Microbiota-derived resveratrol metabolites: new biomarkers of red wine 1 consumption are inversely associated with inflammation in a longitudinal 2 study of a Mediterranean population 3

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20 **Objectives:** To evaluate the association between urinary microbiota-derived resveratrol metabolites, which may serve as specific biomarkers of red wine consumption, and plasma circulating proinflammatory markers. 21 22 Design, settings, and participants: One-year longitudinal study included 179 participants at high 23 cardiovascular risk (mean age 69 years, 49% women) enrolled in the PREDIMED trial. Measurements: 24 Plasma inflammatory biomarkers and urinary microbiota-derived resveratrol metabolites were analyzed 25 using xMAP technology and high-performance liquid chromatography coupled to mass spectrometry, 26 respectively. Receiver operating characteristic (ROC) analyses were performed to evaluate the reliability of 27 urine resveratrol metabolites as biomarkers of red wine consumption, as reported in the food frequency 28 questionnaires (FFQs) of the participants. The relationship between baseline values and 1-year changes in 29 urinary microbiota-derived resveratrol metabolites and plasma levels of circulating inflammatory molecules 30 were assessed. Results: ROC curves confirmed that urinary dihydroresveratrol glucuronide (DHRg) [AUC 31 = 0.835] and sulfate (DHRs) [AUC = 0.803] metabolites are reliable and specific biomarkers of red wine 32 consumption. Baseline urinary concentrations of DHRs were negatively associated with plasma levels of 33 soluble vascular cell adhesion molecule-1 (sVCAM-1) (-0.40 ng/mL per 1-SD increase, p = 0.012). After one 34 year of follow-up, changes in urinary concentrations of DHRg also showed a negative association with 35 plasma circulating sVCAM-1 levels (-0.39 ng/mL per 1-SD increase, p-value = 0.028). No significant associations were detected at baseline and after one year of follow-up when FFQ information of red wine 36 37 consumption was used to perform the regression analysis with circulating inflammatory molecules. 38 **Conclusions:** Light to moderate red wine consumption (10 to 20 grams of alcohol per day), which can be 39 monitored by microbiota-derived resveratrol metabolites excreted in urine, is associated with lower plasma 40 concentrations of sVCAM-1, an inflammatory biomarker related to atherosclerosis. Biomarkers of 41 consumption offer advantages compared to FFQ data, since they provide objective and more accurate 42 information about nutrient intake and metabolism. Without specific biomarkers of red wine consumption, no 43 significant associations would have been found in the present study.

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45 Keywords: Anti-inflammatory; Antiaging; Biomarker; Healthy diet; Dihydroresveratrol; Bioactives; Health

46 Abbreviations: BMI, body mass index; CVD, cardiovascular disease; CRP, C-reactive protein; DHRg, 47 dihydroresveratrol glucuronide; DHRs, dihydroresveratrol sulfate; EVOO, extra virgin olive oil; FFQ, food

48 frequency questionnaire; IL-1A; interleukin-1 alpha; IL-6, interleukin-6; IQR, interquartile range; MedDiet,

- 49 mediterranean diet; METs, metabolic equivalent tasks; MCP-1, monocyte chemoattractant protein-1; NSAID,
- 50 non-steroidal anti-inflammatory drug; PREDIMED, PREvención con Dieta MEDiterránea; ROC, receiver
- 51 operating characteristic; ROS, reactive oxygen species; SD, standard deviation; sICAM-1, soluble
- 52 intercellular adhesion molecule-1; sVCAM-1, soluble vascular cell adhesion molecule-1; TNF- α , tumor
- 53 necrosis factor alpha; TRMs, total resveratrol metabolites.

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54 1. Introduction

Resveratrol, a (poly)phenol with manyfold health benefits (1), is found in some plant-based foods, such as grapes, berries, cocoa or nuts. Red wine is usually the main source of resveratrol in wine drinkers, which may also synergize with other phenolic compounds found in wine to produce their reported health benefits (2, 3).

Food intake was traditionally evaluated through food frequency questionnaires (FFQs), which suffer from methodological limitations and systematic errors. These include the under- or overestimation of the amount and frequency of food consumption, especially alcohol intake (4). Furthermore, FFQs do not consider interactions within the food matrix and with the gut microbiota (4, 5).

