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Review article

Utility of mass spectrometry for the diagnosis of the unstable coronary plaque

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ABSTRACT

Mass spectrometry is a powerful technique that is used to identify unknown compounds, to quantify known materials, and to elucidate the structure and chemical properties of molecules. Recent advances in the accuracy and speed of the technology have allowed data acquisition for the global analysis of lipids from complex samples such as blood plasma or serum. Here, mass spectrometry as a tool is described, its limitations explained and its application to biomarker discovery in coronary artery disease is considered. In particular an application of mass spectrometry for the discovery of lipid biomarkers that may indicate plaque morphology that could lead to myocardial infarction is elucidated.

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INTRODUCTION

Mass spectrometry is an indispensable tool for chemical analysis owing to its speed, sensitivity, and versatility. The last two decades have seen rapid and significant developments in MS instrumentation, experimental methods and data analysis approaches.¹⁻³ These developments have led to the possibility of lipidomic analyses where thousands of lipid ions are measured. Software suited to analyzing mass spectrometry data sets can identify the lipids, determine their relative concentrations between samples and statistically analyze significant differences. This ability has led to this procedure being used for complex samples such as can be found in biological fluids, tissues and cell cultures.^{4,5} Therefore the field of lipidomics can now be applied to a number of applications related to understanding mechanisms of disease and in the determination of prognostic markers of disease.⁵ This article provides a summary of the use of mass spectrometry in the field of biomarker discovery in coronary artery disease (CAD) using the lipidomics platform.

VASCULAR BIOLOGY OF CORONARY ATHEROGENESIS

The first step to atherogenesis is lipoprotein accumulation in the arterial intima due to a high cholesterol and saturated fat diet.⁶ Leukocyte recruitment and accumulation also occurs early in lesion generation and move through the endothelial layer into the intima. The leukocytes then accumulate lipids and become foam cells.⁷ These foam cells are also rich in proinflammatory mediators and these mediators promote inflammation in the plaque.^{8,9} The innate immune system is also known to respond to the lesion by the recognition of danger-associated molecular patterns found on oxidized-low density lipoproteins and apoptotic cells that provide a continuous trigger for inflammatory responses.¹⁰ There is also evidence of adaptive immunity involvement in plaque progression with candidate antigens including modified lipoproteins.¹¹ Following atheroma initiation, smooth muscle cells (SMC) accumulate in the advancing atheroma after recruitment from the underlying media into the intima and become morphologically distinct from the less mature phenotype seen in the normal arterial medial layer.¹² These SMCs undergo cell replication and cell death and add to the complication of the atherosclerotic plaque. Extracellular matrix, such as collagen, secreted by the SMCs then builds up to make up much of the volume of the advanced plaque and forms a fibrous cap over the growing plaque. The plaque also develops areas of calcification.

Initially the plaque grows outward in an abluminal direction; however after the plaque burden exceeds approximately 40% of the cross-sectional area of the artery, luminal stenosis starts to occur. But rather than the progressive growth of the intimal lesion to a critical stenosis, thrombosis of a not necessarily occlusive plaque most often causes episodes of unstable angina and MI. Thrombosis occurs either by fracture of the fibrous cap or superficial erosion of the intima.

Fracture of the fibrous cap accounts for the cause of two-thirds of acute MI. The strength of the plaque's fibrous cap undergoes dynamic regulation and thinning occurs perhaps as a result of reduced collagen synthesis and increased degradation. The site of the fracture is usually poor in SMCs responsible for collagen synthesis and rich in macrophages which secrete matrix-degrading enzymes that break down collagen. In addition, the rupture site is rich with foam cells. Superficial erosion of the intima accounts for one quarter of acute MIs that result in sudden death. The pathobiology of superficial erosion is not understood well. However, desquamation of epithelial cells and degradation of nonfibrillar collagen found in the basement membrane are thought to contribute. Repeated cycles of plaque disruption, thrombosis *in situ* and healing are thought to contribute to lesion evolution and plaque growth.¹³

