

## Metabolomics in the Context of Forensic Omics Biomarkers

Research Article

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### Abstract

Search for biomarkers is supported on any of the great omics, but the given omics is rarely discussed or even named in the literature as being the basis of the target biomarker. In this context, metabolomics biomarkers exist even before this omics discipline was defined as such, but the fact that a biomarker is based on the changes in the concentration of one or several metabolites does not seem to be enough reason for giving to it the name of metabolomics biomarker. This omission is discussed here for forensic omics in general and for forensic metabolomics in particular. Present forensic biomarkers belonging to different omics are compared and the present and foreseeable future of forensic metabolomics biomarkers discussed.

**Keywords:** Biomarkers; Omics Disciplines; Forensic Metabolomics.

**Abbreviations:** AMI: Acute Myocardial Infarction; BAC: Blood Alcohol Concentration; CDT: Carbohydrate Deficient Transferrin; CF: Cystic Fibrosis; CK: Creatine Kinase; CODIS: Combined DNA Index System; CRP: C-Reactive Protein; DSM: Mental Disorders; EtG: Ethyl Glucuronide; EtS: Ethyl Sulfate; LC-MS/MS: Liquid Chromatography Coupled to tandem Mass Spectrometry; LC-MS QqQ: Liquid Chromatography Coupled to Mass Spectrometry with Triple Quadrupole; LDH: Lactate Dehydrogenase; LISH: Ligation in Situ Hybridization; MALDI: Matrix-Assisted Laser Desorption/Ionization; MS: Mass Spectrometry; PEth: Phosphatidylethanol; PK: Pyruvate Kinase; PSA: Prostate-Specific Antigen; Q: Quadrupole; QTOF: Quadrupole Time-of-Flight; UHPLC: Ultra-High Pressure Liquid Chromatography.

### Introduction

Scientific investigations on biological traces occurring on a crime scene are carried out through a series of sequential steps involving generic diagnosis, species diagnosis, regional diagnosis and individual diagnosis. All together these steps allow researchers to reconstruct the dynamics of the criminal event and to check the reliability of assertions by putative suspect people. The so-called biomarkers help in the successful development of one, several or all the steps in the series.

### Definition of Biomarkers and their Role in Forensics

The term 'biomarker' has been defined differently depending on the scientific area to which it belongs. For example, in toxicology (also applicable in the forensics area) a biomarker could be defined as 'a component (or components) in biological fluids, cells,

tissues, or whole organisms that indicate the presence, magnitude, and exposure of toxicants or of host response' [1]. In the clinical area (also applicable in forensics) a biomarker is defined as 'a characteristic that can be objectively measured and evaluated as an indicator of a physiological or pathological process or as a pharmacological response to a therapeutic intervention' [2]. Otherwise, the World Health Organization defines a biomarker as 'any substance, structure, process or its products its products that can be measured in the body and influence or predict the incidence of outcome or disease'. In spite of all the different definitions of biomarker, they all coincide on the idea of a biomarker as almost any measurement reflecting an interaction between a biological system and a potential hazard, which may be chemical, physical, or biological [3].

Even though biomarkers are by definition objective and quantifiable characteristics of biological processes, they may not be nec-

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essarily associated to an individual's experience or health status. This is the main reason why biomarkers identification requires their relevance and validity to be established. Thus, their assessment involves repeated evaluation taking into account distinct points of view in order to establish its reliability to characterize a specific situation or the individual health status [3]. Final validation is based on comprehensive application to a number of cases that ensures representativeness.

In forensic sciences, the term 'biomarker' has different meanings depending on the forensic discipline and some definitions coincide with those used in other areas, as is the case with toxicological or clinical biomarkers. In dealing with forensic environmental geochemistry, biomarkers are defined as compounds derived from biological sources (i.e., natural products) that retain some, if not all, of the structural characteristics of their parent precursor molecule after being preserved in the geological record or released into the environment [4]. Even though the use of biomarkers in forensic science still needs notable research, it is highly spread through the different areas in this field, as can be found in the literature [5, 7].

