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Metabolomics as a tool in the identification of dietary biomarkers

Helena Gibbons^{1,2} and Lorraine Brennan^{1,2*}

¹ Institute of Food & Health, UCD School of Agriculture and Food Science, University College Dublin (UCD), Belfield, Dublin, Ireland ²UCD Conway Institute of Biomolecular Research, UCD, Belfield, Dublin, Ireland

* Address correspondence to Prof. Lorraine Brennan, UCD School of Agriculture and Food Science, Belfield, University College Dublin, Dublin 4, Ireland. E-mail: lorraine.brennan@ucd.ie

Metabolomics in dietary biomarker discovery

Metabolomics: Dietary biomarkers: Diet and nutrition: Dietary assessment

1 **Abstract**

2 Current dietary assessment methods including food-frequency questionnaires (FFQs), 24-hour
3 recalls and weighed food diaries are associated with many measurement errors. In an attempt to
4 overcome some of these errors, dietary biomarkers have emerged as a complimentary approach to
5 these traditional methods. Metabolomics has developed as a key technology for the identification of
6 new dietary biomarkers and to date, metabolomics based approaches have led to the identification
7 of a number of putative biomarkers. The three approaches generally employed when using
8 metabolomics in dietary biomarker discovery are; i) acute interventions where participants consume
9 specific amounts of a test food, ii) cohort studies where metabolic profiles are compared between
10 consumers and non-consumers of a specific food and iii) the analysis of dietary patterns and
11 metabolic profiles to identify nutritypes and biomarkers. The present review critiques the current
12 literature in terms of the approaches used for dietary biomarker discovery and gives a detailed
13 overview of the currently proposed biomarkers, highlighting steps needed for their full validation.
14 Furthermore, this review also evaluates areas such as current databases and software tools which are
15 needed to advance the interpretation of results and therefore enhance the utility of dietary
16 biomarkers in nutrition research.

17

18

Dietary biomarkers and the concept of metabolomics

19 The contribution of diet to the increasing burdens of cardiovascular disease (CVD), diabetes,
20 obesity and cancers has been recognised since the 1970s⁽¹⁾. Selected foods and nutrients as well as
21 dietary patterns are now known to interact with various metabolic processes contributing to a
22 reduction or an increase in the risk of disease⁽²⁾. For example, it is well established that high salt
23 consumption raises blood pressure⁽³⁾ and high consumption of red meat has been associated with
24 increased incidence of type 2 diabetes^(4; 5), CVD⁽⁶⁾ and cancers⁽⁷⁾. In contrast dietary patterns such
25 as the Dietary Approaches to Stop Hypertension (DASH) diet, which emphasises consumption of
26 fruit and vegetables, low-fat dairy foods and whole grains and reduced intake of red meats and
27 sugars has been shown to decrease blood pressure and CVD risk^(8; 9). Similarly, the Mediterranean
28 diet which emphasises high fruit, vegetable and olive oil consumption has been shown to reduce
29 CVD and type 2 diabetes risk^(10; 11). As diet is a key environmental risk factor, the identification
30 and targeting of dietary factors with the greatest prospective for reducing or increasing disease risk
31 is of major scientific and public health importance⁽¹²⁾. It is therefore essential that dietary
32 assessment methods are reliable and accurate for the advancement of our understanding of the links
33 between diet and health.

34 Diet is traditionally measured via self-reporting methods such as food-frequency
35 questionnaires (FFQs), 24-hour recalls and weighed food diaries. There is however a number of
36 methodological issues associated with each of these assessment methods, including energy under-
37 reporting, recall errors and difficulty in assessment of portion sizes^(2; 13; 14). Such errors can lead to
38 reduced power, underestimated associations and false findings which may contribute to
39 inconsistencies in the field of nutritional epidemiology^(14; 15). In an effort to address some of these
40 measurement issues, the use of dietary biomarkers, which are found in biological samples and are
41 related to ingestion of a specific food or food group, have emerged⁽¹⁶⁾. Currently dietary
42 biomarkers exist for salt, protein, sucrose/fructose intake (sodium/nitrogen/sucrose and fructose
43 measured in 24 h urine samples) and energy expenditure (the doubly labelled water technique)^(2; 17).
44 These dietary biomarkers can be used in conjunction with traditional dietary assessment methods to
45 improve the accuracy of dietary intake measurement and can also be used to more accurately
46 associate dietary intake with disease risk and nutritional status⁽¹⁸⁾.

47 In recent years, metabolomics has developed as a key technology for the identification of
48 new dietary biomarkers. Metabolomics provides a powerful approach for the comprehensive
49 description of all low molecular weight molecules present in biological samples⁽¹⁶⁾. In
50 metabolomics research the analytical platforms predominantly used are nuclear magnetic resonance
51 (NMR) spectroscopy and mass spectrometry (MS) coupled with a chromatographic step, for

52 example, gas chromatography (GC) or liquid chromatography (LC). Each of these techniques are
53 associated with a number of advantages and disadvantages, for example MS-based techniques have
54 high sensitivity and therefore may detect metabolites below the detection limit of NMR
55 spectroscopy, however sample treatment is necessary before MS-based analysis, while little or no
56 pre-treatment is required for NMR ⁽¹⁹⁾. While in the past many articles detailed the advantages and
57 disadvantages of different approaches there has now been a realisation that using one platform alone
58 will not give complete coverage of the metabolite profile; therefore, a combination of technologies
59 and approaches is usually recommended for optimal coverage. Analysis of metabolomic data is
60 commonly performed using multivariate statistics and there are an increasing selection of databases
61 and tools available to assist in the interpretation of these multivariate results ⁽²⁰⁾.