Insufficient control of risk factors associated with coronary artery disease (CAD) such as obesity, smoking, hypertension, diabetes mellitus, dietary patterns and psychosocial factors cause a high rate of hospital admissions due to acute myocardial infarction (MI).¹⁴ Strategies to detect MI before it occurs could aid healthcare professionals to prevent the occurrence of the MI event in susceptible patients. This task is made difficult by the fact that MI and sudden cardiac death are the first manifestations of coronary atherosclerosis in the majority of patients.^{15,16} Therefore a safe and low cost prognostic technology for the detection of MI in asymptomatic patients is required.

PREDICTING RISK FOR CORONARY ARTERY DISEASE IN ASYMPTOMATIC PERSONS

Current risk stratification strategies for CAD involve exercise stress testing with electrocardiography or with radionuclides and echocardiography. This assessment works well for the evaluation of patients

with symptoms and known coronary heart disease, however, it has low predictive value in asymptomatic patients.¹⁷ Risk modeling based on epidemiological studies to estimate the probability of future death or myocardial infarction (MI) in an individual suffer from several flaws, in particular the inability to incorporate new risk factors, the impact of diet, estrogens, personality traits and physical activity.¹⁷ Coronary artery calcium (CAC) scanning by computed tomography without the use of a contrast agent is a recently approved technique for estimating the risk of MI.^{18,19} Another potential strategy is to test for a biochemical signature to indicate the presence of CAD.

ASSESSMENT OF CORONARY PLAQUE VULNERABILITY BY COMPUTED TOMOGRAPHY ANGIOGRAPHY

Coronary computed tomography (CT) angiography (CCTA) permits the non-invasive detection of vulnerable plaques which may help to identify patients at risk for developing acute coronary events.²⁰ Plaques prone to rupture – also termed thin cap fibroatheroma (TCFA) – have a large necrotic core (area > 1.0 mm² in 80% of cases) with a thin fibrous cap (thickness < 65 μm).²¹ Unfortunately, the limited CT spatial resolution and plaque detection threshold (> 1 mm) precludes the assessment of fibrous cap thickness and necrotic core area by current CT scanners.²²

CCTA enables quantification of total coronary plaque burden and allows accurate and reproducible measurement of coronary atheroma volume especially with automated 3D quantification software.²³ The culprit plaques in patients with acute coronary syndrome (ACS) have a larger volume than stable plaques (193 mm³ vs. 104 mm³ respectively, $p = 0.001$).²⁴ Moreover, a direct relation has been observed between increased coronary plaque volume and subsequent adverse cardiac events in a systematic review of six serial intravascular ultrasound (IVUS) trials; each standard deviation increase in atheroma volume had a 1.3-fold higher risk for a major cardiac adverse events, myocardial infarction, or coronary revascularization.²⁵

Coronary artery calcification (CAC) is a surrogate for coronary atherosclerosis and closely correlates with the extent and severity of atherosclerosis.^{26–28} Calcium increases the shear stress and hence the risk of rupture of coronary plaques. CAC is considered present if a minimum of three contiguous pixels with an attenuation of ≥ 130 Hounsfield Units (HU) are detected along the course of a coronary artery. Several studies have reported that spotty calcification is highly prevalent in vulnerable plaques associated with ACS and is associated with increased adverse cardiac events and accelerated progression of coronary atherosclerosis.^{29–31} The CCTA cut-off to define a small calcification as spotty is < 3 mm, however micro-calcifications in approximately two thirds of ruptured plaques cannot be detected by current CT scanners.²⁰ In addition, current scoring techniques make several assumptions related to calcium density, location of calcium, spatial distribution of calcium and micro-calcification that may affect the prediction of a future cardiac event.³²