### Single and Multiple Biomarkers

Biomarkers can be classified attending to different criteria; one of them is the capability to characterize an organism situation (single biomarker) or the necessity of other biomarkers for complete characterization (multiple biomarkers). An example is found in biomarkers of alcohol consumption, which can reveal recent alcohol exposure or a prolonged risk of alcohol consumption. Among the latter are carbohydrate deficient transferrin,  $\gamma$ -glutamyltranspeptidase and phosphatidylethanol. The last is present in the body only after alcohol intake, while the first two are influenced by factors different from alcohol intake such as sex, age and smoking habit, among others [8]. Therefore, in order to obtain a more complete and unequivocal information multiple biomarkers should be used. A recent and interesting study on the dynamics of multiple biomarkers in mouse excisional wounds for wound age estimation (from 12 h to 10 days) was based on neutrophil and macrophage infiltration, fibroblast and fibrocyte accumulation, their myofibroblastic transformation and some wound healing-related molecules [9]. One other classification of biomarkers is based on the number of compounds forming part of the given biomarker. This classification is characteristic of metabolomics biomarkers, giving place to single metabolite biomarkers and panel metabolite biomarkers [10, 11].

### Scope of Forensics Biomarkers

The sequential steps to which forensic scientists face in their research involve: first, to determine whether a crime has been committed; if so, their assistance focuses on identification of the offender; then, to conduct detailed studies in different areas depending on the evidences they have at their disposal [12]. The areas are specific and well differentiated; this is the main reason why biomarkers are not considered in the same way when scientists work with clinical, environmental or geological samples, among others. Despite forensic biomarkers for clinical samples have so far been more abundant than for environmental samples, advanced techniques and databases have recently been developed in environmental forensic studies to investigate the source, trans-

port, and fate of organic compounds present in the environment. Biomarkers in this discipline consist of compounds that are contained in the target environmental sample (oil, soil, air, etc.), and characterize, correlate and differentiate the sample from others. In this way the source of identification, the determination of its certain composition and distinct relievable factors for the crime investigation are allowed. Nowadays, several spillages of refined oils frequently occur during their production, transportation, storage, and use. These may cause significant environmental problems and this is the reason why researchers perform fingerprinting analysis of oil spills for site contamination assessment, and they also determine the legal liability for the spill [5]. These biomarkers are one of the most important hydrocarbon groups in petroleum for chemical fingerprinting, which are usually stable and show little or no changes in structures from their parent organic molecules [6]. However, recent research has demonstrated that different factors, such as weather, could be involved in the changes [7].

In dealing with clinical samples, forensic biomarkers are particularly desirable. These biomarkers are very helpful, for instance, to evaluate elder abuse - including abrasions, lacerations, bruising, fractures, restraints, decubiti, weight loss, dehydration, burns, cognitive and mental health problems, hygiene issues, and sexual abuse [13]. Their identification is crucial to the medical and legal establishment of whether elder abuse or neglect has occurred [14].

### Pursued Objectives

The aim of this article was first to give a call of attention to the fact that biomarkers in general and forensic biomarkers in particular are supported on given omics that must be specified by the authors; then, to discuss the present and foreseeable future of forensic metabolomics biomarkers.

### Omics in the Context of Forensic Biomarkers

Since Jeffreys et al. introduced in 1985 the DNA fingerprinting in the field of forensic genetics, proving that some regions from the DNA contain repetitive sequences which are variable among individuals [15], the results of DNA analysis have been accepted as evidence in the court in many countries [16]. When in 1992 the European Council issued the Recommendation No. 92, regarding the use of the DNA analysis in the criminal justice, the DNA test was accepted in the Court [17].