62 Examination of the literature reveals that there are three approaches generally employed for
63 dietary biomarker discovery. These can be summarised as : i) acute or medium interventions where
64 participants consume specific amounts of a test food and biological samples are collected post
65 consumption, ii) cohort studies where metabolic profiles are compared between consumers and non-
66 consumers of a specific food and iii) the analysis of dietary patterns and metabolic profiles to
67 identify nutritypes and biomarkers. Although these study designs have led to the identification of a
68 number of biomarkers in the literature in recent years, each of these approaches have a number of
69 limitations associated with them. Awareness of these is important in the interpretation and potential
70 use of such biomarkers. Therefore the objective of this review is to give an overview of currently
71 proposed biomarkers and secondly this review aims to critique the current literature in terms of
72 approaches for dietary biomarker discovery, highlighting steps needed for their full validation.

73

74 **Dietary biomarker discovery using intervention studies**

75 Dietary intervention studies involve participants consuming specific amounts of a test food in a
76 single meal (acute intervention) or for a short to medium term intervention the test food is
77 consumed in repeated meals. In this approach baseline and postprandial biofluids are collected and
78 following analysis, potential biomarkers are identified. This approach has led to the identification of
79 a number of putative biomarkers of specific foods and beverages as summarised in Table 1. An
80 excellent example of a biomarker successfully identified using this approach is proline betaine, a
81 robust biomarker of citrus fruit intake. Proline betaine was originally identified by Atkinson et al.
82 ⁽²¹⁾ and following this Heinzmann and colleagues performed an acute intervention study with a
83 mixed-fruit meal, which consisted of apples, grapes, oranges, and grapefruit ⁽²²⁾. Eight participants
84 consumed standardised meals over three days and on the second day the mixed-fruit meal was
85 consumed ⁽²²⁾. Urine samples were collected and analysed using NMR spectroscopy. Following
86 multivariate analysis proline betaine was identified as a potential biomarker. To assign the origin of

87 urinary proline betaine excretion after the mixed-fruit meal, concentrations of proline betaine in
88 fruits and fruit juices were measured. Concentrations of proline betaine were higher in citrus fruit
89 compared with other commonly available fruit and fruit juices tested. The urinary excretion profile
90 of proline betaine was then measured in 6 individuals after consumption of orange juice. This
91 biomarker was confirmed using data from participants in the INTERMAP U.K. cohort and
92 demonstrated a high sensitivity and specificity for citrus fruit consumption (90.6 and 86.3%
93 respectively) ⁽²²⁾. Lloyd and colleagues also identified proline betaine and a number of
94 biotransformed products in postprandial urine samples after consumption of 200ml of orange juice
95 as part of a standardised test breakfast ⁽²³⁾. Subsequent biomarker validation demonstrated
96 sensitivities and specificities of 80.8–92.2% and 74.2–94.1% respectively, for elevated proline
97 betaine in high reporters of citrus fruit consumption ⁽²³⁾. Following on from these acute studies, a
98 medium term intervention study used MS to profile the urinary metabolomes of 12 volunteers that
99 consumed orange juice regularly for one month as part of their habitual diet. Proline betaine was
100 again identified as a potential marker of citrus fruit ⁽²⁴⁾. Considering the range of studies that
101 consistently report proline betaine as a marker of citrus fruit intake the evidence base is strong to
102 support its use.

103 A number of research groups have also used dietary interventions to investigate biomarkers
104 of cruciferous vegetables ^(25; 26; 27). Andersen and colleagues performed a controlled cross-over meal
105 study with nine brassica-containing New Nordic Diet (NND) meals in 17 subjects ⁽²⁶⁾. 24 h urine
106 samples were collected and analysed by ultra-performance liquid chromatography quadruple time-
107 of-flight MS (UPLC-qTOF-MS). To investigate the food sources of the biomarkers found in the
108 meal study, a range of small single food studies were performed with 3–4 participants in each.
109 Using a sensitivity and specificity analyses to select the most promising biomarkers, a range of
110 conjugated isothiocyanates were identified as PEMs of brassica intake ⁽²⁶⁾. Further PEMs of other
111 foods, including fish were also identified ⁽²⁶⁾. To validate the biomarkers from this study, Andersen
112 et al. carried out a 6-month parallel dietary intervention study where 107 participants were
113 randomised into two distinct dietary patterns ⁽²⁷⁾. Combining LC-MS data from 24 h urine samples
114 and data from 3-day weighed dietary data this study again identified conjugates of isothiocyanates
115 as brassica biomarkers. However, using this approach it was only possible to verify 23% of
116 potential biomarkers observed in the previous-meal studies ⁽²⁷⁾. As this was a less controlled
117 intervention that included a wider selection of foods with varied amounts of intake and different
118 preparation methods, it highlights the need for the validation of biomarkers in different subjects and
119 study settings ⁽²⁷⁾.

120 A number of red meat and fish biomarkers have been identified using this intervention
121 approach ^(7; 28; 29). Most recently, metabolomics has been applied to compare the different effects of

122 meat and fish on the plasma metabolome ⁽³⁰⁾. Ross et al. carried out an intervention study analysing
123 the differences in the postprandial plasma metabolic response to meals containing baked beef,
124 baked herring and pickled herring ⁽³⁰⁾. 17 males consumed three test meals in a crossover design
125 with one week washout between the meals. Postprandial blood plasma samples were taken over
126 seven hours and analysed by GC-MS. Concentrations of 2-aminoadipic acid, β -alanine and 4-
127 hydroxyproline were significantly higher following the beef meal compared to the baked herring
128 meal. Herring intake led to a greater plasma postprandial response from docosahexaenoic acid
129 (DHA) and cetoleic acid compared with beef ⁽³⁰⁾. However, further studies are needed to confirm
130 these dietary biomarkers and decipher their specificity.