CT also allows the identification of individual plaque components with correlation to virtual histology IVUS (VH-IVUS).²³ Plaques can be classified into calcified (plaques with more than 50% calcium), mixed (plaques with less than 50% calcium), and non-calcified plaques (NCPs) (Figure 1).³³ NCPs are further classified into low CT attenuation “lipid-rich” plaques and those with predominantly fibrous tissue on the basis of CT attenuation values. Low CT attenuation (defined as < 30 HU) has been identified in 88% of ruptured plaques compared with 18% of the stable lesions ($P < 0.001$).³⁴ In addition, a ring-like CT attenuation pattern of NCP - a central area of low CT attenuation and a surrounding ring like higher attenuation “napkin ring sign” - may indirectly indicate unstable plaque with large lipid-rich necrotic core.³⁵

Intravenous injection of novel contrast agents may be an adjunct to detect inflammatory cells within coronary plaques with CT scanners in several animal studies. Macrophages in atherosclerotic plaques of rabbits can be detected with CT after the intravenous injection of iodinated nanoparticles dispersed with surfactant.³⁶ In addition, multicolour CT detected gold-labelled high density lipoproteins (HDL) nanoparticles targeted to activated macrophages in a mouse model.³⁷

CCTA is a promising technique for the detection of unstable plaque. However, the cost related to running the test routinely in patients showing low- or no-risk is not feasible. In addition if contrast reagents are used the potential side-effects of the applied radiation are a deterring factor. Therefore, a safer potential strategy is to test for a biochemical signature to indicate the presence of CAD. A biochemical signature that can be detected by sampling peripheral blood, although invasive, does not involve the potential side effects of CCT thereby avoiding high cost and unwarranted risks for asymptomatic patients.

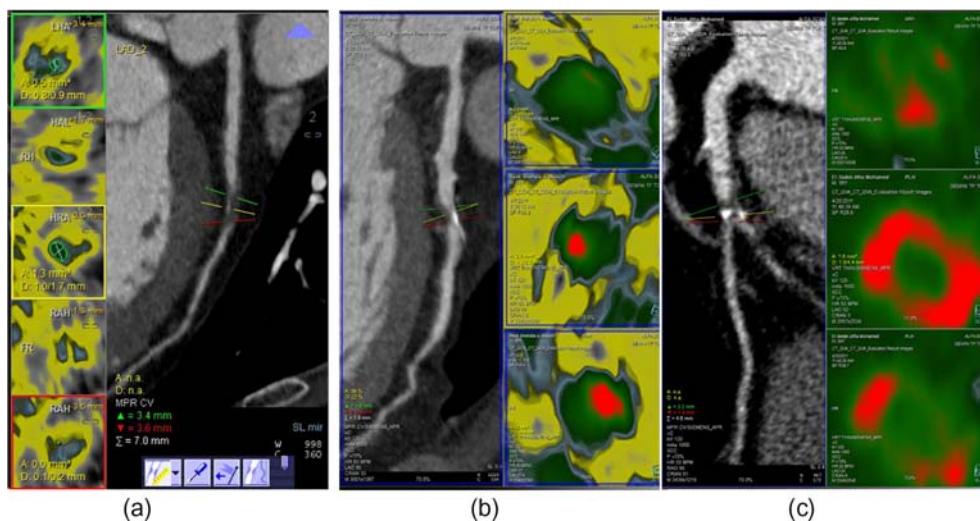


Figure 1. Coronary Plaque Characterization by MDCT: Non-calcified plaque (a), Mixed plaque (b), Calcified plaque (c). Red colour: calcium.