64 In this context, biomarkers of consumption can serve as a valuable tool to enhance the 65 accuracy of FFOs. Tartaric acid, total resveratrol metabolites (TRMs), and gallic acid metabolites have been postulated as biomarkers of wine consumption (6-8). A recently 66 published paper suggested anthocyanins and resveratrol derivates as the most selective 67 biomarkers for regular wine consumption (9). Resveratrol is 10-fold higher in red wine. 68 69 When wine is consumed, resveratrol is hydrogenated to dihydroresveratrol by gut microbiota prior to absorption (10). Dihydroresveratrol is metabolized mainly in the liver 70 to dihydroresveratrol sulfate (DHRs) and dihydroresveratrol glucuronide (DHRg) (11). 71 These microbiota-derived resveratrol metabolites can be quantified in urine and to date 72 73 have not been assessed as specific biomarkers of red wine consumption in human 74 intervention studies.

Light to moderate wine consumption is defined as up to one drink per day for women (1 drink \approx 10 grams of alcohol) and two drinks per day for men (12). Although several studies suggest that moderate wine consumption, especially red wine, may reduce proinflammatory biomarkers (13, 14), some others have not found these benefits (15, 16), or even reported acute postprandial proinflammatory responses (17).

80 The aim of the present study was to corroborate the usefulness of microbiota-derived 81 resveratrol metabolites excreted in urine as specific biomarkers of red wine consumption. 82 Additionally, we evaluated the advantages of using these biomarkers over FFQ data to 83 investigate associations between wine consumption and plasma circulating inflammatory 84 molecules.

85 2. Methods

86 2.1 Study Design

This study included samples from 179 participants from the IDIBAPS and Navarra recruitment centers as part of the PREDIMED trial (<u>www.predimed.es</u>), from which additional data on inflammation biomarkers and urine metabolites were available, serving as one of the inclusion criteria for the present study. PREDIMED trial was a large parallelgroup, multicenter, randomized, controlled intervention trial that involved 7,447 participants at high cardiovascular risk. Study design, inclusion and exclusion criteria and methodology were previously described (18, 19). After one year of intervention, FFQ data

- 94 from 6 participants were excluded as their energy intake was above predetermined limits,
- 95 and 5 participants dropped out during the intervention.
- 96 *2.2. Assessment of covariates*

Food consumption was assessed using a semi-quantitative validated FFQ (20).
Mediterranean diet (MedDiet) adherence was evaluated using a validated 14-item screener
(21). Physical activity was assessed using a validated Spanish iteration of the Minnesota
physical activity questionnaire, measuring metabolic equivalent tasks minutes per day
(METs min/day) (22).

102 2.3. Inflammatory biomarkers

103 Plasma concentrations of soluble adhesion molecules were determined using Bio-Plex Pro 104 Human Cytokine 17-plex Assay on the Luminex platform and analyzed with Bio-Plex 105 ManagerTM Software. Five potential inflammatory biomarkers were determined: soluble 106 vascular cell adhesion molecule-1 (sVCAM-1), soluble intercellular adhesion molecule-1 107 (sICAM-1), interleukin-6 (IL-6), tumor necrosis factor-alpha (TNF- α), and monocyte 108 chemoattractant protein-1 (MCP-1).

109 2.4. Urinary dihydroresveratrol metabolites

DHRg and DHRs were determined in the first spot urine. 20 µL of urine were diluted 1:5
(v:v) with Milli-Q Water and formic acid at 0.05 % prior to analysis through LC- ESIMS/MS with abscisic acid D6 as internal standard. Calibration curves of the aglycon form
in synthetic urine were used for the quantification of the two dihydroresveratrol
metabolites.

