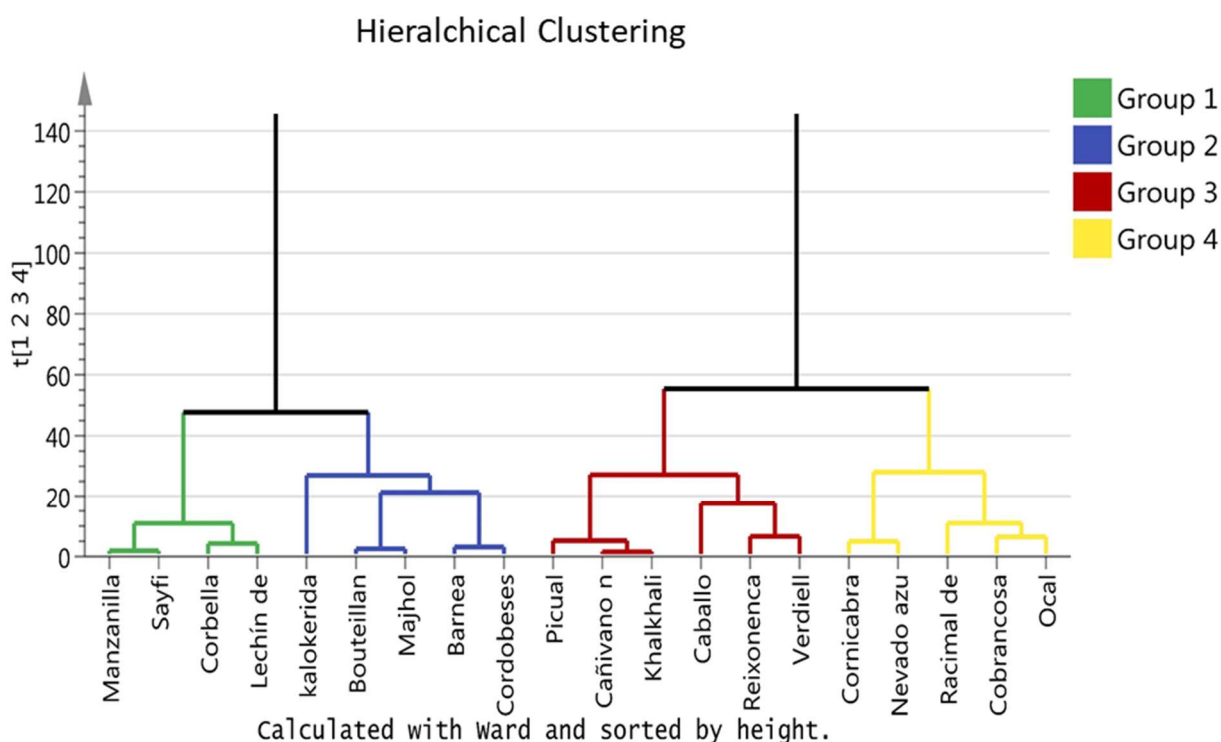


Figure 4. Dendrogram obtained by PCA using the ward method of 40 peptides correlated with hypocholesterolemic capacities to reduce the micellar cholesterol solubility, bind bile acids, inhibit the pancreatic cholesterol esterase and inhibit the HMG R from 20 varieties of olive seeds.

439 According to the PCA loading plot, the capacity to inhibit 447
 440 cholesterol esterase enzyme was situated in the opposite side to 448
 441 capacity to inhibit HMG-CoA R enzyme (see Figure 5B). Thus, when 449
 442 peptide is good to inhibit one enzyme, it will have a low or 450
 443 capacity to inhibit the action of the other. An example is pep 451
 444 VFDGEVK that is close to the capacity to inhibit cholesterol ester 452
 445 and far from the inhibition of the HMG-CoA R. On the other hand 453
 446 the capacity to reduce the micellar cholesterol solubility and to bind

bile acids were close to each other in the loading plot which means that both capacities were related and peptides with high capacity for one assay, will contribute positively to the other one (Figure 5B). For instance, NFFVVK, GNEVL, and SSPL, which are located near to these capacities in the loading plot are positively correlated with both mechanisms. These conclusions confirm results withdrew from the correlation analysis (see Figure 3 and S3).