MASS SPECTROMETRY FOR BIOCHEMICAL ANALYSIS

The ‘omics fields, including genomics, transcriptomics, proteomics, lipidomics and metabolomics are associated fields in systems biology where a complex interaction between biological systems is studied (Figure 2). Metabolomics is primarily concerned with the high-throughput identification and quantification of small metabolites that are less than 1500Da. Lipidomics is considered a subset of metabolomics and attempts to describe a complete lipid profile. Proteomics is the study of the entire set of proteins produced or modified by an organism. Both the proteome and metabolome of any organism varies with time and under distinct conditions such as disease states.³⁸ A common instrument used for the analysis of samples for proteomic, lipidomic and metabolomic studies is the mass spectrometer (MS).

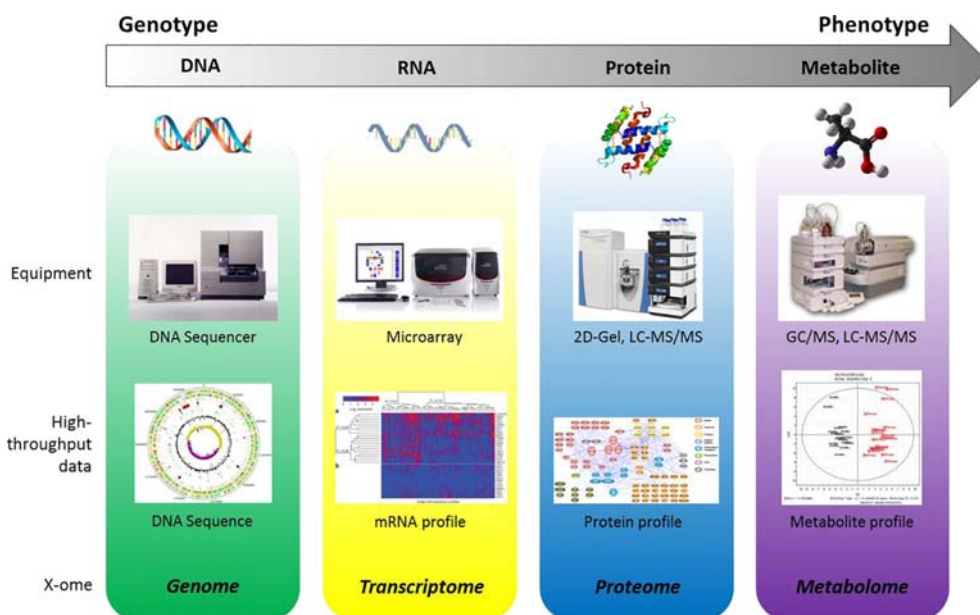


Figure 2. The interconnection of systems biology showing the equipment used for analysis and the data generated.

The incorporation of novel biomarkers to improve current models of prediction of preclinical CAD has been an on-going area of research. The use of two well-known biomarkers, Cardiac Troponin and Creatine-Kinase-MB isoform, used for the diagnosis of MI, has revolutionized the management of

patients presenting with chest pain. Due to the late-rise of troponin, a number of new candidate biomarkers are also being tested for the diagnosis of acute coronary syndrome.

INVESTIGATIVE BIOMARKER RESEARCH FOR CORONARY ARTERY DISEASE

The global analysis of lipids by mass spectrometry is an untargeted form of chemical analysis where experimental hypotheses are not yet formed. The workflow – from sample collection to results – is simplified in Figure 3. It requires unbiased acquisition of data in the hope that trends can be discerned