115 Chromatographic separation was performed on a Kinetex F5 100Å (50 x 4.6 mm x 2.6 µm) reverse column from Phenomenex[®] coupled to a SecurityGuard[™] (UHPLC F5 4.6mm). 116 High-resolution mass spectrometry was conducted on an Agilent 6560 Ion Mobility QTOF 117 LC/MS working in negative mode, at the Separation Techniques Unit of the Scientific and 118 119 Technological Centers (CCiTUB). The mobile phases were (A) 0.05% acetic acid in water 120 and (B) 0.05% acetic acid in acetonitrile. The column temperature was maintained at 40°C throughout the analysis. A 5 µL sample was injected into the chromatographic column, with 121 a constant flow rate of 0.750 mL/min, using the following non-linear gradient: 1.7 min, 2% 122 123 B; 4.7 min, 8%B; 6 min, 20%B; 7.3 min, 30%B; 7.4 min, 50%B; 8.7 min, 100%B; 10 min, 124 2%B. Agilent Mass Hunter Software was used to identify and quantify DHRg and DHRs.

125 2.5. Statistical analyses

126 Student's t-test was used to assess differences in quantitative variables and chi-square tests 127 for categorical. Baseline values of inflammatory biomarkers in plasma (ng/mL) and dihydroresveratrol metabolites in urine (nmol/mL) were log-normalized and scaled to a 128 mean of 0 and standard deviation (SD) of +1. Changes in these variables were calculated 129 130 and were also normalized and scaled. Receiver operating characteristic (ROC) curve analysis was conducted using logistic regression, with wine (consumers/non-consumers) as 131 the dependent variable and urinary dihydroresveratrol metabolites concentrations as the 132 133 exposure variable. Multivariable-adjusted linear regression models were used to assess 134 associations between baseline and one-year changes in urinary dihydroresveratrol

135 metabolites concentrations and inflammatory biomarkers per 1-SD increment. Adjustment models of increasing complexity were applied. Model 1 was adjusted for age (continuous, 136 years) and sex (categorical, men/women); Model 2 was further adjusted for recruitment 137 center (categorical, Barcelona/Navarra), body mass index (BMI) (continuous, kg/m²), 138 physical activity (continuous, METs-min/d), smoking habit (categorical, yes/no), diabetes 139 (categorical, yes/no), hypercholesterolemia (categorical, yes/no) and hypertension 140 141 (categorical, yes/no); and model 3 was additionally adjusted for total energy intake 142 (continuous, kcal/d), intake of omega-3 fatty acids (continuous, g/d), statins intake 143 (categorical, yes/no), aspirin consumption intake (categorical, yes/no), non-steroidal anti-144 inflammatory drugs (NSAIDs) intake (categorical, yes/no) and consumption of grapes and raisins (continuous, g/d). One-year changes were further adjusted for baseline levels of 145 146 resveratrol metabolites (continuous, nmol/mL) and inflammatory molecules (continuous, 147 ng/mL or pg/mL), and the intervention group (categorical, EVOO/nuts/low-fat).

148 All analyses were conducted with robust variance estimates to correct for intra-cluster 149 correlations and two-sided significance was determined at p < 0.05. Analyses were 150 performed using Stata 16.0.

151 **3. Results**

152 *3.1. General characteristics of the participants*

General characteristics of the participants are summarized in Table 1 and detailed in *Supplementary Table S1, S2, S3 and S4.* Plasma levels of circulating inflammatory molecules at baseline and after one year of follow-up are reported according to red wine consumption in *Supplementary Table S5.* As shown in Table 1, the mean age of participants was 68.9 years and 49.2% were female. As expected, based on the inclusion criteria of the PREDIMED trial, the mean BMI indicated overweight and the prevalence of cardiovascular risk factors was 49.7% for diabetes, 64.8% for dyslipidemia, and 81.6% for hypertension.

160 Most participants were either non-smokers (85.5%) or had a low educational level (75.4%).

Table 1

Baseline characteristics of the participants (n = 179).

