Metabotyping and its application in targeted nutrition: an overview

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Abstract

Metabolic diversity leads to differences in nutrient requirements and responses to diet and medication between individuals. Using the concept of metabotyping – that is, grouping metabolically similar individuals – tailored and more efficient recommendations may be achieved. The aim of this study was to review the current literature on metabotyping and to explore its potential for better targeted dietary intervention in subjects with and without metabolic diseases. A comprehensive literature search was performed in PubMed, Google and Google Scholar to find relevant articles on metabotyping in humans including healthy individuals, population-based samples and patients with chronic metabolic diseases. A total of thirty-four research articles on human studies were identified, which established more homogeneous subgroups of individuals using statistical methods for analysing metabolic data. Differences between studies were found with respect to the samples/populations studied, the clustering variables used, the statistical methods applied and the metabotypes defined. According to the number and type of the selected clustering variables, the definitions of metabotypes differed substantially; they ranged between general fasting metabolism types, more specific fasting parameter subgroups like plasma lipoprotein or fatty acid clusters and response groups to dietary recommendations or drug treatments for disease conditions. This demonstrates that the term ‘metabotype’ has a subjective usage, calling for a formalised definition. In conclusion, this literature review shows that metabotyping can help identify subgroups of individuals responding differently to defined nutritional interventions. Targeted recommendations may be given at such metabotype group levels. Future studies should develop and validate definitions of generally valid metabotypes by exploiting the increasingly available metabolomics data sets.

Key words: Metabotypes; Metabotyping; Metabolic phenotypes; Targeted nutrition: enable Cluster

The human metabolome is influenced by genetic, transcriptional and post-transcriptional factors as well as by the gut microbiome and environmental factors like diet and other lifestyle determinants1,2. It is well known that individuals show large differences in their nutrient requirements and responses to diet and medication according to their metabolic characteristics3–5. Specific dietary recommendations or drug treatments for disease states should thus be tailored to optimise the benefit to the individual. Equally important, specific treatments should not be provided to individuals with only a minor response or a lack of positive response to the intervention. The concept of personalisation is supposed to be more effective with respect to individual benefit: risk ratio and health-care costs than currently used general dietary recommendations and standard treatments for chronic disease5–8.

Such efforts have led to the concept of metabotyping or metabolic phenotyping, which describes the categorisation of individuals based on their metabolic or phenotypic characteristics into more homogeneous subgroups, the so-called metabotypes or metabolic phenotypes. This concept implies that individuals within a subgroup show a high metabolic similarity and those in different subgroups show a high dissimilarity. Metabotyping could, thus, allow the identification of subpopulations or specific patient groups responding differently to a defined dietary or medical intervention.

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intervention, promising better nutritional and medical treatment at the metabolotype level\(^{6,7–13}\).

The metabotyping approach has been used widely in healthy animals\(^{14,15}\) as well as in rodent models of disease for testing drug effects\(^{16,17}\). On this basis, it was possible to separate strain-specific metabolic phenotypes or strain subtypes based on the plasma, urine or fecal metabolic profiles, thereby finding diagnostic and prognostic biomarker differences between groups\(^{14–20}\). Strain subtypes could be established by sex\(^{19,22–25}\), age\(^{22}\), diet\(^{20,26}\) or diurnal time of sample collection\(^{18,21,25}\).

Further, several human studies have been conducted to define specific metabotypes, but these studies used a variety of methods and inconsistent definitions, indicating that the term ‘metabotype’ is often used with quite a different meaning. In reviews on personalised nutrition, O’Donovan et al.\(^{26}\) and Brennan\(^{13}\) proposed the concept of metabotyping and provided examples of articles using the metabotyping approach.

The aim of this paper was to review the existing literature on metabotyping in human studies, to show its application in targeted nutrition and, thus, to provide recommendations for future studies in this field.

**Methods**

A comprehensive literature search was performed using PubMed, Google and Google Scholar up to May 2016. However, this is not a strictly systematic review as described, for example, by the Cochrane Collaboration\(^{27}\) because of many open questions. The first search strategy addressed the definition of metabotypes in healthy individuals or population-based samples to find evidence for differences in metabolism and corresponding subgroups. The second search was conducted on the definition of metabotypes in patients with chronic diet-related metabolic diseases (obesity, metabolic syndrome, diabetes, dyslipidaemia, hyperlipidaemia, hyperuricemia, gout and hypertension) for diagnosing or establishing metabolically homogeneous patient subgroups.