131

132 **Dietary biomarker discovery using cohort studies**

133 Searching for new dietary biomarkers in cohort studies requires the use of self-reported dietary data
134 to identify low and high consumers of a specific food. Following this, the metabolomic profiles are
135 compared between low and high consumers and potential biomarkers are identified. Putative
136 biomarkers of foods, identified using this approach, are presented in Table 2. Work in our lab
137 combined this approach with an acute intervention to identify and confirm a panel of biomarkers
138 indicative of sugar sweetened beverage (SSB) intake ⁽³¹⁾. Heat map analysis was performed to
139 identify correlations between NMR spectral regions and SSB intakes in the cohort study. A panel
140 of 4 biomarkers; formate, citrulline, taurine and isocitrate were identified as markers of SSB intake.
141 Following the acute consumption of the SSB all 4 metabolites were shown to increase in the urine
142 and the panel of biomarkers were successfully identified in the SSB ⁽³¹⁾. Another study using this
143 cohort study approach, analysed the correlations between serum profiles and dietary data collected
144 using FFQs in participants from the Prostate, Lung, Colorectal, and Ovarian (PLCO) Cancer
145 Screening Trial ⁽³²⁾. The application of untargeted metabolomics to this epidemiologic data set
146 detected 39 metabolites of known identity that were correlated with a total of 13 dietary groups, for
147 example citrus intake was associated with stachydrine, chiro-inositol, scyllo-inositol and N-methyl
148 proline, fish with 3-carboxy-4-methyl-5-propyl-2-furanpropanoic acid, DHA and EPA, peanut
149 intake with tryptophan betaine and 4-vinylphenol sulfate and coffee intake was associated with
150 trigonelline-N-methylnicotinate and quinate ⁽³²⁾. To complicate interpretation further, the intake of
151 foods is highly correlated making identification of specific biomarkers difficult and this highlights
152 the need for the validation of biomarkers. The majority of biomarkers identified using cohort
153 studies have been predominantly identified in urine, this study demonstrates the potential use of
154 serum samples in dietary biomarker discovery. However, the proposed biomarkers identified are
155 only based on associations and some biomarkers were not food specific, for example DHA was

156 correlated with fish and rice intake. Further validation in intervention studies is therefore necessary
157 to demonstrate responsiveness to intake.

158 Wittenbecher and colleagues also demonstrated the use of serum samples when identifying
159 biomarkers of red meat intake in a subset of participants from the European Prospective
160 Investigation into Cancer and Nutrition (EPIC)-Potsdam cohort (n=2047) ⁽³³⁾. Total red meat
161 consumption was assessed using FFQs and serum samples were analysed using a targeted
162 metabolomics approach. Ferritin, glycine, 4 diacyl phosphatidylcholines, 11 acylalkyl
163 phosphatidylcholines, 2 lysophosphatidylcholines and 2 sphingomyelins were associated with total
164 red meat consumption and 6 of these biomarkers were also found to be associated with type 2
165 diabetes risk ⁽³³⁾. This is the first study evaluating a large set of metabolites as potential mediators of
166 the association between red meat intake and diabetes risk, however, dietary information relied on
167 estimates of habitual consumption over the past year by FFQs and metabolites were measured at a
168 single time point. Furthermore, total red meat was defined as processed and unprocessed meat and
169 therefore did not identify biomarkers of specific types of meat. Additional study is essential to
170 validate the biomarkers identified and to further dissect such relationships with disease risk.

171 Biomarkers of bread intake have also been investigated in 155 subjects from the PERIMED
172 study ⁽³⁴⁾. A 137-item FFQ was used to stratify subjects into three groups: non-consumers of bread
173 (n = 56), white-bread consumers (n = 48) and whole-grain bread consumers (n = 51). Fasting urine
174 samples, analysed by untargeted high-performance liquid chromatography quadruple time-of-flight
175 MS (HPLC-qTOF-MS), identified higher concentrations of compounds including benzoxazinoids
176 and alkylresorcinol metabolites and compounds produced by gut microbiota (enterolactones,
177 hydroxybenzoic and dihydroferulic acid metabolites) in bread consumers. 2, 8-dihydroxyquinoline
178 glucuronide was also found to be more abundant in whole-grain bread consumers ⁽³⁴⁾. The
179 biomarkers identified are based on a FFQ; therefore further validation is essential to demonstrate a
180 direct relationship with bread consumption.

181

182 **Dietary biomarker discovery using dietary patterns**

183 The third approach; analysing dietary patterns and metabolomic profiles to identify nutritypes (ie,
184 metabolic profiles that reflect dietary intake) and biomarkers have been demonstrated by a number
185 of research groups (see Table 3). One of the first examples emerged from our laboratory when a k-
186 means cluster analysis was performed on self-reporting dietary data and 3 distinct dietary patterns,
187 which were associated with unique food intakes were identified ⁽³⁵⁾. Dietary clusters were reflected
188 in the urinary metabolomic profiles of the 125 participants and a number of metabolites were
189 identified and linked to the intake of specific food groups ⁽³⁵⁾. These nutritypes have the potential to
190 aid dietary assessment by unobjectively classifying people into certain dietary patterns. Further

191 work within our research group, applying the concept of using biomarkers to reflect dietary
192 patterns, has focused on lipidomics, a subfield of metabolomics that concentrates on the global
193 study of lipids ⁽³⁶⁾. Dietary data, measured by FFQs and lipid profiles measured from serum
194 samples, in 34 Metabolic Challenge Study (MECHE) participants were used for this analysis. PCA
195 reduced lipid profiles into lipid patterns and these were regressed against dietary data to identify
196 biomarkers related to the intake of certain foods and nutrients. 6 lipid patterns were identified
197 including lipid pattern 1 which was found to be highly predictive of dietary fat intake (AUC of
198 0.82), lipid pattern 4 which was highly predictive of alcohol intake (AUC=0.81) and lipid pattern 6
199 which had a reasonably good ability to predict dietary fish intake (AUC=0.76).
200 Lysophosphatidylcholine alkyl C18:0 (LPCeC18:0) was identified as a potential biomarker of
201 alcohol consumption and lysophosphatidylethanolamine acyl C18:2 (LPEaC18:2) and
202 phosphatidylethanolamine diacyl C38:4 (PEaC38:4) were identified as potential biomarkers of fish
203 intake ⁽³⁶⁾. This approach demonstrates the utility of serum in the identification of key dietary
204 factors that influence the lipidomic profile. However, again validation of the biomarkers through
205 use of intervention studies is needed.

