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Introduction

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1.1 A Brief Introduction to Metallomics

Metals and metalloids play vital role in life and even death, acting as catalysis, structural components, signal transmitters or electron donors [1–3], etc. However, metals or metalloids do not work alone; they may interact with each other through synergism or antagonism in biological systems. The systematic understanding on the roles of all the metals and metalloids in biological systems is called “metallomics,” which was proposed by Haraguchi in 2002 as “integrated biometal science,” [4, 5] while the term “metallome” was first used by Williams in 2001, referring to “an element distribution or a free element content in a cellular compartment, cell or organism.”[6] In 2010, metallomics was defined by the International Union of Pure and Applied Chemistry (IUPAC) as a research field focusing on the systematic study of the interactions and functional connections of metallome with genes, proteins, metabolites, and other biomolecules within organisms [7]. Metallomics aims to provide a global understanding of the metal uptake, trafficking, role, and excretion in biological systems, and potentially to be able to predict all of these in silico using bioinformatics [8, 9].

Metallomics aims to understand the biological systems and life process at the atomic level [10], which is similar to ionomics in this regard [11–13]. However, metallomics also works at molecular levels like the study on metalloproteins [14] and speciation study [15, 16]. Therefore, it covers both the atomic and molecular levels of metallome. The metallome has been proposed as a fifth pillar of elemental – vis-à-vis molecular-building blocks alongside the genome, proteome, lipidome, and glycome in life [17] as illustrated in Figure 1.1. With the technical advances, it is expected that metallomics will be evolved to elementomics [18–21], which will cover all the elements in the periodic table.

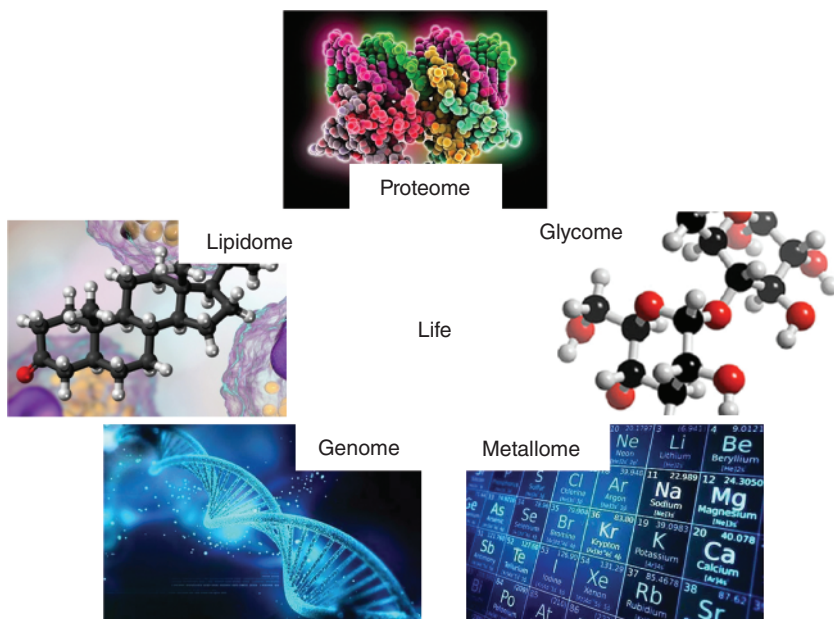


Figure 1.1 Metallome as one of the five pillars in life alongside the genome, proteome, lipidome, and glycome. Source: abhijith3747/Adobe Stock; Yu-Feng Li (Author).

Metallomics is considered both a basic science to understand the chemical structures and biological functions of metallome and an applied science in convergence with many research fields [5, 17]. Metallomics has gained increasing attention among scientists working outside the biological science, such as nanoscience, environmental science, agricultural science, medical science, food science, geoscience, toxicological science, materials science, and metrological science [8–10, 15, 22–28]. The convergence of metallomics with these research field has led to new branches of metallomics such as nanometallomics [22, 29–31], environmentalomics [32–34], agrometallomics [35], metrometallomics [36], clinimetallomics [37], radiometallomics [38], archaeometallomics [39], and matermetallomics [40]. A special issue called “Atomic spectroscopy for metallomics” published in *Atomic Spectroscopy* covered some of these topics [10].