Forensic genetics has experienced a strong development during the last 20 years supported on the new discoveries and technologies in molecular biology. Identification of people present in a crime scene is based on analysis of DNA samples extracted from biological fluids such as blood, saliva, semen, or urine; or from tissues such as bones or hairs. DNA analysis has long been able to provide information about an individual's biological sex [18, 19]. More recently, it has also been shown that DNA can be used to learn other externally visible characteristics about the donor, such as eye color, race, and sex [20]. DNA analysis is strongly considered the gold standard in forensic analysis of blood samples because of its highly accurate results (if a DNA match is made the chance of it being a false positive or a coincidental match is on the scale of 1 in 34 million [21]). This is due to the comparative assessment between the genetic profiles obtained from biological

traces found on the crime scene and the profile of a suspect. The profile is entered and logged into the Combined DNA Index System (CODIS) so that a comparison can be made to a person who has been previously arrested [15, 22, 23]. If there is no suspect in custody or no match in the CODIS database either the chromosomal DNA found in the nucleus or the mitochondrial DNA, the profile is essentially useless for the police. Other no minor shortcomings of DNA analysis are the time, price, and technical skill required to analyze a single blood sample.

Continuous improvements in sample preparation in genetics have a clear example in the evolution experienced from the known as Nano String technique to handle damaged mitochondrial RNA-which requires both expensive instrumentation and reagents and has limited sensitivity - to ligation in situ hybridization (LISH), cheaper and less expensive. Addition of LISH probes to damaged mitochondrial RNA allows turning them into sequences of mostly DNA that can be amplified and sequenced without reverse transcription [24].

Proteins, contrary to DNA, were rarely considered as sources of useful biological traces during the first years of proteomics life and were scarcely used in crime scene investigations because: (i) they tend to be less stable than DNA and are easily degraded. (ii) Individual diagnosis by protein identification is impractical because protein variability is low. (iii) The amount of sample available cannot be amplified by "PCR-like" procedures--this aspect can be partially overcome by the possibility of including the original biomarker in a single biocatalytic cascade for amplifying its effect on the final analytical output signal [25]. (iv) Generally, higher amounts than in genomics or extremely high sensitive analytical techniques are required in proteomics. After more than 20 years of proteomics research [26], also the forensic area has been highly benefited from this omics. For example, proteomics has proved that the biological sex, ethnicity, and age of a blood sample can all be determined using multi-enzyme assays [27, 28]. This type of system was used to conduct research using the markers creatine kinase (CK) and lactate dehydrogenase (LDH), in combination with pyruvate kinase (PK) to distinguish between African American and Caucasian blood sample originators [25]. In a similar reaction combining CK, PK, LDH, and alanine transaminase sex of a blood sample originator was determined [28, 29]. In analyzing the use of this assay the samples were allowed to age for up to 120 h and it was determined that the assay could also be used to know the time since a sample was deposited [30]. In addition, a one-enzyme biocatalytic cascade has been used to distinguish between young and old people, independently of the sex, by analysis of blood alkaline phosphatase based on photometric monitoring of *p*-nitrophenol at 450 nm [31]. In this way, the traditional methods applied in forensic serology (usually based on immunoassay [32] or DNA [33]/RNA [34] analysis) with involvement of sophisticated equipment and highly skilled personnel [35] can be substituted by a simple enzymatic assay performed directly at a crime scene, thus giving rapid results for identification of a pool of possible suspects. Given the value of modern crime scene DNA analysis for gathering specific information on the age, sex and race, the enzymatic assay cannot substitute for a DNA 'fingerprint' as it only narrows a group of suspects with some uncertainty. However, its advantage lies in quick, on-site analysis, which is markedly absent in modern crime scene analysis.

The development of a proteomic-based approach to identify un-

ambiguous protein biomarkers for each individual matrix with the aim to constitute a specific database for matrix characterization fulfilled the requirements of forensic science for the rapid determination of biological matrices. In fact, mass spectrometry (MS)-based proteomics procedures can be used to identify the most prominent proteins specifically present in each biological matrix found at a crime scene (blood, saliva, semen, vaginal fluid, nasal secretion or urine). One single test is sufficient to determine unambiguously the identity of the biological matrices, even in complex mixtures. In addition, species identification is also possible, and the analysis is performed on the first "washing" step of DNA extraction, thus saving most of the sample for subsequent DNA analysis. The protein biomarkers for the most frequently encountered biological matrices (saliva, blood, semen and lacrimal fluid) have been clearly identified in real forensic samples [31].

