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# **Advances in visualization of copper in mammalian systems using X-ray fluorescence microscopy**

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# **Abstract**

Synchrotron-based X-ray fluorescence microscopy (XFM) has become an important imaging technique to investigate elemental concentrations and distributions in biological specimens. Advances in technology now permit imaging at resolutions rivaling that of electron microscopy, and researchers can now visualize elemental concentrations in subcellular organelles when using appropriate correlative methods. XFM is an especially valuable tool to determine the distribution of endogenous trace metals that are involved in neurodegenerative diseases. Here, we discuss the latest research on the unusual copper (Cu) storage vesicles that were originally identified in mouse brains and the involvement of Cu in Alzheimer's disease. Lastly, we provide an outlook of how future improvements to XFM will drive current trace element research forward.

#### **Keywords**

X-ray fluorescence microscopy; copper storage vesicles; copper dyshomeostasis in Alzheimer's disease

# **1. Introduction**

Synchrotron-based x-ray fluorescence microscopy (XFM) is a robust technique to quantitatively determine the distribution of trace elements like metals in a biological specimen with high sensitivity and, if needed, high resolution. The method does not require dyes or other labeling steps because detection of each element is based on its intrinsic fluorescence properties (i.e. photoelectric effect). XFM therefore allows one to directly quantify the abundance of a specific element. Samples are raster scanned through a focused

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Declaration of interests

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x-ray beam in an x/y pattern and two-dimensional elemental distributions are produced from the emitted fluorescence spectra at each pixel (Figure 1).

Typically, x-rays fully penetrate biological samples  $(> 10 \,\mu m)$  and elemental concentrations can be calculated in three dimensions if the thickness of the specimen is known. Because biological material is almost transparent to high energy x-rays (weak absorption contrast), highly brilliant x-ray sources are needed to produce a detectable x-ray fluorescence response signal over a micro to nanometer scale. As a consequence, XFM experiments on biological samples requiring micron to submicron resolution are usually carried out at synchrotron sources, though commercial benchtop instruments like the Sigray AttoMap Micro XRF are rapidly improving in performance and resolution (<8 μm).

XFM and its related applications have enabled the research community to obtain rich information about the distribution and speciation of elements in organs, tissues and cells (Figure 1). In fact, over the past two decades the use of biological XFM has expanded from 'exploratory' elemental imaging [2] to include narrowly focused investigations of the distribution and speciation of platinum in tumor cells [3] or iron (Fe) in hemozoin deposits in mouse macrophages [4]. XFM has also been invaluable to studies of copper (Cu) that identified unexpected and highly concentrated Cu pools within biological systems (Figure 1 and [5]), contributed to a better understanding of disease processes associated with impaired Cu handling [6] and facilitated targeted development of therapies for Cu handling disorders [\*7]. These advances are in part attributable to improvements in focusing optics (decreased spot size and increased photon yield), energy dispersive detector technologies (increased energy resolution), read-out electronics (increase of maximum number of photons processed per second) and data acquisition software. This review will focus on how XFM has advanced our understanding of Cu homeostasis in the brain and how it has begun to illuminate the role of Cu in neurodegenerative diseases over the past 3 years.

# **2. Cu storage vesicles (CSVs) in mammals**

Work by Pushkar and colleagues previously showed that Cu accumulates to high concentrations in small puncta termed CSVs in astrocytes within the periventricular region of the lateral ventricle in rat and mouse brains [5]. Cu levels within CSVs were found to exceed 100 mM, a concentration that is cytotoxic when used in cell culture. We detected the same Cu foci around all ventricles of the mouse brain (Figure 1) and, upon investigating the development of these CSVs in greater detail, found that they grow deeper into the brain parenchyma (interstitium) with age (Figure 2). Our current hypothesis is that these CSVs act as a 'filter' to tightly control the Cu content of the interstitial fluid that is available to neurons. The majority of Cu entering the brain traverses the cells of the choroid plexus and passes into the cerebral spinal fluid (CSF), which then freely diffuses through the ependymal layer of the ventricles into the brain parenchyma and becomes interstitial fluid [9]. Elevated Cu concentrations in the CSF will thus be buffered by what may be specialized astrocytes, which import Cu with high affinity and store it within CSVs. The importance of balancing the Cu concentration in interstitial fluid was underscored by a remarkable high resolution study from Perrin and colleagues in primary rat hippocampal neurons [10]. The authors showed how local Cu and zinc (Zn) distributions were fundamental for tubulin- and actin-

