**Open Access** 

# Untargeted Metabolomics in the Discovery of Novel Biomarkers for Atherosclerotic Cardiovascular Diseases

### Jun-Long Zhong\*

Department of Cardiology, the Fifth Affiliated Hospital of Sun Yat-Sen University, Zhuhai 519000, Guangdong, China

# Introduction

Cardiovascular Disease (CVD) is the main source of mortality and bleakness around the world. Four out of five CVD passing are because of myocardial dead tissue or stroke. Regardless of numerous drives that have been set up for CVD anticipation and hazard the executives, and new treatments to treat existing CVD, patients keep on dieing from cardiovascular occasions. Plainly, we need to recognize new restorative targets and procedures. Metabolomics offers a novel answer for this issue, as metabolomics-based biomarkers don't just demonstrate the presence or nonattendance of an illness, but at the same time are equipped for evaluating dangers of fostering the sickness and identifying the infection preceding the presence of obvious clinical indications.

### Method

In this audit, we depict the scientific strategies and work process utilized in untargeted metabolomics. We additionally distinguish a few contextual investigations that feature the utilization of untargeted metabolomics in cardiovascular examination.

### **Biomarkers**

Preventive cardiovascular risk assessment relies on established risk factors, including smoking, hypertension, dyslipidaemia, and diabetes; however, approximately half the people developing coronary heart condition (CHD) are classified as having low or intermediate risk supported current risk algorithms [1]. Although biomarkers seem to be a rather novel research field the term 'biomarker' was already introduced in 1980.5 In fact, 'biomarker' within the broad sense, being 'a characteristic that's objectively measured and evaluated as a sign of normal biologic processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention',6 covers also traditional risk factors that are used for the above-mentioned risk algorithms. Hence, 'biomarkers' are going to be utilized in the subsequent as markers measured in biological specimens, like cells or serum.

The clinical value of serological biomarkers for the diagnosis and prediction of clinical manifestations of atherosclerotic disease has been assessed in numerous clinical studies. Meta-analyses and reviews are widely available in international literature summarizing diagnostic and predictive properties of both, cardiac-specific markers (e.g. produced/released by the heart muscle and hence likely reflecting coronary atherosclerosis) and non-cardiac-specific markers (systemic markers like lipids, creatinine, glycaemia and glycated hemoglobin, essentially reflecting metabolic risk factors). In spite of the massive number of biomarkers that are tested, the ecu Society of Cardiology

\*Address for Correspondence: Jun-Long Zhong, Department of Cardiology, the Fifth Affiliated Hospital of Sun Yat-Sen University, Zhuhai 519000, Guangdong, China, Email: conjugatelogic@yahoo.com

**Copyright:** © 2021 Jun-Long Zhong. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Received 10 July 2021; Accepted 26 July 2021; Published 2 August 2021

(ESC) guidelines only recommend the utilization of troponin for the diagnosis and prognosis within the management of acute coronary syndromes (ACS), alongside the assessment of lipid profile, creatinine, and glycaemia. The event of high-sensitivity (hs) assays for troponin I and T has improved the diagnostic sensitivity for acute myocardial infarct (MI), decreased the time to diagnosis and led to guicker rule-out of myocardial ischaemia. Additionally, elevated hstroponin has been related to adverse outcomes in patients with stable CHD and within the general population. However, troponin doesn't have sufficient independent prognostic value to advise systematic measurements in patients with stable CHD. actually, during this condition, the present guidelines don't recommend testing any biomarkers beyond lipids, creatinine, glycaemia and glycated haemoglobin, adding the organ specific BNP or NT-proBNP as long as coronary failure is suspected.9 Specifically, the utilization of hsCRP or the other novel biomarker isn't recommended. However, the amount of routinely measured biomarkers which will be wont to predict MI or presence of clinically silent atherosclerotic disease is quite limited and systemic markers may have some limitations, because although atherosclerosis are often considered a systemic disease, in some cases it's going to be progressing at different rates in several arterial beds or individuals counting on variables like age, ethnicity, etc. Thus, tentative new biomarkers got to be robust enough to be ready to indicate progression of disease albeit it happens during a relatively small a part of the arterial tree.

Guidelines for biomarker use to assess presence of atherosclerotic disease within the absence of an acute event are scarce. The explanations for this might be found in our limited scientific understanding of biomarkers thus far or the described limited added value of biomarkers on top of the predictive value of traditional risk factors for prediction of adverse events [2]. This is often in sharp contrast with biomarker guidelines for the diagnosis of coronary failure where NTpro-BNP is an accepted standard.

For the prediction of incident cardiovascular events, markers with strong potential are mainly related to lipids and lipoproteins. For recurrent cardiovascular events, markers are mostly related to ischaemia. There's an ongoing debate which biomarkers should be applied in patients with low, intermediate, and high 5- to 10-year risk for MI. for instance , the National Academy of Clinical Biochemistry guidelines from 2009 discussed the utilization of the foremost often used commercially available biomarkers like hsCRP and fibrinogen.16 Their conclusion was that there's no need for further biomarker screening in low-risk patients and just in case of intermediate risk much is left to the discretion of the medical man .

Biomarkers that reflect the inflammatory state aren't recommended for routine use in non-high-risk subjects. Recommendations for hsCRP screening slightly differ between US and EU standards. While both American Heart Association (AHA) and ESC recommend hsCRP measurements in patients with moderate or unusual CHD risk profile, asymptomatic high-risk patients, and patients with hypertension categorized as intermediate risk by Framingham criteria to assess 10-year CHD risk the AHA also recommends screening of asymptomatic low-risk patients.