Different combinations of the following keywords were used to search for studies that performed metabotyping in healthy subjects or in population-based samples: ‘metabotype’, ‘metabolic phenotype’, ‘metabolomic phenotype’, ‘molecular phenotype’, ‘clinical phenotype’, ‘biochemical phenotype’, ‘metabolic profile’, ‘metabolomic profile’, ‘metabolic pattern’, ‘nutritional phenotype’, ‘nutritype’, ‘metabolome’, ‘metabolomics’, ‘metabolitism’ or ‘metabolic response’ and ‘cluster’, ‘pattern’, ‘subgroup’, ‘subtype’, ‘cluster analysis’ or ‘principal component analysis’. In addition, an extended search was conducted on this topic including information on underlying causes for differences in metabolism between individuals, namely with regard to genetics, epigenetics, transcriptomics or the microbiome\(^{50}\). To this end, the search terms ‘genetics’, ‘genotype’, ‘SNP’, ‘epigenetics’, ‘transcriptomics’, ‘gut microbiota’ or ‘enterotype’ were added to the search strategy mentioned above.

The literature search concerning the definition of metabotypes in patients was restricted to frequent chronic metabolic diseases with a strong relation to diet. This selection was based on the worldwide growing prevalence of diet-related metabolic diseases such as obesity and type 2 diabetes, on the one hand, and on the fact that, besides tailored medical treatments, targeted dietary intervention could also have an important effect on diet-related diseases, on the other\(^{20}\). Thus, in addition to the keywords mentioned above concerning the definition of metabotypes in healthy subjects or population-based samples, the following search terms referring to common metabolic diseases were included in the search strategy: ‘obesity’, ‘adiposity’, ‘metabolic syndrome’, ‘diabetes’, ‘dyslipidaemia’, ‘hyperlipidaemia’, ‘hyperuricemia’, ‘gout’ or ‘hypertension’. Again, extended searches with keywords addressing underlying causes of metabolic differences were performed.

Relevant articles were selected by first checking titles and abstracts and subsequently the full text of the search results in accordance with the inclusion criteria. Additional studies were identified through supplementary screening of the reference lists of all articles analysed.

The following inclusion and exclusion criteria were used in the literature search: original research articles in English language on human studies, which established homogeneous groups of individuals using statistical analyses based on metabolic data from the body fluids blood and urine. Studies using exclusively other information like genetic, epigenetic, transcriptomic, microbiome, anthropometric or lifestyle data for group establishment were excluded, except in combination with metabolic and/or metabolomics data. In addition, studies in which metabotyping was based only on the combination of simple cut-off points of metabolic variables instead of on statistical analyses, as in the definition of the metabolic syndrome, were not included in this review. In general, all types of study designs were accepted and there were no restrictions on sample size. However, the study populations were limited to healthy subjects or population-based samples in the first search and – for the definition of patient subgroups – to individuals affected by common chronic metabolic diseases in the second search. Extreme or rare chronic diet-related metabolic diseases were not included.

**Results**

In total, thirty-four articles met the inclusion criteria, of which twenty-five articles were related to the definition of metabotypes in healthy subjects or population-based samples, and nine articles were related to the definition of patient subgroups with common metabolic diseases revealed by metabotyping.

**Definition of metabotypes in healthy subjects or population-based samples**

Tables 1 and 2 summarise the key features of the twenty-five articles identified according to the definition of metabotypes in healthy subjects or population-based samples. Table 1 gives an overview of twenty articles defining metabotypes based on fasting data. Table 2 shows an additional five articles defining metabotypes on the basis of metabolic response data for different dietary interventions. Both tables present the respective study objectives, designs and samples, the variables for clustering and their pre-processing, the clustering methods used and their validation as well as the main findings. With the exception of four
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<td>O’Sullivan et al.(30)</td>
<td>Metabolic phenotypes</td>
<td>Intervention study (n 135 healthy subjects) of participants aged 18–63 years in Ireland</td>
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<td>O’Donovan et al.(31)</td>
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<td>Cardiometabolic risk patterns</td>
<td>Cebu Longitudinal Health and Nutrition Survey (CLHNS) (n = 1621 individuals aged 21 (± 0-0) years) in the Philippines</td>
<td>Eight cardiometabolic biomarkers (TAG, HDL, LDL, CRP, systolic and diastolic BP, HOME-IR and glucose)</td>
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<td>CVD risk factors</td>
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IDL, intermediate-density lipoprotein; hs-CRP, high-sensitivity C-reactive protein; GLM, general linear model; HOMA-IR, homeostasis model assessment of insulin resistance; OSC-PLS-DA, orthogonal signal-correction partial least squares discriminant analysis; BP, blood pressure; HOMA2-IR, homeostasis model assessment of insulin sensitivity; PCA, principal component analysis; AIC, Akaike information criterion; BIC, Bayesian information criterion.
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<td>Bouwman et al. [51]</td>
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**References:** Objective study sample Variables for clustering Preprocessing of variables Clustering method Validation of cluster solutions Main findings