Dedicated analytical techniques are required for the characterization of metallome and their interactions with genome, proteome, metabolome, and other biomolecules in the biological systems. Commercially available instruments like inductively coupled plasma optical emission spectroscopy (ICP-OES) and inductively coupled plasma optical mass spectrometry (ICP-MS) have been widely applied in metallomics for the quantification of metallome [15, 24–26]. On the other hand, there are scientific instruments which are commercially less available but accessible to scientists, i.e. large research infrastructures (LRIs). LRIs are built to solve the strategic, basic, and forward-looking scientific and technological problems in economic and social development [41].

Particle accelerators are such kinds of LRIs, which produce beams of fast-moving, electrically charged atomic or subatomic particles, such as electrons, positrons, protons, or ions [42]. They are used for particle physics and nuclear physics like the structure of nuclei, the nature of nuclear forces, and the properties of nuclei not found in nature [43]. They are also used for radioisotope production, industrial radiography, radiation therapy, sterilization of biological materials, and radiocarbon dating [44, 45], etc. Furthermore, the particle accelerator-derived electrons, positrons, protons, or ions beams have many advantages compared to the commercially available ones, which make them superb tools in many research fields including metallomics.

1.2 Key Issues and Challenges in Metallomics

It is desired to know which and how many elements are there in a biological system, and this includes the high-throughput quantification of elements, their species, and also the metal/metalloid-binding molecules like metalloproteins.

For the quantification of metallome, it is required to know first which metallome is to be quantified. There are over 20 elements like C, N, O, F, Na, Mg, Si, P, S, Ca, Fe, Cu, Zn, and I that have been proved to be essential elements for humans [46]. Plants also require B, while some bacteria need W, La, and Ce instead of Ca [47]. In some marine diatoms, Cd-containing carbonic anhydrase was found [48]. It is also desired to quantify the presence of non-essential elements in the biological system since new technologies and manufacturing practices lead to new industrial emissions, releases, or discharges to the environment. For example, the electronic industry uses rare-earth elements and many transition elements in the periodic table. With nearly 60 million tonnes of electronic waste generated in 2021 alone, it is also desired to know to which extent that humans, plants, animals, and microorganisms are exposed to these elements [49]. Another example is the increased production and application of nanomaterials these years, which inevitably lead to the environmental burden of nanomaterials themselves or their degraded products [31, 50]. Therefore, it is desired to quantify as many elements as possible or even the whole elements in the periodic table in a high-throughput way; however, this indeed is one of the big challenges for the quantification of metallome since huge concentration difference of elements exists in the biological systems [21].

The speciation of elements is also required since different species of the same element may have different biological effects. One example is Cr. Cr^{3+} is positive on glucose on lipid metabolism, while Cr^{6+} in the form of chromate is a carcinogen [46]. Another example is Hg. It is known that mercury selenide (HgSe) is stable and generally not bioavailable, while methylmercury (MeHg) is highly toxic and bioaccumulative in biological systems [51]. For the speciation in metallomics, the challenge is to identify the species in situ. This is also required for the quantification of metalloproteins and other non-protein complexes of metal ions in metallomics study.

Besides knowing the concentration and speciation of metallome in a whole biological system, it is also desired to know how many of them exist in a particular location, i.e. the distribution of metallome. Seeing is believing. This includes knowing the two-dimensional (2D) and three-dimensional (3D) distribution of metallome in a biological system, which is called spatial metallomics [52–54]. Spatial metallomics is the study on the distribution of metallome at the subcellular, cellular, tissue, and whole-body levels including human-sized objects or even larger ones [55], requiring the spatial resolution at the nanometer, micrometer, millimeter, centimeter, and even larger ones [56].

The challenge for mapping the metallome in 2D and 3D is to have a tunable spatial resolution, which will greatly facilitate the study on the distribution of metallome in a biological system through a coarse scan first, following by a fine scan of the samples [57]. For 3D mapping, high-speed data acquisition is highly desired, while non-destructive analysis is highly preferred.

The 2D and 3D spatial distribution of chemical species is also required in the metallomics study. This includes the *ex situ* and *in situ* study, while the *in situ* chemical speciation is always desired. The study on the distribution of metals/metalloids in metalloproteins and other non-proteins complexes, i.e. their 3D structure can also be included in spatial metallomics.