The clinical value and appreciation of biomarkers could also be hampered by many determinants like intra-individual variability, lack of tissue specificity, inter-lab variability, analytical sensitivity and accuracy, age, weight, renal function, gender differences, or differences among ethnicities. Also, progression of atherosclerosis might not be homogeneous in several areas, and different degrees of peripheral artery disease are described for similar degrees of CHD [3]. This fact could limit theoretically the knowledge given by a cardiac biomarker on the progression of atherosclerosis in other areas and the other way around. Finally, unmonitored and unaccounted differences in pre-analytical sample handling (e.g. time from collection to storage, isolation protocol, and room temperature) and marker stability could also be additional limitations. This strongly depends on storage conditions; number of freeze-thaw cycles, etc., and is molecule specific and thus not generalizable.

Moreover, biomarkers with causal involvement are usually regarded more valuable for risk stratification as they'll even be utilized in testing drug efficacy or applied as companion diagnostic. However, Mendelian randomization studies have shown that a number of the foremost widely applied biomarkers for disorder aren't causally related with disease progression.

#### **Microparticles**

(MPs; often also called micro vesicles) belong to the family of extracellular vesicles released from activated or apoptotic cells. Micro particles ( $\sim 100-1000$  nm in diameter) stem from the cellular plasma membrane, whereas exosomes, which are 70%), plasma levels of leukocyte CD11b+CD66b+MPs are associated with plaque instability.91 In patients with familial hypercholesterolemia, levels of CD45+CD3+ lymphocyte MPs help to discriminate lipid-rich plaques from fibrous lesions.92

Taken together, these findings indicate that MPs from endothelial cells and leukocytes could provide useful tools to identify patients at high risk for future cardiovascular events. Furthermore, the complex MP composition (proteins, lipids, and nucleic acids) might be an interesting source for –omics.

#### Micro-RNAs

Micro-RNAs are small non-coding RNAs that control organic phenomenon by binding to focus on mRNAs, thereby inducing mRNA degradation or repression of protein translation. Besides their important intracellular functions and potential value as therapeutic targets, 97–99 extracellular miRNAs have also been detected in various body fluids including the blood. the amount of circulating miRNAs are modulated in disease states and, therefore, yield potential value as disorder biomarkers.

Proteomic technologies allow comparing the expression of hundreds or thousands of proteins from two biological specimens, including fluids, tissue, or cells. as an example , arteries with and without atherosclerosis are often compared or the effect of various therapies are often assessed.128 Over the past decade, proteomics analyses have evolved from protein separation by two-dimensional electrophoresis to mass spectrometry (MS)-based approaches.128 at the present , a spread of proteomic platforms are available. Their selection depends on the specimens and therefore the sort of proteins to explore

In general, there are two MS approaches: First, the untargeted discovery approach, during which samples are analysed without a priori assumptions and peptides are prioritized for fragmentation supported their relative abundance. This approach is restricted by its bias towards abundant proteins since there's currently no technological platform to resolve the whole human plasma proteome. The results of an untargeted discovery proteomic experiment may be a list of proteins, among which potential biomarker candidates are selected consistent with their highest statistical significance and relevance. Second, targeted MS offers an alternate approach, during which a pre-selected panel of proteins is measured with high precision. This method is termed using multiple reaction monitoring and was selected naturally Methods as technology of the year in 2012.

## **Results**

Five contextual investigations that utilize untargeted metabolomics ways to deal with distinguish biomarkers for cardiovascular danger, myocardial ischemia; transient ischemic assault, episode coronary illness, and myocardial dead tissue hazard expectation are portrayed. The utilization of the untargeted metabolomics is still somewhat new in cardiovascular examination. All things considered, there stays a requirement for future headway in metabolomics advancements. Key issues in metabolic profiling in epidemiology

Quantitative metabolic profiling can aid biomarker discovery in an unbiased and unsupervised manner by providing molecular information across multiple pathways: all metabolic measures can then be separately tested for the potential disease association or incidence. This could be followed by appropriate independent replication of the candidate biomarkers identified within the discovery cohort. Unfortunately, the promise of metabolomics in biomarker discovery has not been fully realized; albeit various papers are published, there's little or no consistency and rigor within the metabolomics works during this area as recently acknowledged .173 We involve a stringent attention to statistics and replication within the field of metabolomics to strengthen the scientific value of the work, regardless of the analytical platform used. Particularly when aiming for clinical applications, recent frameworks are recommended to strengthen the methodological rigour and quality for the prediction models

Proteomic approaches allow screening to detect differences in protein expression between different biological specimens. Although this approach isn't freed from limitations, it's considerably increased our ability to get novel biomarkers of atherosclerosis as untargeted or targeted protein analysis are often performed by MS without a priori assumptions and without the necessity for the supply of excellent antibodies to a selected protein of interest.

### Conclusion

Early finding of CVDs and ID of patients at high danger of creating unfriendly occasions would take into consideration opportune intercession that forestalls genuine outcomes or demise. There is a need to set up touchy and non-obtrusive CV biomarkers, and novel remedial focuses for the counteraction and treatment of CVDs.

## References

- Imo E, Hoefer, Sabine, Steffens, Mika, Ala-Korpela, and Magnus, Back, et al. "Novel methodologies for biomarker discovery in atherosclerosis." Eur Heart J 36(2015): 2635-2642.
- Elmien Heyneke." Characterization of the Wheat Leaf Metabolome during Grain Filling and under Varied N-Supply". Front Plant Sci 10(2017).
- Wei Zhang, Rawi Ramautar."CE-MS for metabolomics: Developments and applications in the period 2018–2020"Wiley Analytical Science, USA (2020).

How to cite this article: Jun-Long Zhong. "Untargeted Metabolomics in the Discovery of Novel Biomarkers for Atherosclerotic Cardiovascular Diseases." *Metabolomics (Los Angel)* 11 (2021):297.