- **oGTT:** oral glucose-tolerance test; **GLM:** general linear model; **hs-CRP:** high-sensitivity C-reactive protein; **HOMA-IR:** homoeostasis model assessment of insulin resistance; **PCA:** principal component analysis; **PLS-DA:** partial least squares discriminant analysis.
The following two studies are examples for the establishment of metabotypes using metabolite profiles obtained in the fasting state and the subsequent investigation of differences in response to dietary interventions between the subgroups. O’Sullivan et al.\(^{(30)}\) described metabotypes in an Irish intervention study with 135 healthy individuals aged 18–63 years. After z-standardisation, thirteen blood \(^1\)H NMR biochemical markers of the metabolic syndrome and serum vitamin-D levels were used in a \(k\)-means cluster analysis. Five distinct biologically meaningful clusters were found. Among these, one group with lower serum vitamin-D levels and higher levels of adipokines showed a positive response to vitamin-D supplementation on parameters of the metabolic syndrome. The stability of the cluster result was verified using a 5-fold cross-validation method. Second, Vázquez-Fresno et al.\(^{(52)}\) investigated fifty-seven subjects at a high cardiovascular risk aged \(\geq 55\) years in a randomised and controlled cross-over study. \(k\)-Means cluster analysis revealed four well-differentiated and biologically meaningful clusters using sixty-nine blood and urine \(^1\)H NMR biochemical markers and anthropometric variables identifying red wine polyphenol-responsive metabotypes. In addition to cross-validation, cluster indices like Dunn analysis and Figure of Merit analysis were used.

An example for the definition of metabotypes based on metabolic response data to a dietary intervention is the Irish Metabolic Challenge (MECHE) study, which included 116 participants aged 18–60 years\(^{(59)}\). Mixed-model clustering of blood glucose curves revealed four distinct metabotypes with different responses to an oral glucose-tolerance test, of which one group was identified as a high-risk phenotype. The stability of the differentiated clusters was confirmed by another intervention, an oral lipid-tolerance test. Wang et al.\(^{(50)}\) described metabotypes in a dietary intervention with carotenoid-rich beverages in a cross-over design based on twenty-three healthy subjects in the USA. In each carotenoid arm, the responses to all plasma carotenoids were analysed individually. \(k\)-Means cluster analysis revealed five distinct subgroups with different temporal responses. Subsequently, strong and weak responders to individual dietary carotenoids were identified. The different responses were induced by genetic variants of the carotenoid-metabolising enzyme \(\beta\)-carotene 15,15'-monoxygenase 1.

**Definition of patient subgroups with metabolic diseases by metabotyping**

Table 3 presents nine publications that were selected during the literature search on the definition of metabotypes in patients with chronic diet-related metabolic diseases for diagnosing or establishing metabolically homogeneous patient subgroups. All articles were published within the last 10 years and, again, a majority of the studies were performed in Europe and the USA with differences in study design, sample size (between fifty and 50,000 participants) and the age range of adults. Both sexes were considered in all studies. The articles describe the diagnosis and subgrouping of patients affected by diabetes, obesity, the metabolic syndrome or dyslipidaemia. Here, again, the definitions of patient subgroups varied according to the use of different numbers of metabolic clustering variables. In addition, the types