Concerning metabolomics - the youngest of the great omics, the field it and its subdisciplines open to the forensic science is in developing yet. Isolated incursions in metabolomics subdisciplines for forensic biomarkers were made years ago. Boccardet et al., in 2011, proposed an approach based on an analytical platform involving an ultra-high pressure liquid chromatograph (UHPLC) and a quadrupole time-of-flight (QTOF) mass spectrometer for untargeted steroidomics in urine samples from a clinical trial for the discovery of relevant biomarkers of testosterone undecanoate oral intake. In this way, a wide door was open to the untargeted simultaneous evaluation of a high number of potential biomarker candidates [36]. Since then, metabolomics has provided numerous biomarkers in the clinical area in general and in forensics in particular, despite it is hardly taken into account most times. For example, in the characterization of the salivary epigenome, the importance of previous work in dealing with the salivary microbiome, proteome, endocrine analytes, genome, and transcriptome was highlighted [37], but the possible role of metabolomics was ignored, despite its crucial importance in unraveling epigenetic behavior [10]. At present, the importance of metabolomics biomarkers increases at a fast rhythm [38, 39], even surpassing well-established proteomics biomarkers. This is the case with ethanol consumption in which metabolites from this drug are clearly better biomarkers of chronic drinkers than well known indirect biomarkers such as enzymes (e.g., aspartate transferase, alanine transferase,  $\gamma$ -glutamyltransferase), mean corpuscular volume of the erythrocytes or carbohydrate-deficient-transferrin, as can be seen in a section below.

It is remarkable that, despite an omics study precedes the discovering of a new biomarker, most authors do not specify in their publications the omics to which their investigated biomarkers belong, but only the sample and their forensic use [40].

### Analytical Tools for Search and Determination of Biomarkers in Forensic Metabolomics

Traditional assays using as detector the naked eye after spraying on the target common reagents such as phenolphthalein or luminol, or even using ultraviolet light, for in situ analysis in the crime scene, the most popular and the only known by people addicted to television police series, are not the subject of this section. We consider here equipment for analysis of metabolomics biomarkers proposed in the literature and its desirable evolution in the light of the present and foreseeable developments.

Distinction is made between the search for metabolomics biomarkers and their quantitation in a given sample once the panel has been assessed; that is, between untargeted and targeted metabolomics analysis, respectively.

The first and crucial step in the search for metabolomics biomarkers or for their quantitation is sample preparation. This step can vary from direct insertion of the sample either into the detector (or more commonly into previous separation equipment), to the use of microfluidic (chip-based) devices coupled to capillary high-resolution separation tools [41], or solid-phase extraction commercial equipment on-line connected to LC-MS triple quadrupole (QqQ) arrangements [42, 43]. These devices constitute a milestone in forensics equipment for analysis of small samples.

Equipment based on time-of-flight (TOF)-either with quadrupole or matrix-assisted laser desorption/ionization (Q or MALDI, respectively)-coupled to liquid or gas chromatographs, depending on the features of the metabolites, is commonly used for identification, followed by metabolites selection using chemometric approaches (ANOVA, PCA, PLS-DA, heat maps, ROC curves, etc.) [38, 39, 42]. The sensitivity and specificity displayed by each metabolite in the ROC curve clearly establish its usefulness as biomarker.

The preferred option for targeted analysis of metabolomics biomarkers is MS in the QqQ approach, as it provides one of the most sensitive tools for metabolites quantitation [10, 43, 44]. It should not be forgotten that absolute quantitation by this tool requires preparing standard curves in the same matrix as the samples under study so that the matrix effect and the extraction efficiency for the target metabolites must be the same in both the standards and samples. Taking into account that, by definition, analyte-free biological matrices do not exist for endogenous compounds, the lack of blank matrices for quantification of endogenous compounds by LC-MS/MS must be addressed by different approaches (e.g., standard addition, background subtraction, surrogate matrix, and surrogate metabolite methods) by comparing their advantages and disadvantages [44].