206 Most recently, Andersen and colleagues used an untargeted metabolomics approach to
207 distinguish between two dietary patterns with the purpose of developing a compliance measure ⁽³⁷⁾.
208 In a parallel intervention study 181 participants were randomly assigned to follow a New Nordic
209 Diet (NND) or an Average Danish Diet (ADD). 24 hour urine samples were collected, analysed by
210 UPLC-qTOF-MS and PLS-DA was applied to develop a compliance model for ADD and NND
211 based on the most discriminative features detected in urine. This resulted in a robust model with a
212 misclassification rate of 19% ⁽³⁷⁾. Metabolites characterising the ADD diet and the NND diet are
213 listed in Table 3. This study demonstrates the potential of metabolomics in discovering biomarkers
214 indicative of dietary patterns but furthermore it highlights a promising approach that may be used to
215 develop compliance measures that cover the most important discriminant metabolites of complex
216 diets.

217

218 **Limitations of current approaches/study designs**

219 In general, metabolomics based approaches have produced reasonably robust models for dietary
220 biomarker identification. However, following the discovery of any biomarker, validation in an
221 independent study is critical to enable the generalisability of the results. This validation step is
222 essential because factors which may not be present in traditional dietary assessment methods
223 including genetic factors, lifestyle and physiological factors, dietary factors, the biological sample
224 or the analytic methodology could skew biomarker measures of dietary intake ⁽³⁸⁾. For many of the

225 study designs discussed, validation of the biomarker is often absent, making it difficult for the
226 translation of these biomarkers into practice.

227 It has been proposed that the confirmation of dietary biomarkers should occur in two stages,
228 firstly the dose–response effect should be included in intervention studies and secondly the
229 suitability of the candidate biomarker in a free-living population should be investigated using a
230 (controlled) habitual diet ⁽³⁹⁾. Evaluation of the dose–response relationship is critical as it allows for
231 the assessment of the suitability of the biomarker over a range of intakes ⁽²⁰⁾. Unfortunately, in
232 many studies, this important step is often absent. Biomarkers identified using samples from cohort
233 studies do not assess the direct relationships of food amounts consumed and levels of biomarkers
234 and do not demonstrate responsiveness to intakes, therefore the relationship is only an association
235 ⁽¹⁶⁾. Such studies should ideally be combined with intervention studies to demonstrate direct
236 relationships and dose-response relationships. Conversely, dietary biomarkers identified within
237 acute intervention studies advantageously allow for the examination of dose-response relationships,
238 however, to date few studies have incorporated such designs.

239 When using self-reporting dietary data from cohort studies in the biomarker discovery
240 process, one should be aware of reporting errors and the potential for missing important correlations
241 and attenuation of results. May and colleagues investigated the metabolomic profiles of participants
242 consuming a high-phytochemical diet compared with a diet without fruits and vegetables in a
243 randomised controlled trial and also investigated the metabolomic profiles of participants in a cross-
244 sectional study, where high and low fruit and vegetable diets were identified based on 3-day food
245 records and FFQs. The intervention study found forty-six putatively annotated ions, with MS/MS
246 fragment ion support that were differentially abundant between the two intervention diets, however
247 within the cross-sectional study only one compound annotated with MS/MS support was identified
248 using the 3-day food records and there were no metabolites that significantly separated groups
249 based on FFQ data ⁽⁴⁰⁾. This therefore demonstrates the drawbacks of using self-reported data in
250 dietary biomarker discovery. Furthermore, when using cohort studies to identify or confirm
251 biomarkers it is imperative that it is acknowledged that many of the foods consumed are highly
252 correlated and therefore biomarkers identified may not be specific to the particular food of interest
253 ⁽²⁰⁾. Following identification of putative biomarkers from cohort studies we recommend that the
254 relationship is confirmed using an intervention study in a dose-response manner where the
255 sensitivity and specificity of the biomarkers can also be assessed. The importance of such a step is
256 key to the validation of the biomarkers and important to support their use.

257 Use of acute and medium term interventions is not without limitations in terms of dietary
258 biomarker identification: many of the biomarkers identified using this approach are markers of
259 acute intake. For example proline betaine is excreted rapidly in urine and excretion is almost

260 complete ≤ 24 h⁽²²⁾. These acute biomarkers may therefore only be valid for people that regularly
261 and frequently consume the particular foods. The identification of dietary biomarkers that reflect
262 habitual intake requires longer-term studies. Furthermore, it must also be noted that the majority of
263 the acute and medium term intervention study designs involve only a small number of participants
264^(22; 24; 41). The proposed dietary biomarkers identified using these approaches therefore cannot
265 always be extrapolated to population studies in free-living individuals. However, this can be in part
266 be dealt with by confirmation in cohort studies with a diverse range of characteristics.

267 While the above describes limitations in study designs, there is also the need for
268 development of databases and software tools to advance the interpretation of metabolomics results
269 and therefore enhance the utility of dietary biomarkers in nutrition research. Current databases such
270 as the Human Metabolome Database (HMDB) provides access to an online database containing
271 detailed information about small molecule metabolites (>40,000) found in the human body⁽⁴²⁾.
272 Since it was first described in 2007, it is constantly being expanded and updated and has become a
273 valuable resource that contains spectroscopic, quantitative, analytic and physiological information
274 about human metabolites⁽⁴²⁾. The Food Metabolome Database (FooDB), is another database of
275 >28,000 food constituents that contains information about food sources and food concentrations⁽⁴³⁾.
276 This resource provides an aid for the identification of new metabolites that are reflective of food
277 intake. While this resource is valuable, the identification of metabolites originating from food
278 remains difficult and there is a need for sharing of databases to aid identification. Most recently, a
279 comprehensive and electronically accessible human urine metabolome database, which includes
280 quantitative concentrations of metabolites in urine samples was established⁽⁴⁴⁾. This database also
281 represents a significant development and resource for biomarker identification and quantification.
282 Other new software tools include BAYESIL, this system provides fully automated and fully
283 quantitative NMR-based metabolomics of complex mixtures⁽⁴⁵⁾. This will have a significant impact
284 on NMR spectroscopy and NMR-based metabolomics.