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**References**

1. O’Sullivan et al.\(^{(30)}\)
2. Vázquez-Fresno et al.\(^{(52)}\)
3. Wang et al.\(^{(50)}\)
4. Sullivan et al.\(^{(30)}\)
5. Bouwman et al.\(^{(51)}\)
6. All studies included both sexes.
7. The type of the cluster variables differed between the studies using blood or urine metabolites, diverse metabolite classes or specifically selected individual metabolite subclasses like lipoproteins or fatty acids and those using fasting metabolites (Table 1) or metabolic responses to dietary interventions (Table 2).
8. According to the number and type of the selected clustering variables, the definitions of metabotypes differed considerably; they ranged between general fasting metabotypes, more specific fasting parameter subgroups like plasma lipidoprotein\(^{(29,33)}\) or fatty acid clusters\(^{(39)}\) and response groups to defined meal challenges or dietary interventions. However, in most studies, at least some standard clinical markers such as glucose, TAG and cholesterol were included. Besides metabolic data, the inclusion of additional phenotypic factors for the definition of metabotypes was implemented in some studies: for example, the consideration of anthropometric parameters like BMI or waist circumference\(^{(32,36–38,41,43–45)}\) and blood pressure\(^{(34–38,40–43,45,46)}\).
9. However, only the study by Bouwman et al.\(^{(51)}\) also assessed some underlying causes for differences in metabolism between sub-populations in the clustering process using transcriptomics data.
10. Before grouping individuals into metabotypes, diverse preprocessing steps were applied in the studies analysed to the cluster variables such as outlier exclusion, log-transformation of skewed data, dimension reduction (e.g. by multiple-correspondence analysis) and standardisation (e.g. range-scaling or z-standardisation). Different unsupervised learning methods were used in the studies to define relatively homogeneous metabolic groups of individuals. These included \(k\)-means cluster analysis, hierarchical clustering and combinations of the two, principal component analysis (PCA), latent class analysis\(^{(33)}\) and mixed-model clustering\(^{(9,45)}\). Then, supervised learning methods, such as partial least squares regression as well as statistical tests like the \(t\) test and ANOVA, were used to find discriminatory variables between the established groups. Clustering indices, cross-validation procedures, repetitions with different cluster seeds and cluster numbers as well as different clustering methods were applied to validate the clustering results. Biologically meaningful metabotypes, which were differentiated using discriminatory variables, also confirmed the clustering results.
11. Using the clustering methods, different numbers of metabotypes were found, ranging between two and eight groups. Some studies identified subgroups of individuals with differential response to nutritional interventions; others only described differences between the subgroups, mainly in the fasting state.
Table 3. Definition of patient subgroups with metabolic diseases by metabotyping