A desirable option in metabolomics biomarkers is the use of no destructive analysis, particularly when the sample is scant and several parameters should be analyzed in it. A discussion on the application of no destructive techniques in metabolomics biomarkers analysis is given in the section below.

The trend to miniaturization of analytical instruments leads to portable equipment either for identification or quantitation of metabolomics biomarkers for their on site use. Fast and accurate analysis, as facilitated by this equipment, could be crucial in some forensics research. An example is the Huynh et al.'s proposal for the use of a portable Raman instrument for analysis to be done entirely on site, thus avoiding any risk of sample damage [45].

### Present Metabolomics Biomarkers in Forensics

To omit the name of the omics to which the biomarker belongs is a general situation in forensics biomarkers, more remarkable in the case of metabolomics biomarkers. It could be a consequence of the use of metabolites as biomarkers before metabolomics was

defined, as the determination of chloride in sweat as biomarker of cystic fibrosis (CF) [46]. An enormous number of metabolomics biomarkers are daily used in forensics analyses without mentioning this omics (even without awareness of the existence of metabolomics by the forensic analyst). Most of the published articles on the proposal of new metabolomics biomarkers ignore the omics to which they belong. A representative example is the article by Halánek et al. on the sex determination by metabolites (amino acids in this case that they recognize as metabolites) in the sweat contained in fingerprints [45]. This sample has also been used previously to discriminate people from different demographic groups and sexes [47], who had also been discriminated using more invasive sampling as blood [27]. Even age has been determined from blood found at a crime scene [30] without mentioning metabolomics as the discipline whose previous development has allowed the target metabolite(s) to be established as biomarkers.

Countless are also metabolomics biomarkers of drug intake (including alcohol), clearly based on the determination of metabolites from the drug found in samples as varied as hair [40], blood [8], urine [36], saliva [48], human breath [49] or sweat [50].

When biomarkers of a given target situation based on different omics exist, that (or those) based on metabolomics usually offer advantages as compared with those based on other omics.

### Metabolomics Biomarkers that Surpass those based on other Omics: Alcohol Biomarkers

The fact that metabolomics biomarkers clearly surpass those based on any other omics with similar aims is supported on the requirement by the formers of cheaper reagents, simpler sample preparation and shorter analysis time. A representative example are ethanol biomarkers, as this is one of the most analyzed drugs in a daily basis in forensic and clinical cases of chronic and sporadic alcohol misuse, including driver licensing, workplace testing, and abuse rehabilitation. Both indirect and direct biomarkers of ethanol intake have been widely studied using blood as preferred sample in the former case and a variety of samples (blood, hair, urine, etc.) in the latter [51].

Indirect biomarkers are used in Europe for excessive alcohol intake screening. However, there is not standard protocol for selecting the most appropriate biomarkers to determine alcohol consumption or a defined cut-off level. Furthermore, in North America, indirect parameters of ethanol consumption are not systematically applicable according to the law [52]. This situation is a consequence of the low specificity and sensitivity of indirect biomarkers, as commented in the introduction section [8], since they can be affected by factors different from alcohol consumption. Examples of indirect biomarkers are carbohydrate deficient transferrin,  $\gamma$ -glutamyl transpeptidase, aspartate transferase, alanine transferase, mean corpuscular volume of the erythrocytes, and even serotonin metabolites such as 5-hydroxytryptophol, which allow consumption detection in body fluids (mainly in blood) providing different type of information.

Direct biomarkers of alcohol consumption --e.g., blood alcohol concentration (BAC), ethyl glucuronide (EtG), ethyl sulfate (EtS), phosphatidylethanol (PEth) - have also been widely investigated [8]. Figure 1 schematizes the oxidative and no oxidative pathways

of ethanol metabolism and formation of the biomarkers from it [51]. Particularly EtG proves to be very sensitive and specific for identification of active heavy drinkers, and guarantees excellent diagnostic accuracy--with negligible false positive and false negative results, provided an appropriate cutoff value is established [52]. Owing to its short half-life in blood, EtG is not usually determined in this biofluid; therefore, EtG in urine is more commonly used, while hair is used as a longer marker of ethanol use [50]. Fatty acid ethyl esters also increase with chronic alcohol consumption, and are deposited in hair with comparable mechanism and sensitivity/specificity to EtG [53].