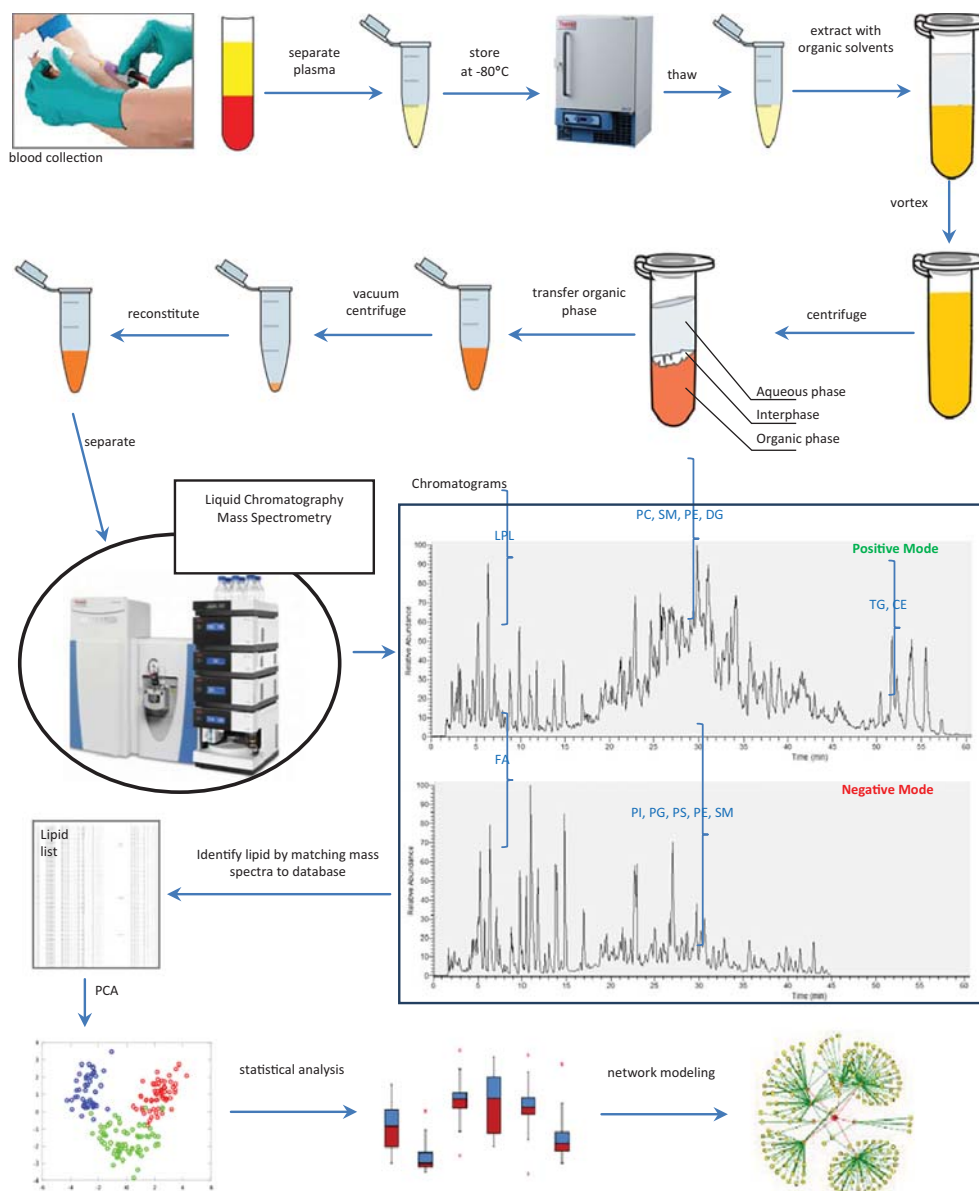


Figure 3. A typical workflow of a lipidomics experiment. Blood is separated and stored as plasma. On the day of the analysis the required volume of plasma is extracted with organic solvents and the organic phase concentrated and injected on a liquid chromatography mass spectrometry system. The liquid phase is ionised with the application of positive and negative voltages and corresponding chromatograms of detected ions are recorded. The classes of lipids commonly seen in blood plasma isolate to certain regions of the chromatogram. The data is matched against a database to identify the lipids. Once samples are analyzed, statistical analysis commonly performed are principal components analysis (PCA) of samples from patients at different stages of disease. Network modeling is used to identify metabolic pathways that have changed. Abbreviations: FA-fatty acid, LPL-lysophospholipid, PC-phosphatidylcholine, PI-phosphatidylinositol, PG-phosphatidylglycerol, PS-phosphatidylserine, PE-phosphatidylethanolamine, SM-sphingomyelin, MG-monoglycerol, DG-diglycerol, TG-triglycerol, CE-cholesteryl ester.