The temporal change of metallome in a biological system forms series of live pictures of metallome in a biological system, i.e. the movie of metallome. The study on this can be called temporal metallomics. Furthermore, the study on the spatial distribution of metallome with a temporal resolution in a biological system can be called the spatiotemporal metallomics [52]. This shows the dynamic changes of metallome in a biological system.

For both the temporal and spatiotemporal metallomics, a challenge lies in the *in situ* monitoring of the dynamic changes of metallome in the biological system, especially at the single-cell level, which is called single-cell metallomics [17, 52]. Besides, considering the individual variations in mixed communities of organisms like cells, metametallomics was proposed to cover this [17, 26]. Temporal and spatiotemporal metallomics also include the study on the dynamic changes of metals in metalloproteins and other biomolecules.

1.3 About the Structure of this Book

As abovementioned, with the fast development in the last 20 years, metallomics has been converging with different research fields such as nanoscience, environmental science, agricultural science, biomedical science, toxicological science, materials science, archaeology, and analytical science to form new metallomics branches like nanometallomics, environmetallomics, agrometallomics, and medimetallomics. Dedicated tools through synchrotron radiation, neutrons, protons and other commercially available techniques can be applied in metallomics study. Besides, the methodology of metallomics including targeted or non-targeted metallomics, spatial metallomics (including single-particle/single-cell metallomics), temporal

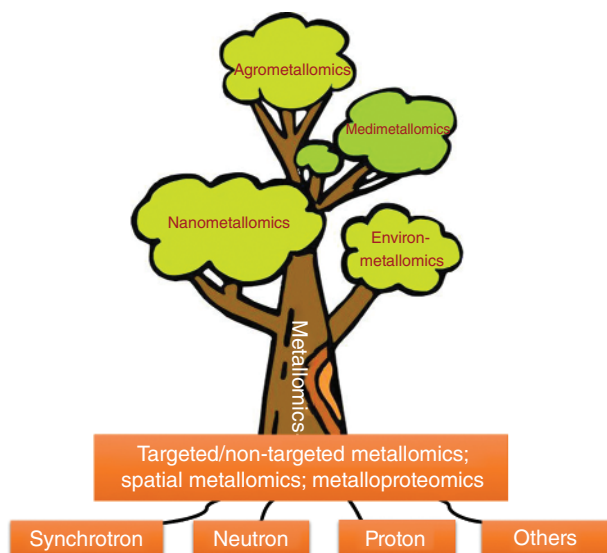


Figure 1.2 The different branches of metallomics and the methodologies and tools.
Source: Yu-Feng Li.

metallomics, spatiotemporal metallomics, and metalloproteomics is also formed (Figure 1.2).

Therefore, from Chapters 2–11, these metallomics branches will be introduced: Chapter 2, Nanometallomics (coordinated by Yu-Feng Li); Chapter 3, Environ-metallomics (coordinated by Ligang Hu); Chapter 4, Agrometallomics (coordinated by Xuefei Mao); Chapter 5, Metrometallomics (coordinated by Liuxing Feng); Chapter 6, Medimetallomics and clinimetallomics (coordinated by Qun Xu and Huiling Li); Chapter 7, Matermetallomics (coordinated by Zheng Wang); Chapter 8, Archaeometallomics (coordinated by Xiangqian Feng); Chapter 9, Metallomics in toxicology (coordinated by Ming Xu); Chapter 10, Pathometallomics: Taking neurodegenerative disease as an example (coordinated by Qiong Liu); and Chapter 11, Oncometallomics: Metallomics in cancer studies (coordinated by Xin Wang and Chao Li). Each chapter covers both the analytical techniques and the application of metallomics in a definite discipline or more. This is also why we call this book *Applied Metallomics*. Since metallomics is expected to be evolved to elementomics, an introduction and application of bio-elementomics is presented in Chapter 12, Bio-elementomics (coordinated by Jingyu Wang).

In addressing the key issues and challenges of metallomics, methodologies and tools, especially ICP-MS, machining learning and data mining are introduced in Chapter 13, Methodology and tools for metallomics (coordinated by Qiuquan Wang); Chapter 14, ICP-MS for single-cell analysis in metallomics (coordinated by Bin Hu); Chapter 15, Novel ICP-MS-based techniques for metallomics (coordinated by Meng Wang); and Chapter 16, Machine learning for data mining in metallomics (coordinated by Wei Wang).

Through all these efforts, this book is intended to reflect the latest development and application of metallomics in different research fields.

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