PEth is a direct alcohol metabolite present in cell membranes with a half-life of four days [54]. Up to 48 different PEth homologues have been identified and demonstrated their suitability in forensics analysis as biomarkers of alcohol consumption by a simple, easy and cheap test. The selection of one or other of the homologues depends on how old ethanol consumption is searched, allowing, in the case of PEth, differentiating between social drinking behavior (PEth<700 ng/mL) and excessive alcohol consumption (PEth≥700 ng/mL) [8]. The combination of analyses of biomarkers related to alcohol intake in different samples is very useful to provide predictive models for the diagnosis of alcohol misuse with forensic purposes. For instance, recent studies deal with indirect biomarkers in blood and direct ones in hair [51]; thus is, use of multiple biomarkers.

### Future of Metabolomics Biomarkers in Forensics

The search for new metabolomics biomarkers that fulfill the necessities of forensic sciences should encompass those considered below.

*Biomarkers for which counterparts based on other omics exist, but that can be surpassed by new metabolomics biomarkers because these can be simpler, cheaper, with shorter response time, etc.* Examples should be metabolomics biomarkers of vaginal exposure to semen, which overcome the shortcomings of present biomarkers based on other omics such as those of seminal plasma, among which prostate-specific antigen (PSA) is the best characterized; and biomarkers

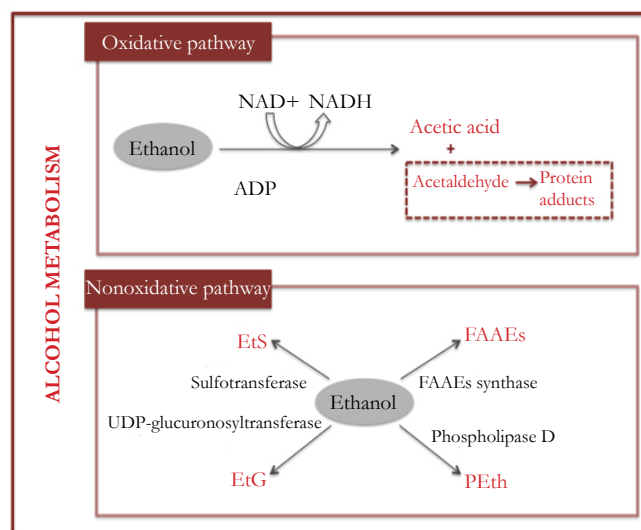
of spermatozoa and other cells present in semen; none of which are ideal biomarkers [55-57]. The useful and interesting substitution of PSA by a metabolites panel as that recently reported for prostate cancer biomarkers [11] could be an example for promoting forensic research in this area.

*Traditional metabolomics biomarkers that can be improved either by changing the type of sample in which they are investigated or by changing the target metabolite biomarker using the same sample.* Despite increased levels of chloride in sweat is a well established metabolomics biomarker for CF, present studies consider saliva of CF patients contains increased calcium (resulting in insoluble calcium-protein complexes) which causes turbidity of saliva [58, 59], elevated phosphate levels that could explain a higher occurrence of calculus [60], and more neutral lipids, phospholipids and glycolipids as a consequence of the altered physico-chemical properties of saliva [61]. In addition, there are elevated levels of urea, uric acid, and total protein, especially in submandibular saliva [62]. A multi- or single-metabolite biomarker could easily monitor CF in saliva, which offers a simpler, faster, and cheaper sampling than sweat by the commercial Macroduct<sup>®</sup> sampler.