285

286

287

288 **Conclusion**

289 The use of dietary biomarkers in nutrition research holds great promise. However, prior to having a
290 suite of reliable dietary biomarkers that could be used in nutrition research a number of validation
291 steps need to be considered. Furthermore, the challenges identified in this review need to
292 be acknowledged and addressed. Appropriate validation steps are essential, otherwise the robustness of
293 biomarkers will remain uncertain and the translation of these biomarkers into practice will be
294 challenging. Longer-term studies are also needed for the identification of dietary biomarkers

295 reflective of habitual dietary intake. Until well validated biomarkers are identified it is unlikely we
296 will see uptake by the research community of the emerging biomarkers. The challenge for the
297 researchers working in this field, in the coming years, will be to develop a suite of well validated
298 biomarkers. To this end the JPI funded programme FoodBall will address some of these issues and
299 pave the way forward (<http://foodmetabolome.org/>). They may also have the potential for the
300 assessment of compliance to dietary interventions in both a clinical and a research setting.
301 Ultimately these dietary biomarkers will be used to further elucidate the proposed links between
302 certain foods and disease.

303

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310

311 Authorship

312 H.G. drafted the outline of the manuscript, conducted the literature search and drafted the
313 manuscript. L. B. was responsible for critically reviewing the manuscript. Both authors read and
314 approved the final manuscript before submission.

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Table 1: Summary of putative biomarkers identified using a metabolomics approach in intervention studies

| Dietary Factor | Study duration | No. of subjects | Sample | Metabolomic technique | Biomarker | Author |
|-----------------------|-----------------------|------------------------|------------------------------|------------------------------|---|--------------------------------------|
| Citrus fruit | Acute intervention | 8 | Fasting & postprandial urine | NMR | Proline betaine | Heinzmann et al. ⁽²²⁾ |
| Citrus fruit | Acute intervention | 4 | 24 h urine | LC-ESI-qTOF, LTQ-Orbitrap | Proline betaine, hydroxyproline betaine, hesperetin 3'- <i>O</i> -glucuronide, naringenin 7- <i>O</i> -glucuronide, limonene 8,9-diol glucuronide, nootkatone 13,14-diol glucuronide, N-Methyltyramine sulfate | Pujos-Guillot et al. ⁽²⁴⁾ |
| Citrus fruit | 4 weeks intervention | 12 | 24 h urine | LC-ESI-qTOF, LTQ-Orbitrap | Proline betaine, hydroxyproline betaine, hesperetin 3'- <i>O</i> -glucuronide, naringenin 7- <i>O</i> -glucuronide, limonene 8,9-diol glucuronide, nootkatone 13,14-diol glucuronide, N-Methyltyramine sulfate | Pujos-Guillot et al. ⁽²⁴⁾ |
| Citrus fruit | Acute intervention | 12 | Fasting & postprandial urine | FIE-FTICR-MS | Proline betaine, hydroxyproline betaine | Lloyd et al. ⁽²³⁾ |
| Citrus fruit | 6 month intervention | 107 | 24 h urine | LC-qTOF | Proline betaine, hesperetin-3-glucuronide | Andersen et al. ⁽²⁷⁾ |
| Red cabbage | 6 month intervention | 107 | 24 h urine | LC-qTOF | 3-Hydroxy-3-(methylsulfinyl)propanoic acid, 3-hydroxyhippuric acid-sulfate, 3-hydroxyhippuric acid, iberin N-acetyl-cysteine, N-acetyl-S-(N-3-methylthiopropyl)cysteine, N-acetyl-S-(N-lylthiocarbamoyl)cysteine, sulforaphane N-acetylcysteine | Andersen et al. ⁽²⁷⁾ |
| Beetroot | 6 month intervention | 107 | 24 h urine | LC-qTOF | 4-Ethyl-5-aminopyrocatechol sulfate, 4-ethyl-5-methylaminopyrocatechol sulfate, 4-ethylpyridine-2-carboxylic acid glycine conjugate | Andersen et al. ⁽²⁷⁾ |
| Walnuts | 6 month intervention | 107 | 24 h urine | LC-qTOF | 5-Hydroxyindole-3-acetic acid | Andersen et al. ⁽²⁷⁾ |
| Strawberries | 6 month intervention | 107 | 24 h urine | LC-qTOF | 2,5-Dimethyl-4-methoxy-3(2H)-furanone-sulfate | Andersen et al. ⁽²⁷⁾ |
| Chocolate | 6 month intervention | 107 | 24 h urine | LC-qTOF | 6-Amino-5-(N-methylformylamino)-1-methyluracil, theobromine, 7-methyluric acid | Andersen et al. ⁽²⁷⁾ |
| Raspberries | Acute intervention | 24 | Fasting & postprandial urine | FIE-FTICR-MS, GC-TOF-MS | Caffeic acid-sulfate, methylepicatechin-sulfate | Lloyd et al. ⁽²⁸⁾ |