<table>
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<th>Main findings</th>
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<td>Zák et al.</td>
<td>Diagnosis and identification of distinct phenotypes of the metabolic syndrome</td>
<td>Study (n = 354 individuals (166 patients with the metabolic syndrome and 188 controls)) in the Czech Republic</td>
<td>Initially twenty-two but reduced to six plasma fatty acids in plasma (dihomo-γ-linolenic, stearic, myristic, DHA, DPA and linoleic acids)</td>
<td>Examination of extreme values, Power transformation for symmetry and constant variance Variable reduction by linear discriminant analysis with forward variable selection using Wilk's λ criterion</td>
<td>Hierarchical cluster analysis (Ward's method with Euclidean distance)</td>
<td>Well-differentiated individuals by discriminatory metabolites (t test, Wilcoxon's test, Benjamin–Hochberg correction, ANCOVA adjustments) Biologically meaningful groups</td>
<td>Diagnosis of the metabolic syndrome Two distinct subgroups of the metabolic syndrome with differences in concentrations of glucose, NEFA, HOMA-IR and conjugated dienes in LDL</td>
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<td>Schader</td>
<td>Subtypes of type 2 diabetes</td>
<td>GWAS (Framingham Heart Study (FRAM), MESA, SHARe Study (MESA), Atherosclerosis Risk in Communities study (ARIC)) (13 459 study participants aged 30–84 years (832 cases during follow-up for clustering and 12 066 controls) in the USA</td>
<td>Ten metabolic and anthropometric characteristics before diagnosis of type 2 diabetes (sex, BMI, waist: hip ratio, TAG, HDL, glucose, insulin, cholesterol, systolic BP and diastolic BP)</td>
<td>Standardisation</td>
<td>k-Means cluster analysis (Euclidean distance)</td>
<td>Well-differentiated individuals by discriminatory metabolites (t test, Cox proportional hazards model) Stability of cluster results (Calinski method, twenty-five iterations) Biologically meaningful groups</td>
<td>Two distinct subtypes No statistical significant differences in genetic risk factors between the subtypes</td>
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<tr>
<td>Li et al.</td>
<td>Subtypes of type 2 diabetes</td>
<td>Mount Sinai BioMe Biobank Program (n = 11 210 individuals mean aged 55–5 years, of whom 2551 were patients with type 2 diabetes in the USA)</td>
<td>Seventy-three clinical data from high-dimensional electronic medical records</td>
<td>Feature selection (&gt;50 % of patients with non-missing values)</td>
<td>Topological analysis (cosine distance)</td>
<td>Well-differentiated individuals by discriminatory metabolites (t test, ANOVA, χ² test) Stability of cluster results (random training and test sets, stability and robustness statistics) Biologically meaningful groups</td>
<td>Three distinct subtypes characterised by increased diabetic nephropathy and retinopathy in subtype 1, cancer malignancy and CVD in subtype 2 and CVD, neurological diseases, allergies and HIV infections in subtype 3 Association of subtypes with specific SNP</td>
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<td>Amato et al.</td>
<td>Subtypes of type 2 diabetes</td>
<td>Cross-sectional study (n = 96 patients with type 2 diabetes aged 62–40 (so 6–36 years) (range = 51–75 years)) in Italy</td>
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<td>Well-differentiated individuals by discriminatory metabolites (t test, χ² test, Fisher's exact test) Stability of cluster results (silhouette coefficient) Biologically meaningful groups</td>
<td>Two distinct subgroups with higher levels of glycated Hb, glucagon, fasting glucose and lower levels of C-peptide in subgroup 1</td>
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<td>Frei et al.</td>
<td>Subtypes of obesity</td>
<td>Study (n = 50 patients aged 21–61 years) in Brazil</td>
<td>Blood parameters before and after the surgery (BMI, LDL, HDL, VLDL, Hb, platelets, leucocytes, TAG, glucose and bilirubin)</td>
<td>z-standardisation</td>
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<tr>
<td>Arguelles et al.</td>
<td>Subtypes of the metabolic syndrome</td>
<td>Hispanic Community Health Study/Study of Latinos (HCHS/SOL) (n 15,825 Hispanics/Latinos aged 18–74 years in the USA)</td>
<td>Metabolic syndrome components (waist circumference, systolic and diastolic BP, HDL, TAG, glucose, medication use)</td>
<td>Log-transformation and multiplication by 100 were used for skewed variables</td>
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<td>Two distinct subgroups for men and women, respectively (‘metabolic syndrome’ cluster and ‘non-metabolic syndrome’ cluster) Association of subgroups with covariates and CVD No identification of additional subtypes of the metabolic syndrome</td>
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<td>Kim et al.</td>
<td>Subtypes of prediabetes</td>
<td>Large Cohort (n 52,139 adult Mayo Clinic patients) in the USA</td>
<td>Diagnoses (obesity, hyperlipidaemia, hypertension, renal failure, various cardiovascular conditions, vital signs (BP, pulse), laboratory results (glucose, lipids), use of medication (aspirin, medication for hypertension and hypercholesterolaemia)</td>
<td>Binary transformation of variables</td>
<td>Bisecting divisive hierarchical cluster analysis</td>
<td>Well-differentiated individuals by discriminatory metabolites</td>
<td>A subgroup with higher and another subgroup with lower risk for diabetes than the general population Identification of twelve highest-risk groups (out of twenty-six clusters) and their relevant risk factors Use of clustering as a diabetes index outperforming the Framingham risk score</td>
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<td>Mäkinen et al.</td>
<td>Subtypes of type 1 diabetes</td>
<td>Finnish Diabetic Nephropathy (FinnDiene) Study (n 613 patients with type 1 diabetes) in Finland</td>
<td>Blood serum $^1$H NMR spectrum</td>
<td>Several preprocessing steps of $^1$H NMR spectra Adjustment of intensity units to equal variance</td>
<td>Self-organising map (9 × 9 hexagonal sheet of map units, Gaussian neighbourhood function)</td>
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<td>Six subgroups Different diabetic complications, clinical and metabolic characteristics between subgroups</td>
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<tr>
<td>Botelho et al.</td>
<td>Subgroups of dyslipidaemia</td>
<td>Patient data bank at the Dante Pazzanese Institute of Cardiology (n 57 individuals aged 30–80 years with dyslipidaemia controlled by statins) in Brazil</td>
<td>Four plasma biomarkers of oxidative stress (malondialdehyde, ferric reducing ability power, 2,2-diphenyly-1-picrylhydrazyl radical and oxidised-LDL)</td>
<td>Dimension reduction by PCA</td>
<td>Hierarchical cluster analysis (Ward’s method, Euclidean distance)</td>
<td>Well-differentiated individuals by discriminatory metabolites (ANOVA, Tukey’s post hoc test)</td>
<td>Five distinct subgroups No difference in dietary pattern between the subgroups</td>
</tr>
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</table>