*Metabolomic biomarkers proposed in the clinical area that can be useful in forensic analysis.* New biomarkers for cardiovascular diseases such as acute myocardial infarction (AMI) based on gene expression analysis [63] or serum-based proteomics have been investigated [64] for a diagnostic better than that provided by traditionally used biomarkers (e.g., ST-elevation or saddle back pattern of Q-wave [65]). The search of the authors' group for evaluation of coronary artery disease constitutes a strong support to future developments in the forensic field [39]. The research involved discrimination among patients with stable angina, non-ST elevation myocardial infarction and AMI [38], and monitoring of atherosclerotic patients for myocardial infarction prevention [66] (all them developed by LC-QTOF MS/MS or LC-MS QqQ).

*Search for cardiovascular disease omics biomarkers using no traditional samples.* The presence of C-reactive protein (CRP) molecules in saliva provides an opportunity for development of non-invasive assessments of cardiovascular diseases risk factors [67]. The use of this

**Figure 1. Scheme of Oxidative and Nonoxidative Pathways of Ethanol Metabolism and Generation of Alcohol Biomarkers. FAAE: Fatty acid ethyl ester.**



simple no invasive sample requires the establishment of salivary CRP reference ranges and their correlation with serum concentrations, which have not been investigated in detail yet. A subsequent step could be to study the metabolism of CRP and establish a relationship between the levels of some of its characteristic metabolites and the given disease. Another potential metabolomics biomarker research could result after the characteristics of dry sweat as compared to fresh sweat are well established. This sample could be used for forensic purposes in dealing with lung cancer screening [10].

*The key appearance of metabolites from wound-healing processes.* A number of wound healing-related molecules (e.g., IL-1b, IL-6, TNF-a, IFN-g, MCP-1, CXCL12, VEGF-A, EGF, KGF, pro-col Ia2 and pro-col IIIa1, and also fibroblasts and fibrocyte spartially transformed into contractile myofibroblasts) have provided fundamental information for wound age estimation by comprehensive analysis of these molecules from the perspective of morphometrics, protein and gene expressions. This information can be of great interest in forensic analysis [9]. Transformations of these molecules during the wound healing process undoubtedly produce characteristic metabolites that can provide information on the process by simpler, cheaper and faster analyses. Nevertheless, no metabolomics biomarkers of wound-healing processes have been reported so far.

*New drugs, new metabolites, new analytical methods for them.* The endless appearance of new design drugs of abuse makes mandatory the continuous research on methods for their identification and that of their metabolites, crucial for the assessment of drug exposure [68]. In general, these metabolites are formed only in vivo and are not available as analogs on the illicit drug market. Their presence in biological samples such as urine and hair positively confirms exposure to the parent drug. Also, analysis of drug metabolites reduces the likelihood of false negatives when the parent drug is not detected [69] as the metabolites of many drugs of abuse can be detected in urine for days and sometimes weeks after exposure [70].

*The effect of weathering on biomarkers.* As in other biomarker fields forensic metabolomics biomarkers require to study the effects of weathering on the given metabolites as a function of the climatic conditions to which the target has been subjected [7].

*Use of diseases-associated biomarkers.* New proposals on biomarkers in the forensics field include the use of diseases-associated biomarkers as a provisional tool for identifying individuals in complicated forensic challenges. Such is the case of systemic lupus erythematosus, one among the diseases associated with the release of different biomarkers in body fluids. These biomarkers could help a differential identification of individuals at acceptable level of validity; however, the main drawback to face this proposal is the previous establishment of a disease-related biomarker bank [71].

*Better knowledge about the metabolism of potential biomarkers.* An in-depth study on the metabolism of biomarkers based on any omics is mandatory for accurate monitoring of a given compound through the alternative metabolic pathways it can follow depending on personal characteristics of the target individual, thus avoiding or reducing the possibility of false negatives.

*Evolution of forensic psychiatric diagnosis toward omics biomarkers.* The

recent publication by Brown "From bibles to biomarkers: the future of the statistical manual on mental disorders (DSM) and forensic psychiatric diagnosis" shows as the once immovable psychiatric world has evolved towards the use of omics biomarkers that may involve metabolomics [72].

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