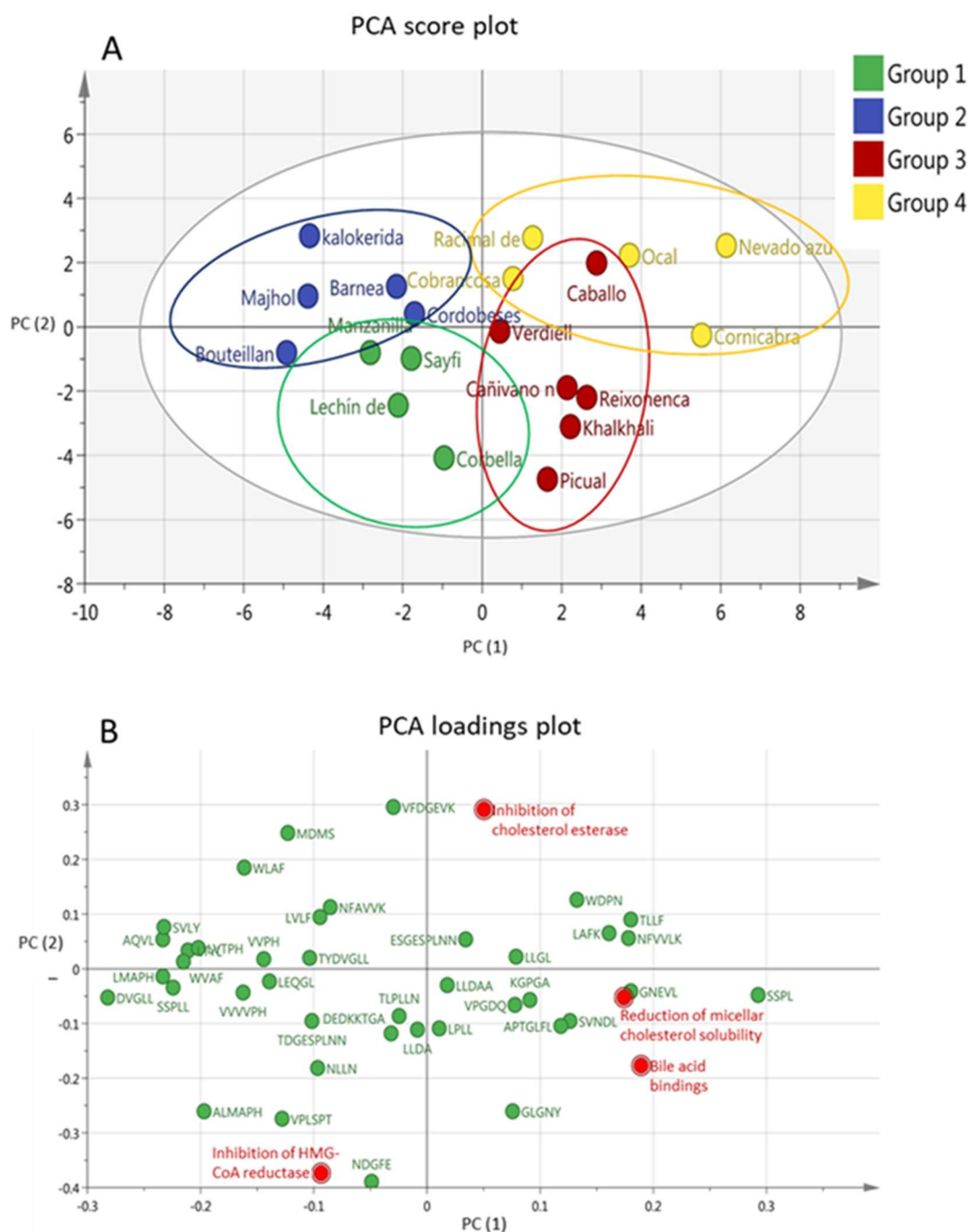


Figure 5. (A) Score plot resulting from a PCA (arbitrary groups are represented by ellipses and the colours showed the groups obtained in the HCA) of 40 peptides correlated with hypocholesterolemic capacity and their capacities to reduce the micellar cholesterol solubility, bind bile acids, inhibit the pancreatic cholesterol esterase and inhibit the HMG R from 20 varieties of olive seeds. (B) Loading plot obtained from a PCA (green colour represents peptides while red colour means hypocholesterolemic capacities).

454 **Conclusions**

455 This work demonstrates that the presence of certain peptides
 456 in olive seed hydrolysates modulates their lipid-lowering
 457 properties. Forty peptides among the 130 identified within
 458 hydrolysates showed a significant effect, positive or negative,
 459 on the capacity of hydrolysates to reduce exogenous
 460 cholesterol absorption (by the reduction of the micellar
 461 cholesterol solubility, the binding of bile acids or the inhibition
 462 of cholesterol esterase enzyme) or to inhibit cholesterol
 463 biosynthesis (by the inhibition of HMG-CoA R enzyme).
 464 Univariate analysis enabled to observe that peptide NFVVK
 465 displayed the strongest correlation with the capacity to reduce
 466 the micellar cholesterol solubility and, in general, with the
 467 capacity of hydrolysates to reduce exogenous cholesterol
 468 absorption while the presence of peptide WVAF was related
 469 with the capacity of hydrolysates to reduce endogenous
 470 cholesterol. Multivariate analysis confirmed these results and
 471 enabled to observe a strong negative correlation between the
 472 capacity of peptides to inhibit the cholesterol esterase and the
 473 HMG-CoA R enzymes and a strong positive correlation between
 474 the capacity of hydrolysates to reduce the micellar cholesterol
 475 solubility and to bind bile acids. An opposite correlation
 476 between the capacity of hydrolysates to inhibit the absorption
 477 of dietary cholesterol and to inhibit cholesterol biosynthesis
 478 was observed in some cases. According to their peptide profile
 479 and hypocholesterolemic ability, olive varieties were grouped
 480 into 4 groups. Results show that every olive genotype can
 481 release peptides with a different lipid-lowering capacity and
 482 that their selection is a powerful tool to tune the
 483 hypocholesterolemic properties.

484 **Conflicts of interest**

485 There are no conflicts to declare.

486 **Acknowledgements**

487 This work was supported by the Spanish Ministry of Economy,
 488 and Competitiveness (ref. AGL2016-79010-R) and the
 489 Comunidad Autónoma of Madrid and european funding from
 490 FSE and FEDER programs (S2018/BAA-4393 AVANSECAL-II-CM)
 491 I. P. thanks the Comunidad Autónoma of Madrid and FEDER
 492 program (S2013/ABI-3028, AVANSECAL-CM) for her research
 493 contract.

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