HOMA-IR, homoeostasis model assessment of insulin resistance; GWAS, genome-wide association study; MESA, Multi-Ethnic Study of Atherosclerosis; SHARe, SNP Health Association Resource; BP, blood pressure; GLP-1, glucagon-like peptide-1; GIP, glucose-dependent insulinotropic polypeptide; AIC, Akaike information criterion; BIC, Bayesian information criterion; ABIC, sample size-adjusted BIC; PCA, principal component analysis.
of clustering variables differed, often depending on the particular disease investigated. For example, Mäkinen et al.\(^{(60)}\) used a full blood serum \(^{1}H\) NMR spectrum for the subgrouping of patients with type 1 diabetes. In contrast, Arguelles et al.\(^{(58)}\) tried to identify subgroups of the metabolic syndrome using only components of this syndrome (waist circumference, systolic and diastolic blood pressure, HDL, TAG, fasting glucose and medication use) for the clustering procedure. Few studies used additional variables such as anthropometry\(^{(54,57,58)}\) or medication use\(^{(58,59)}\) along with the metabolic information in the clustering process. As a result, the studies identified different patient subgroups depending on the metabolic data assessed. After the application of various preprocessing steps to the cluster variables as described above, clustering methods like \(k\)-means cluster analysis, hierarchical clustering and combinations of the two, topological analysis\(^{(55)}\), latent class analysis\(^{(58)}\) and self-organising maps\(^{(60)}\) were applied. Discriminatory variables between the resulting disease subgroups were again identified using test statistics. Moreover, biological meaning, clustering indices, cross-validation procedures, repetitions with different cluster seeds and cluster numbers as well as different clustering algorithms were applied to validate the clustering results. Different numbers of disease subgroups were formed, mainly two to four groups.

An example for the establishment of type 2 diabetes subgroups is the study by Schader\(^{(54)}\) using three studies in the USA with a total of 852 patients with type 2 diabetes aged 30–84 years. Applying \(k\)-means cluster analysis with ten standardised metabolic and anthropometric characteristics assessed before the diagnosis of type 2 diabetes, two subgroups of the disease were found. Despite the stability of the clustering results, measured using the Calinski method and twenty-five repetitions of the clustering method, and strong differentiation of individuals based on discriminatory variables, no statistically significant difference was found between the genetic risk factors among the subgroups. In a smaller sample size of ninety-six patients with type 2 diabetes, Amato et al.\(^{(56)}\) used three fasting incretins in a two-step cluster analysis to identify two subgroups of this disease.

**Discussion**

This review analysed the literature on metabolotyping of individuals in metabolic and nutrition research. In total, thirty-four studies were included in this analysis covering a wide range of populations and using various clustering variables and statistical methods to identify different numbers of metabolotypes. Consequently, it is difficult to draw meaningful conclusions regarding the establishment of metabolotypes based on these rather heterogeneous studies using different approaches in metabolotyping. However, this paper includes all available human studies using metabolotyping in healthy subjects, population-based samples and patients with chronic metabolic diseases, and thereby represents the current state of knowledge.

**Differences in study populations**

We found a considerable variation in metabolotypes across the countries in which the studies were performed, and this could be due to different genetic characteristics, environmental influences (like dietary and cultural behaviour), risk factors and disease rates\(^{(5,62–64)}\). This variation was seen to be particularly large between Western countries and East Asian countries, whereas metabolotypes across different Western countries displayed substantial overlapping\(^{(62,64)}\). As most studies we review here were conducted in Western populations in Europe and the USA, the defined metabolotypes seem to be transferable and comparable between these studies. However, there is a lack of data as to whether these metabolotypes can be transferred to other ethnic populations.

Comparing metabolotypes between different age ranges may be hampered by the physiological ageing process itself, which is characterised by marked changes in metabolism or metabolic flexibility\(^{(65)}\). However, it was shown in some studies that the plasma metabolotypes (metabolite profiles) of individuals remain relatively stable over a few years\(^{(66,67)}\) and only large differences in age seem to be relevant. As many metabolites differ between men and women – for example, steroid hormones or branched chain amino acids\(^{(62,68,69)}\) – studies need to consider sex differences. This could be achieved by the exclusion of these sex-specific variables from the clustering process or by separate analyses for men and women.