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|------------------------|----------------------|----|-----------------------------------|-----------------------|---|------------------------------------|
| Cruciferous vegetables | 2 week intervention | 20 | Fasting & postprandial urine | NMR | S-methyl-L-cysteine sulfoxide | Edmands et al. ⁽²⁵⁾ |
| Cruciferous vegetables | Acute intervention | 17 | Fasting & postprandial urine | UPLC- qTOF - MS | N-acetyl-S-(N-3- methylthiopropyl) cysteine, N-acetyl-S-(Nallylthiocarbamoyl) cysteine, Iberin N-acetyl-cysteine, N-acetyl-cysteine conjugate, 4-iminopentylisothiocyanate, Sulforaphane N-acetyl- cysteine, Erucin N-acetyl-cysteine, N-Acetyl-(N ⁷ -benzylthiocarbamoyl)- cysteine, Sulforaphane N-cysteine | Andersen et al. ⁽²⁶⁾ |
| Broccoli | Acute intervention | 24 | Fasting & postprandial urine | FIE-FTICR-MS | Tetronic acid, xylonate/lyxonate, threitol/erythritol | Lloyd et al. ⁽²⁸⁾ |
| Coffee | Acute intervention | 5 | Fasting & postprandial urine | NMR | 2-furoylglycine | Heinzmann et al. ⁽⁴¹⁾ |
| Coffee | Acute intervention | 9 | Fasting, morning spot, 24 h urine | HILIC-MS/MS | N-Methylpyridinium, trigonelline | Lang et al. ⁽⁴⁶⁾ |
| Black tea | Acute intervention | 20 | Fasting & postprandial urine | NMR | Hippuric acid, 4-hydroxyhippuric acid, 1,3-dihydrophenyl-2- <i>O</i> -sulfate, allic acid, 4- <i>O</i> -methylgallic acid | Van Velzen et al. ⁽⁴⁷⁾ |
| Black tea | Acute intervention | 3 | 24 h urine | NMR | Hippuric acid, gallic acid, 1,3-dihydroxyphenyl-2- <i>O</i> -sulfate | Daykin et al. ⁽⁴⁸⁾ |
| Black and green tea | 2 day intervention | 17 | 24 h urine | NMR | Hippuric acid, 1,3-dihydrophenyl-2- <i>O</i> -sulfate | van Dorsten et al. ⁽⁴⁹⁾ |
| Chamomile tea | 2 week intervention | 14 | Spot urine | NMR | Hippuric acid | Wang et al. ⁽⁵⁰⁾ |
| Mixed nuts | 12 week intervention | 42 | 24 h urine | LC-qTOF, LTQ-Orbitrap | 10-Hydroxydecene-4,6-diyonic acid-sulfate, tridecadienoic/tridecynoic acidglucuronide, dodecanedioic acid, 1,3-dihydroxyphenyl-2- <i>O</i> -sulfate, <i>p</i> -coumaroyl alcohol-glucuronide and -sulfate, <i>N</i> -acetylserotonine-sulfate, 5-hydroxyindoleacetic acid, urolitin A-glucuronide, sulfate, sulfate glucuronide | Tulipani et al. ⁽⁵¹⁾ |
| Beef | Acute intervention | 17 | Postprandial plasma | GC-MS | 2-aminoadipic acid,β-alanine, 4-hydroxyproline | Ross et al. ⁽³⁰⁾ |

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| Herring | Acute intervention | 17 | Postprandial plasma | GC-MS | Cetoleic acid, docosahexaenoic acid | Ross et al. ⁽³⁰⁾ |
| Salmon | Acute intervention | 24 | Fasting & postprandial urine | FIE-FTICR-MS | Anserine, methylhistidine, TMAO | Lloyd et al. ⁽²⁸⁾ |
| Red meat | 15 day intervention | 17 | 24 h urine | Ion exchange chromatography | 1 and 3 methylhistidine | Cross et al. ⁽⁵²⁾ |
| Red meat | 15 day intervention | 12 | 24 h urine | NMR | Carnitine, creatinine, TMAO, acetyl-carnitine, taurine, 1 and 3 methylhistidine | Stella et al. ⁽²⁹⁾ |
| Cruciferous vegetables, citrus and soya | 2 week intervention | 10 | Fasting urine | LTQ-FT LC-MS/MS | Proline betaine, sulforaphane, hippuric acid, genistein, daidzein, equol, glycitein, O-desmethylangolensin, trigonelline, (iso)valerlglycine, hydroxyphenylacetyl-glycine, nicotinuric acid | May et al. ⁽⁴⁰⁾ |
| Lingonberries | Acute intervention | 14 | Postprandial urine | NMR | Hippuric acid, 4-hydroxyhippuric acid | Lehtonen et al. ⁽⁵³⁾ |
| Wine | 28 day intervention | 61 | 24 h urine | NMR | Tartrate, 4-hydroxyphenylacetate, mannitol, ethanol | Vazquez-Fresno et al. ⁽⁵⁴⁾ |
| Mixed red wine/grape juice extracts | 4 week intervention | 58 | 24 h urine | NMR, GC-TOF-MS | Syringic acid, 3-hydroxyhippuric acid, 4-hydroxyhippuric acid, 3-hydroxyphenylacetic acid, 4-hydroxymandelic acid, vanilmandelic acid, hippuric acid, 3-hydroxyphenylpropionic acid, 1,2,3-trihydroxybenzene, 4-hydroxybenzoic acid, homovanillic acid, dihydroferulic acid, phenylacetylglutamine | van Dorsten et al. ⁽⁵⁵⁾ |
| Mixed red wine/grape juice extracts | 4 day intervention | 35 | 24 h urine | GC-MS, LC-MS | Syringic acid, 3-hydroxyhippuric acid, pyrogallol, 3-hydroxyphenylacetic acid, 3-hydroxyphenylpropionic acid, 3,4-dihydroxyphenylpropionic acid, indole-3-lactic acid, hippuric acid, catechol, 4-hydroxyhippuric acid, 3,4-dihydroxyphenylacetic acid, vanillic acid | Jacobs et al. ⁽⁵⁶⁾ |
| Dietary fibres (oat bran, rye bran, & sugar beet fibres) | 5 week intervention | 25 | Fasting plasma | LC-qTOF-MS | 2-aminophenol sulphate, 2,6-dihydroxybenzoic acid, hydroxylated and glucuronidated nuatigenin | Johansson-Persson et al. ⁽⁵⁷⁾ |
| Dietary fibre | 6 month intervention | 77 | 24 h urine | NMR | Hippuric acid | Rasmussen et al. ⁽⁵⁸⁾ |
| Whole-grain rye bread | 4 week intervention | 20 | 24 h urine | LC-qTOF | 3-(3,5-Dihydroxyphenyl)-1-propanoic acid-sulfate and -glucuronide, enterolactone- glucuronide, azelaic acid, 2- | Bondia-Pons et al. ⁽⁵⁹⁾ |