based on known sample variability. Lipidomic approaches to the identification of disease biomarkers rely principally on the comparative analysis of lipids in normal and diseased patients, animal models or cell cultures to identify aberrant concentration changes that may represent new lipid biomarkers or elucidate a disease mechanism. The global analysis of lipids using mass spectrometry has proven to be a useful tool in the study of cardiac diseases.

Lipidomics for the prediction of CAD

The eukaryotic lipidome might comprise of 10,000 to 100,000 individual species of lipids originating from a few hundred lipid classes.^{39–41} These lipids are distributed as part of the biological membrane, energy storage substances and sometimes function as signal transducers.^{42–44} Lipidomics relies on tandem mass spectrometry performed with on-line liquid chromatography to identify the individual fatty acid chains and any polar head groups. Due to the structure of the aliphatic fatty acid chains present at varied lengths in lipids, any lipid having two or more fatty acids are difficult to identify as there are several possible isomers that are isobaric with identical molecular elements. However with the speed and mass accuracy of current high resolution tandem mass spectrometers, fragmentation of these isobaric compounds leads to correct identification of the exact molecular species within each lipid class (Figure 4).

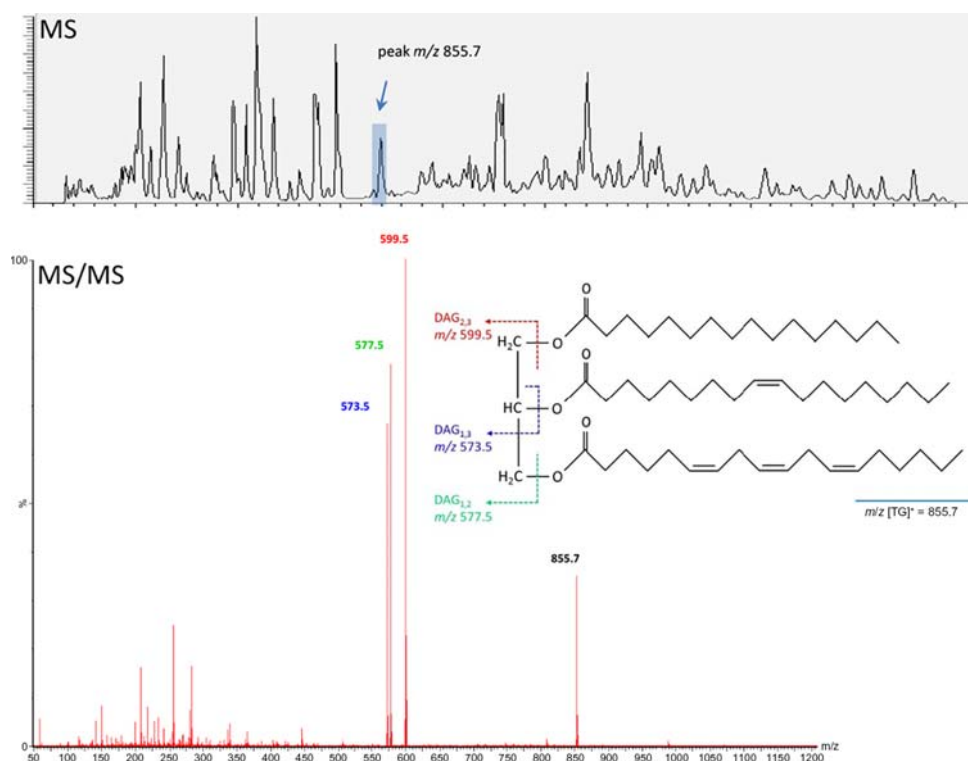


Figure 4. The identification of TG(16:0/18:1/18:3) by tandem mass spectrometry (MS/MS). Peaks corresponding to lipids in the chromatogram are identified by triggering tandem mass spectrometry (MS/MS). When a peak is detected in MS, the ions are selectively fragmented by collision-induced dissociation (CID). During CID, TG breaks characteristically as shown thereby allowing the deduction of the number of carbons and double bonds in each fatty acid chain. The lipid is measured with m/z 855.7 and its fragments due to collision-induced dissociation (CID) are m/z 599.5, 577.5, 573.5.