**Differences in variables used for clustering**

The use of diverse types and numbers of clustering variables does not allow a reasonable comparison of the metabolotypes identified in different studies. At present, the debate on the most important criteria and variables to be used for the definition of a biologically meaningful metabotype remains open. Equally important, the aim of metabotype definition has to be defined \textit{a priori}. In 2000, Gavaghan et al.\(^{(15)}\) defined a metabotype as ‘a probabilistic multiparametric description of an organism in a given physiological state based on analysis of its cell types, biofluids or tissues’. Later, metabolotyping was described in several studies as the ‘process of grouping similar individuals based on their metabolic or phenotypic characteristics’\(^{(6,9–13)}\). These wide and general definitions of metabolotypes allow the inclusion of all studies establishing subgroups based on (1) healthy or sick people (thus also in the diagnosis or subgrouping of patients), (2) the fasting state or response to interventions, (3) a few or a variety of metabolites and (4) specifically selected single metabolite subclasses like lipoproteins, diverse metabolite subclasses or the addition of other variables like underlying causes for differences in metabolism – for example, genetic, epigenetic or gut microbiome information.

The selection of variables plays an important role in the identification and separation of metabolotypes. Grouping of individuals based on a few variables or single specific metabolite classes provides a restricted definition of metabolotypes, as only a small part of human metabolism is taken into account. However, for the establishment of plasma lipoprotein clusters in the studies by van Bochove et al.\(^{(29)}\) and Frazier-Wood et al.\(^{(33)}\), or of plasma fatty acid patterns in the study by Li et al.\(^{(39)}\), restriction to the respective lipid variables seemed to be sufficient for subclassification. Likewise, Wang et al.\(^{(70)}\) considered only the plasma carotenoid levels after a dietary intervention with
carotenoids. The same was the case in the study by Morris et al.\textsuperscript{59} considering only blood glucose levels, measured at several points in time, to identify groups with differential glucose responses to an oral glucose-tolerance test. This is of course in accordance with the current clinical practice for classification of type 2 diabetes based on the plasma kinetics of glucose. In diagnosing or subgrouping patients, the restriction of variables to disease-related parameters could also be sufficient for subclassification. For example, Arguelles et al.\textsuperscript{58} established subgroups of the metabolic syndrome patients based on the standard criteria for disease description, namely waist circumference, systolic and diastolic blood pressure, HDL, TAG, fasting glucose and medication use. The grouping in other studies using plasma fatty acids for the description of the metabolic syndrome\textsuperscript{53} and fasting increments for the subgrouping of diabetes\textsuperscript{50} could be probably refined by the consideration of additional disease-related variables.

There is no consensus yet on a uniform use of the term ‘metabotype’, thus it is subjectively applied, usually based on the respective study objectives. In this review, the definitions of metabotypes differed considerably, they ranged between general fasting metabotypes, more specific fasting parameter subgroups like plasma lipoprotein\textsuperscript{29,33} or fatty acid clusters\textsuperscript{39} and response groups to defined meal challenges or dietary interventions according to the number and type of the selected clustering variables. Although an accepted definition of metabotype seems attractive, there is also the view that there is no need for a strict metabotype definition. On the one hand, it may be argued that a metabotype has by its nature a wide definition and should not be restricted. On the other hand, a better comparability of studies could be achieved using a stricter definition. Even if a strict general definition appears implausible or unrealistic, more precise sub-definitions of metabotypes could be developed, for example for lipid and carbohydrate (glucose) metabolism. Thus, metabolic variables restricted to specific metabolic pathways like to those of lipoproteins may be sufficient depending on the respective study objective.

However, it is assumed that the inclusion of various metabolites originating from different pathways as well as additional information from anthropometry or that obtained by including genetics, epigenetics or the gut microbiome in the process of metabotyping provides a more precise characterisation of individuals and, thus, the establishment of more refined and generally valid metabotypes\textsuperscript{70}. This can be achieved through the use of ‘omics’ data such as metabolomics, genomics and epigenomics, where research is growing rapidly\textsuperscript{2,71,72}. Thus, it may be wise to suggest a stricter definition of generally valid metabotypes in healthy subjects or population-based samples by at least the use of variables originating from different metabolic pathways, preferably the use of targeted or untargeted metabolomics data.