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| | | | | | aminophenol-sulfate, 2,4-dihydroxy-1,4-benzoxazin-3-one, 2-aminophenol-sulfate, 2-4-dihydroxy-1,4-benzoxazin-3-one-sulfate, indolylacryloylglycine, ferulic acid-sulfate, 3,5-dihydroxyphenylethanol-sulfate, 3,5-dihydroxycinnamic acid-sulfate | |
| Whole-grain sourdough rye bread | 8 week intervention | 28 | 24 h urine | FIE-FTICR-MS | HHPAA glucuronide, HPAA sulphate, HBOA glucuronide, N-feruloylglycine sulphate, HHPAA sulphate | Beckmann et al. ⁽⁶⁰⁾ |
| Cheese | 6 week intervention | 23 | 24 h urine | UPLC-ESI-qTOF | Tyramine, sulphate, isobutyryl glycine (and other acyl glycines), xanthurenic acid, 4-hydroxyphenylacetic acid | Hjerpsted et al. ⁽⁶¹⁾ |
| Milk and cheese | 14 day intervention | 15 | Faeces, 24 h urine | NMR | Milk; citrate, creatine, creatinine, urea, cheese; proline betaine, tyrosine, hippurate | Zheng et al. ⁽⁶²⁾ |

NMR, nuclear magnetic resonance. LC, liquid chromatography. ESI, electrospray ionisation. qTOF, quadrupole time-of-flight. LTQ, linear trap quadrupole. FIE, flow infusion electrospray ionisation. FTICR, Fourier transform-ion cyclotron resonance. MS, mass spectrometry. GC, gas chromatography. TOF, time-of-flight. UPLC, ultra-performance liquid chromatography. HILIC, hydrophilic liquid interaction chromatography. TMAO, trimethylamine-N-oxide. LTQ-FT, linear ion trap-Fourier transform mass spectrometer. HHPAA, 2-hydroxy-N-(2-hydroxyphenyl)acetamide. HPAA, N-(2-hydroxyphenyl)acetamide. HBOA, 2-hydroxy-1,4-benzoxazin-3-one. HHPAA, 2-hydroxy-N-(2-hydroxyphenyl)acetamide.

Table 2: Summary of putative biomarkers identified using a metabolomics approach in cohort studies

| Dietary Factor | Dietary assessment tool | No. of subjects | Sample | Metabolomic technique | Biomarkers | Author |
|---|--------------------------|-----------------|-----------------------------------|-----------------------------|--|--------------------------------------|
| Oily fish | FFQ | 68 | Fasting, morning spot, 24 h urine | FIE-FTICR-MS | Methylhistidine | Lloyd et al. ⁽⁶³⁾ |
| Citrus fruit | 24-h dietary record | 80 | Fasting urine | LC-ESI-qTOF, LTQ-Orbitrap | Proline betaine, hydroxyproline betaine, hesperetin 3'-O-glucuronide, naringenin 7-O-glucuronide, limonene 8,9-diol glucuronide, nootkatone 13,14-diol glucuronide, N-Methyltyramine sulfate | Pujos-Guillot et al. ⁽²⁴⁾ |
| Sugar sweetened beverages | 4-day food diary | 565 | Fasting urine | NMR | Formate, isocitrate, citrulline, taurine | Gibbons et al. ⁽³¹⁾ |
| Citrus, green vegetables, red meat, shellfish, fish, peanuts, coffee etc. | FFQ | 502 | Fasting serum | UHPLC-MS/MS,GC-MS | Citrus; Scyllo- & chiro-inositol, Greens; CMPF, Red meat; indolepropionate, Shellfish; CMPF, Peanuts; Tryptophan betaine, 4-Vinylphenol sulfate, Coffee; trigonelline-N-methylnicotinate and quinate | Guertin et al. ⁽³²⁾ |
| Coffee | 24-h dietary record, FFQ | 39 | Morning spot urine | UPLC-qTOF-MS | Atractyligenin glucuronide, Cyclo(isoleucyl-prolyl), 1-Methylxanthine, 1,7-dimethyluric acid, kahweol oxide glucuronide, 1-methyluric acid, trigonelline, dimethylxanthine glucuronide, 5-acetylamino-6-formylamino-3-methyluracil (AMFU), hippuric acid, trimethyluric acid, paraxanthine, 3-hydroxyhippuric acid, 1,3 or 3,7-dimethyluric acid, caffeine | Rothwell et al. ⁽⁶⁴⁾ |
| Coffee | FFQ | 68 | Fasting, morning spot, 24 h urine | FIE-FTICR-MS | Dihydrocaffeic acid | Lloyd et al. ⁽⁶³⁾ |
| Red meat | 24-h dietary record, FFQ | 126 | Fasting urine | Ion exchange chromatography | 1-Methylhistidine | Myint et al. ⁽⁶⁵⁾ |
| Red meat | FFQ | 2047 | Serum | FIA-MS/MS | PC aa 36:0, PC aa 36:4, PC aa 38:0, PC aa 38:4, PC ae 34:2, PC ae 34:3, PC ae 36:3, PC ae 36:4, PC ae 36:5, PC ae 38:4, PC ae 38:5, PC ae 38:6, PC ae 40:4, Lyso-PC 20:4, SM 24:1, Ferritin | Wittenbecher et al. ⁽³³⁾ |