Dusenne enaluerensites of the participants (ii	1/2).	
Age, years	68.9 ± 5.9	
Sex, female	88 (49.2)	
BMI, kg/m ²	29.5 ± 3.6	
Overweight (BMI≥25kg/m ²), n (%)	162 (90.5)	
Physical activity, METs-min/d	267.2 ± 214.0	
Current smoker, n (%)	26 (14.5)	
Medication, n (%)		
NSAIDS	12 (6.7)	
Aspirin	42 (23.5)	
Other antiplatelet drugs	37 (20.7)	
Diuretics	38 (21.2)	
Insulin	14 (7.8)	
Antidepressants	42 (23.5)	
ACE inhibitors	50 (27.9)	
Oral hypoglycemic drugs	58 (32.4)	
Vitamins or supplements	20 (11.2)	
Educational level, n (%)		
Low	135 (75.4)	
High & medium	44 (24.6)	
Diabetes mellitus, n (%)	89 (49.7)	

Dyslipidemia, n (%)	116 (64.8)
Hypertension, n (%)	146 (81.6)
Family history premature CHD, n (%)	43 (24.0)
Total energy intake, kcal/d	2353.8 ± 634.1
Intervention group, n (%)	
MedDiet supplemented with EVOO	60 (33.5)
MedDiet supplemented with nuts	63 (35.2)
Low-fat diet control group	56 (31.3)
Wine consumption (mL/d)	85.8 ± 135.4
Red wine consumption (mL/d)	62.1 ± 110.0
Grape & raisin consumption (g/d)	11.2 ± 20.0
Dihydroresveratrol glucuronide (nmol/mL)	1.1 ± 2.9
Dihydroresveratrol sulfate (nmol/mL)	1.6 ± 5.8
sVCAM-1 (ng/mL)	188.1 ± 51.9
sICAM-1 (ng/mL)	180.0 ± 72.6
IL-6 (pg/mL)	5.0 ± 3.2
TNF-α (pg/mL)	12.7 ± 20.2
MCP-1 (pg/mL)	39.3 ± 22.5

Data are given as mean \pm standard deviation (SD) for continuous variables, and *n* (percentage) for categorical variables.

BMI, body mass index; d, day; EVOO, extra virgin olive oil; IL-6, interleukin-6; MCP-1, monocyte chemoattractant protein-1; MedDiet, Mediterranean diet; METs, metabolic equivalent of tasks; NSAIDS, non-steroidal anti-inflammatory drugs; sICAM-1, soluble intercellular adhesion molecule-1; sVCAM-1, soluble vascular cell adhesion molecule-1; TNF- α , tumor necrosis factor- α .

p < 0.05 were considered significant.

Student's t-test were used for continuous variables and a chi-square test was used for categorical variables.

- 161 *3.2. Dihydroresveratrol metabolites as biomarkers of red wine consumption*
- 162 ROC curves demonstrated that baseline urinary levels of DHRg and DHRs could predict
- 163 red wine consumption, with an AUC = 0.7207 (95% CI: 0.644; 0.797) and AUC = 0.6489
- 164 (95% CI: 0.565; 0.733), respectively (Figure 1A and Figure 1B). After adjusting for
- 165 potential confounders, the predictive value of DHRg and DHRs for red wine intake
- 166 increased, with new values of AUC = 0.835 (95% CI: 0.775; 0.900) and AUC = 0.803 (95%
- 167 CI: 0.736; 0.870), respectively (*Figure 1C and Figure 1D*).



169 Figure 1. Receiver operating characteristic (ROC) curves for predicting baseline red wine 170 consumption (yes/no) using baseline urinary dihydroresveratrol glucuronide (A) and sulfate (B). 171 Adjustments for potential confounders were made to correct baseline urinary values of 172 dihydroresveratrol glucuronide (C) and sulfate (D). Variables used for adjustments were age, sex, 173 physical activity, smoking habit, BMI, diabetes, hypercholesterolemia, hypertension, energy intake, 174 and consumption of grapes and raisins. The analyses were conducted with robust variance estimates 175 to correct for intra-cluster correlation.