Further, there is no agreement as to whether the definition of metabotypes should be based on fasting data (see Table 1) or rather on metabolic response data to interventions (see Table 2), for which we identified only five studies that met the inclusion criteria. An argument for the use of metabolic response data to interventions is the increase of variation between individuals as some metabolic differences are only visible through challenges and would remain undetected using fasting blood values\textsuperscript{73}. However, the establishment of metabotypes by means of fasting data allows extensive measurements of larger study populations and is thus more feasible in the general population. It is important to note that intra-individual variations of metabolite concentrations may also occur because of diurnal time, stress, latent diseases as well as by measurement and storage conditions of the samples\textsuperscript{5,64,74,75}. However, these differences were shown to be smaller than inter-individual differences, suggesting that individual metabotypes are relatively robust\textsuperscript{70}.

**Differences in statistical analyses**

As a variety of statistical methods are available for the establishment of metabotypes\textsuperscript{70}, there is an on-going discussion on which statistical methods should be used to obtain the best spread between subgroups. The preprocessing of variables is especially dependent on the structure of the variables and the requirements of the subsequent clustering methods. Thus, the implementation of outlier exclusion and data transformation has to be decided individually. If the number of clustering variables exceeds one per ten observations, application of data-reduction analyses like PCA or multiple-correspondence analysis must be considered to avoid over adjustment\textsuperscript{77}. In many studies included in this review, standardisation has been applied to the cluster variables to avoid bias from different scales and units in the grouping analyses\textsuperscript{78,79}. The most commonly used method is z-standardisation ($z = \frac{x - \text{mean}}{\text{SD}}$).

Concerning the different clustering methods\textsuperscript{76–82}, k-means cluster analysis and hierarchical cluster analysis were applied most commonly. Each clustering method has its own advantages and disadvantages and must be selected depending on the characteristics of the respective data set (e.g. depending on the scale level or the sample size). k-Means cluster analysis seems to be more suitable for large data sets than hierarchical clustering. However, the number of clusters has to be specified in advance for k-means cluster analysis, whereas hierarchical clustering does not need the number of clusters to be determined\textsuperscript{82}. In addition, there are novel clustering techniques available in the field of bioinformatics, for example the so-called machine learning methods\textsuperscript{83}.

The selection of validation criteria like statistical tests and clustering indices is also dependent on the structure of the data. The reproducibility of metabotypes should be tested in a validation data set to confirm the results and to prove their generalisability.

**Differences in the main findings**

The aim of most studies was to examine metabolic differences between the established metabotypes and to test associations with certain diseases. However, the application of metabotypes, especially the development of targeted interventions for responsive subgroups, is rather limited in the literature. In addition, intervention by supplementation may increase serum levels in all subgroups but with possibly either larger effects in some subgroups or attainment of a threshold concentration considered to be within the normal range. Thus, responsiveness
to an intervention does not necessarily mean benefit and, therefore, outcome parameters also need to be properly defined to evaluate the benefit of interventions, which so far has been rare in previous studies. Only few studies investigated the responsiveness of the established metabotypes to dietary interventions with regard to a specific disease. O’Sullivan et al. [30] identified a subgroup with a positive response to vitamin D supplementation concerning the metabolic syndrome; Vázquez-Fresno et al. [53] detected a subgroup of patients at cardiovascular risk responsive to red wine polyphenols; and Mouzzami et al. [47] identified individuals with reduced insulin sensitivity after consumption of bread. There is only one study that developed tailored dietary recommendations for subgroups using a decision-tree approach [31]. Until now, the established metabotypes have not been transferred to larger populations for specific, tailored interventions.

Conclusion

In conclusion, this literature review shows that metabotyping can help identify metabolically similar subpopulations or patient subgroups responding differently to defined nutritional interventions. Consequently, better tailored and, thus, more precise dietary recommendations than generalised advice may be provided to whole populations at a metabotype group level. The aim of future studies should be the refinement of the definition of generally valid metabotypes in large samples, especially with a possibly more precise phenotype description of individuals based on different ‘omics’ data, particularly metabolomics data. Another aim should be the development of stricter definitions of specific metabotypes for metabolic pathways. The metabotypes should then be tested for differential reactions to diverse dietary factors with regard to properly defined outcome parameters. On the basis of such results, populations may become a future task. Finally, individual health benefits may be improved and the rising costs in the health-care system originating from obesity and other diet-related metabolic diseases may be better controlled.

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