Altered lipid metabolism and dyslipidemia in the context of inflammation and oxidative stress are driving forces in the transition from stable to unstable plaques.⁴⁵ A number of studies have highlighted a characteristic lipid signature within unstable human plaques and also in the circulating blood plasma. One particular triglyceride (TAG) with low carbon number and double-bond content, TAG(54:2), is associated with CVD⁴⁵ suggesting that the relevance of particular TAGs has been underestimated by unwarranted focus on total triglycerides. It is still uncertain whether the TAG levels are related to proatherogenic lipoprotein dynamics or lipoprotein retention in the vessel wall, plaque instability and

thrombogenicity. Lipidomic profiling by mass spectrometry of plaques obtained from endarterectomies show certain cholesteryl esters, in particular CE(16:1), CE(18:1) and CE(18:3), are detectable in only advanced atherosclerotic plaques but not in normal arteries.⁴⁶ The plasma lipidomic profile of the same patients showed that the dominant CEs present in the plaque were also present in the plasma making these potential biomarkers that can easily be tested for. A plasma lipid profiling study of 220 subjects was able to identify 102 differentiated lipids between patients with stable CAD and healthy control individuals and 50 lipids between stable CAD and unstable CAD.⁴⁷ Adding these lipids to a model and also taking into consideration traditional risk factors and the concentration of C-reactive protein, made a marked improvement in the C-statistic which measures how well the model can discriminate between observations at different levels of the outcome.^{47,48} Current testing for CAD is related to the class of lipids rather than the bioactivity of a single lipid species. These studies show that actual species composition of lipid classes is likely to be an atherogenic factor and are therefore potential biomarkers.

Limitations of lipidomic high-throughput analytical mass spectrometry

Mass spectrometry-based quantitative techniques allow the analysis of numerous biomarkers in parallel. However the technique faces its own challenges. Firstly, since the chemical properties of the different classes of lipids vary considerably, only a portion of the lipidome can be examined at one time with one analytical technique. Attempting to cover the entire range of lipids will require several experiments. Secondly, due to the complexity of biological samples, sample preparation techniques to decrease the complexity of sample prior to analysis needs to be used but can result in the loss or poor recovery of particular lipids resulting in an underestimation of concentration values.⁴⁹ If these sample preparation steps are not undertaken, the selectivity of the assay is compromised as isobaric analytes with similar m/z can appear co-eluting with the marker of interest resulting in an overestimation of the marker concentration. For these reasons protein changes related to atherosclerosis, such as allosteric or conformational changes in apolipoprotein molecules that render it antigenic, cannot be detected by a lipidomics platform. Lastly, the reproducibility of results between laboratories is essential and recent studies comparing the correlation of variation of results obtained from the analysis of the same sample in different laboratories with the same technique have proven to be adequate.⁵⁰

CONCLUSION

Mass spectrometry has been widely used to analyze biological samples and has evolved into an indispensable tool for research. In the attempt to fully understand human physiology, advanced technologies that push the boundary of mass spectrometry capabilities has allowed the technique to address an ever-increasing array of biological questions. Advancements in the global lipidomic analysis of samples for the discovery of novel biomarkers are made possible in the last decade due to these instrument improvements. The technique demonstrates enormous potential for the determination of lipid biomarkers indicative of plaque instability in asymptomatic patients as a screening test.

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