Multivariable-adjusted regression model between baseline values of red wine consumption 176 177 and baseline urinary dihydroresveratrol metabolites revealed that higher urinary 178 concentrations of DHRg and DHRs were present in the participants who consumed more 179 red wine ($\beta_0 = 0.707$; $\beta_1 = 0.375$; R-squared = 0.316; p-value = 0.002 and $\beta_0 = 1.352$; β_1 180 = 0.312; R-squared = 0.268; p-value = 0.018, respectively). In contrast, when white wine consumption was modeled instead of red wine, no significant associations were observed 181 182 for either DHRg or DHRs ($\beta o = -2.290$; $\beta 1 = 0.101$; R-squared = 0.089; p-value = 0.239 and $\beta_0 = -2.120$; $\beta_1 = 0.079$; R-squared = 0.091; *p*-value = 0.325, respectively). 183

184 *3.3.* Urinary resveratrol metabolites and circulating inflammatory molecules.

185 As illustrated in *Figure 2A*, after adjustment for potential confounders, participants with 186 higher concentrations of DHRs at baseline showed significantly lower concentrations of

circulating sVCAM-1 (-0.40 (95% CI: -0.66; -0.15) ng/mL per 1-SD increase, *p*-value =

- 188 0.012). No other significant associations were found with other circulating inflammatory
- 189 biomarkers (Supplementary Table S6).

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As shown in *Figure 2B*, after adjustment for potential confounders, participants with higher
 increments in urinary DHRg concentrations after one year of follow-up, presented
 significantly greater decreases in circulating sVCAM-1 concentrations (-0.43 (95% CI:

193 -0.73; -0.13) ng/mL per 1-SD increase, *p*-value = 0.016). No significant associations were 194 found with other circulating inflammatory biomarkers (*Supplementary Table S7*).



195 Figure 2. Multivariable-adjusted regression between baseline dihydroresveratrol sulfate in urine and inflammatory molecules (ng/mL per 1-SD increment) (A) and multivariable-adjusted 196 regression between one-year changes in dihydroresveratrol glucuronide in urine and inflammatory 197 198 molecules (ng/mL per 1-SD increment) (B). Regressions were adjusted for age, sex, recruitment 199 center, intervention group (only **B**), physical activity, smoking habit, BMI, diabetes, 200 hypercholesterolemia, hypertension, intake of energy, intake of omega-3 fatty acids, statins, aspirin, NSAIDs and consumption of grapes and raisins. Analyses were conducted with robust estimates of 201 202 the variance to correct for intra-cluster correlation. sVCAM-1, soluble vascular cell adhesion 203 molecule-1; sICAM-1, soluble intercellular adhesion molecule-1; IL6, interleukin-6; TNF-α, tumor 204 necrosis factor- a; MCP-1, monocyte chemoattractant protein-1.

205 *3.4. Red wine consumption reported in FFQ and circulating inflammatory molecules.*

Multivariable-adjusted regression was performed using red wine consumption reported in 206 FFQ as continuous variable (mL/d) and circulating inflammatory molecules observing no 207 208 significant associations between these two variables either at the baseline (Figure 3A and Supplementary Table S8) or after one year of follow-up (Figure 3B and Supplementary 209 Table S9). An inverse but not significant tendency was observed in case of sVCAM-1 at the 210 baseline (-0.10 (95% CI: -0.61; 0.41) ng/mL per 1-SD increase, p-value = 0.623) and after 211 one year of follow-up (-0.19 (95% CI: -0.50; 0.12) ng/mL per 1-SD increase, p-value = 212 0.162). 213

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Figure 3. Multivariable-adjusted regression between baseline red wine consumption reported in
 FFQ as continuous variable (mL/d) and inflammatory molecules (ng/mL per 1-SD increment) (A)
 and multivariable-adjusted regression between one-year changes in red wine consumption
 reported in FFQ and inflammatory molecules (ng/mL per 1-SD increment) (B). Regressions were

219 adjusted for age, sex, recruitment center, intervention group (only **B**), physical activity, smoking 220 habit, BMI, diabetes, hypercholesterolemia, hypertension, intake of energy, intake of omega-3 221 fatty acids, statins, aspirin, NSAIDs and consumption of grapes and raisins. Analyses were 222 conducted with robust estimates of the variance to correct for intra-cluster correlation. sVCAM-223 1, soluble vascular cell adhesion molecule-1; sICAM-1, soluble intercellular adhesion molecule-224 1; IL6, interleukin-6; TNF- α , tumor necrosis factor- a; MCP-1, monocyte chemoattractant protein-225 1.