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|---|--------------------------|-----|--------------------|-----------------|--|------------------------------------|
| White bread and wholegrain bread | FFQ | 155 | Fasting spot urine | HPLC-qTOF-MS | 2-Aminophenol sulphate, HPAA glucuronide, HHPAA, HMBOA glucuronide, HBOA glycoside, HPPA, HMBOA, DHPPA glucuronide, 3,5-dihydroxyphenylethanol sulphate, DHPPTA sulphate, hydroxybenzoic acid glucuronide, dihydroferulic acid sulphate, enterolactone glucuronide, pyrrolidine, 3-indolecarboxylic acid glucuronide, riboflavin, 2,8-dihydroxyquinoline glucuronide | Garcia-Aloy et al. ⁽³⁴⁾ |
| Cruciferous vegetables, citrus and soya | 3-day food records, FFQ | 93 | Fasting urine | LTQ-FT LC-MS/MS | Proline betaine | May et al. ⁽⁴⁰⁾ |
| Polyphenol rich foods | 24-h dietary record, FFQ | 481 | 24 h urine | UHPLC-qTOF-MS | Coffee; dihydroferulic acid sulfate. Red wine; gallic acid ethyl ester. Citrus fruit; naringenin glucuronide. Tea; 4-O-methylgallic acid. Apples and pears; phloretin glucuronide. Chocolate products; methyl(epi)catechin sulfate | Edmands et al. ⁽⁶⁶⁾ |
| Walnuts | FFQ | 381 | Fasting spot urine | HPLC-qToF-MS | 3-indolecarboxylic acid glucuronide, hydroxyindoleacetic acid sulfate, N-acetylserotonin sulfate, 10-hydroxy-decene-4,6-dienoic acid sulfate, tridecadienoic/tridecynoic acid glucuronide, enterolactone glucuronide, urolithins, | Garcia-Aloy et al. ⁽⁶⁷⁾ |

FFQ, food frequency questionnaire. FIE, flow infusion electrospray ionisation. FTICR, Fourier transform-ion cyclotron resonance. MS, mass spectrometry. LC, liquid chromatography. ESI, electrospray ionisation. qTOF, quadrupole time-of-flight. LTQ, linear trap quadrupole. NMR, nuclear magnetic resonance. UHPLC, ultra-high-performance liquid chromatography. GC, gas chromatography. CMPF, 3-carboxy-4-methyl-5-propyl-2-furanpropanoic acid. FIA, flow injection analysis. PC aa, diacyl phosphatidylcholines. PC ae, acylalkyl phosphatidylcholines. Lyso-PC, lysophosphatidylcholines. SM, sphingomyelin. HPLC, high-performance liquid chromatography. HPAA, N-(2-hydroxyphenyl) acetamide. HHPAA, 2-hydroxy-N-(2-hydroxyphenyl) acetamide. HMBOA, 2-hydroxy-7-methoxy-2H-1, 4-benzoxazin-3-one. HBOA, 2-hydroxy-1,4-benzoxazin-3-one. HPPA, 2-hydroxy-N-(2-hydroxyphenyl) acetamide. DHPPA, 3-(3,5-dihydroxyphenyl) propanoic acid. DHPPTA, 5-(3,5-dihydroxyphenyl) pentanoic acid.

Table 3: Summary of putative biomarkers identified using dietary patterns and metabolomic profiles

| Dietary Patterns | Dietary pattern approach | Sample | Metabolomic technique | Biomarkers | Author |
|--|---------------------------------|----------------|------------------------------|--|---|
| Prudent and Western dietary patterns | PCA | Fasting plasma | ESI-MS/MS | Western dietary pattern; increased amino acids and short-chain acylcarnitines | Bouchard-Mercier et al. ⁽⁶⁸⁾ |
| Healthy, unhealthy, traditional Irish dietary pattern | k-means cluster analysis | Fasting urine | NMR | Healthy; glycine, phenylacetylglutamine and actetoacetate Traditional Irish; TMAO, <i>O</i> -acetylcarnitine and nndimethylglycine | O'Sullivan et al. ⁽³⁵⁾ |
| 7 dietary patterns (e.g. healthy diet, traditional Bavarian) | PCA | Fasting plasma | ESI-MS/MS | Healthy diet; decrease in the degree of saturation of the fatty acid moieties of different glycerol-phosphatidylcholines | Altmaier et al. ⁽⁶⁹⁾ |
| 7 dietary patterns (e.g. dietary fat lipid pattern, alcohol lipid pattern) | PCA | Fasting serum | ESI-MS/MS | Alcohol consumption; LPCeC18:0 Fish consumption; LPEaC18:2, PEaC38:4 | O'Gorman et al. ⁽³⁶⁾ |
| 5 dietary patterns (e.g. energy intake, plant versus animal based diet) | PCA | Fasting plasma | NMR | Energy intake; greater concentrations of lipids related high energy intake, higher circulating phosphatidycholine related to lower energy intake. Animal based diet; higher concentrations of lysine, arginine, glutamine/glutamate, threonine, aspartate/asparagine, citrate and polyol compounds. | Peré-Trepat et al. ⁽⁷⁰⁾ |

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| New Nordic Diet (NND) and an Average Danish Diet (ADD) | | 24 h urine | UPLC-qTOF-MS | NND diet; TMAO, hippuric acid, hydroquinone-glucuronide, (2-oxo-2,3-dihydro-1H-indol-3-yl)acetic acid and 3,4,5,6-tetrahydrohippurate. ADD diet; pyrrolidine, glucuronide conjugated products, theobromine, 7-methyluric acid, 3,7-dimethyluric acid, 7-methylxanthine, 6-amino-5-[N-methylformylamino]-1-methyluracil, proline betaine and glucuronides of perillidic acid. | Andersen et al. ⁽³⁷⁾ |
| Dietary patterns e.g. high intake of butter/low intake of margarine, high intake of red meat and fish/low intake of whole-grain bread, tea and coffee | RRR | Fasting serum | FIA-MS/MS | High intake of butter and low intake of margarine; acylcarnitines, acyl-alkyl-phosphatidylcholines, lysophosphatidylcholines and hydroxy-sphingomyelins. High intake of red meat and fish and low intake of whole-grain bread and tea; hexose and phosphatidylcholines. | Floegal et al. ⁽⁷¹⁾ |

PCA, principal component analysis. ESI, electrospray ionisation. MS, mass spectrometry. LPCeC18:0, lysophosphatidylcholine alkyl C18:0. LPEaC18:2, lysophosphatidylethanolamine acyl C18:2. PEaaC38:4, phosphatidylethanolamine diacyl C38:4. TMAO, trimethylamine-N-oxide. NMR, nuclear magnetic resonance. UPLC, ultra-performance liquid chromatography. qTOF, quadrupole time-of-flight. RRR, reduced rank regression. FIA, flow injection analysis.