226

227 4. Discussion

In this study of older adults at high cardiovascular risk we observed an inverse association
 between urinary microbiota-derived resveratrol metabolites and circulating sVCAM-1
 levels. Moreover, we found a positive and significant association of red wine consumption
 and urinary microbiota-derived resveratrol metabolites.

232 In contrast with microbiota-derived metabolites, no significant associations were detected when FFO-reported values of red wine consumption were used to perform the regression 233 analysis with circulating inflammatory molecules. This outcome highlights the importance 234 of using specific biomarkers of consumption instead of FFQ data, since food biomarkers 235 provide objective and accurate information about nutrient intake, their interaction with 236 microbiota and other food matrixes, absorption, and metabolism. Indeed, without DHRs 237 and DHRg as specific biomarkers of red wine consumption, no significant associations 238 would have been found in the present study. Interestingly, regression models between FFQ 239 240 data and circulating sVCAM-1 showed an inverse association, particularly after one year of follow-up, although it remains non-significant. This supports the hypothesis that red 241 wine consumption reported in FFO was underestimated and can be corrected by using 242 243 accurate and specific biomarkers as reported here.

Our results align with the anti-inflammatory outcomes of wine consumption reported in previous studies (13, 23). The specific correlation between red wine consumption and sVCAM-1 may be explained by the ability of red wine (poly)phenols to suppress VCAM-1 gene transcription, as demonstrated in molecular studies (24). Moreover, Sacanella et al. (25), who also observed the same effect in red wine, highlighted that while ICAM-1 is constitutively expressed by endothelial cells, VCAM-1 is only expressed on activated endothelial cells, providing an additional factor that could explain the observed effect.

It should be emphasized that positive health effects attributed to wine consumption have
only been observed with light to moderate consumption during meals (26), in accordance
with the MedDiet pattern, where main meals are complemented with one or two glasses of
wine (19).

The novelty of the present study lies in the association between red wine consumption and urinary microbiota-derived resveratrol metabolites, with no significant associations with white wine. This high degree of specificity allows, for the first time, differentiation between red wine and other types of wines, which constitutes the main strength of the present study. In addition, longitudinal design and the use of biomarkers for both inflammation and specific biomarkers of red wine consumption further strengthen our work. 261 On the other hand, the small sample size of an older population at high risk of CVD represents a highly specific sample group and constitutes the main limitation of our study. 262 Nevertheless, the sample size was sufficient to detect significant associations between 263 microbiota-derived resveratrol metabolites in urine and plasma sVCAM-1 levels. 264 Moreover, although the participants' data encompassed the most relevant variables that may 265 impact on inflammation, kidney disease information was not available. In addition, we used 266 267 spot urine samples instead of 24-hour urine, the latter being considered the gold standard 268 for estimating nutrient intakes. Finally, we only examined inflammatory biomarkers associated with atherosclerotic plaque development, without assessing other pro-269 inflammatory molecules. 270

271 **5.** Conclusion

Our findings demonstrate that urinary DHRg and DHRs are reliable and specific
biomarkers of red wine consumption, which present advantages compared to FFQ data.
Levels of both resveratrol metabolites were inversely associated with circulating sVCAM1, a recognized biomarker of atherosclerosis progression.

276 **Conflicts of interest**

R.M.L.R. reports fees from Cerveceros de España, UNIDECO, Adventia, Ecoveritas S.A,
from the Fundación Dieta Mediterránea. R.E. reports fees from the Fundación Dieta
Mediterránea, and Cerveza y Salud, Brewers of Europe, Fundación Cerveza y Salud,
Instituto Cervantes, Lilly Laboratories, and Wine and Culinary International Forum. E.R.
reports fees from California Walnut Commission, Alexion, Sociedad Española de
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283 Ethical standards

The study was conducted according to the guidelines of the Declaration of Helsinki. The
Institutional Review Board (IRB) of the Hospital Clinic approved the study protocol.
Controlled Trials number, ISRCTN35739639.

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299 Declaration of generative AI and AI-assisted technologies in the writing process

300	AI or AI-assisted technologies we	ere not used in the writing proces	s of this article.
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