dependent stability of dendrites. XFM scans at 20 nm resolution localized to dendritic spines suggested that either Cu chelation or supplementation at sub-cytotoxic concentrations leads to reduced F-actin and β-tubulin levels, albeit via different mechanisms.

Fu et al. showed previously that the levels of metallothioneins (MT) 1/2 and 3 were dramatically increased in the ventricular zone of rats as they aged [11]. An XFM study by Sullivan et al. found that the number of CSVs, but not their Cu content, was decreased in MT1/2 knockout mice [\*12]. MT1/2 knockout mice also exhibited a decrease in basal Cu in the periventricular region, which led the authors to echo Fu et al. and suggest that all three MT isoforms are involved in the formation and/or maintenance of CSVs (Figure 3a). In MT1/2 knockout mice one would predict that basal Cu storage capacity is lower and fewer Cu loaded MTs are available to form CSVs because MT3 expression is not induced by Cu or Zn and is thus unlikely to compensate for loss of MT1/2 function. In contrast, we expected CSV numbers and Cu content to be unchanged in MT3 single knockout mice when compared to controls because Cu upregulates MT1/2 expression, yet our XFM studies found instead that deletion of MT3 or MT1/2 had comparable consequences on CSV dynamics (Figure 4, unpublished). The fact that MT1/2 did not compensate for the lack of MT3 function suggests an alternative, MT-independent pathway for the formation and regulation of CSVs (Figure 3b,c). In this model, some Cu would still be sequestered by MTs but Cu chaperones like Atox1 or high affinity Cu binding peptides like GSH would transport Cu to vesicles (possibly lysosomes or late endosomes). Cu would then either be actively (via a transporter) or passively (via autophagy) transferred into CSVs. Upon deletion of either MT isoform, cytosolic Cu content is decreased and less Cu is available to populate CSVs owing to reduced expression of the Cu import protein Ctr1 or increased Cu export activity. Insight into how Cu export from CSVs is blocked was provided by work from Ohrvik and colleagues who showed that CSVs are formed throughout mouse brains lacking Ctr2, a mammalian Cu transporter that assists in liberating Cu from transiently formed storage vesicles [14]. Therefore, an attractive hypothesis is that Ctr2 is inactivated in specialized astrocytes harboring CSVs (Figure 3a–c).

Further studies that characterize the regulation of CSV dynamics in mammals may inform us as to how to direct Cu to form CSVs. Such advances in turn would offer new therapeutic avenues for the treatment of Cu overload disorders like Wilson disease where blocked Cu export leads to uncontrolled cellular Cu accumulation and results in aberrant regulation of several important homeostatic processes.

## **3 Alzheimer's Disease**

Dyshomeostasis of transition metals as a contributing factor to Alzheimer's disease (AD) was suggested as early as 1953 [15]. In 2000, a widely cited paper by A. Bush claimed a 'consensus' view of elevated levels of Fe, Cu and Zn levels in AD brain [16]. Subsequent meta-analysis by Schrag et al. [17] and bulk quantitative analysis of these elements in AD patient brains and controls decisively debunked this claim [18]. In fact, it was shown that Cu levels were lower in AD brains, while Fe and Zn concentrations were elevated and unchanged respectively. In recent years, transition metal studies in AD have focused on further characterizing Aβ plaque pathology and investigating a possible role of transition

metal chemistry. Using correlative XFM and IR spectroscopy, Leskovjan and colleagues reported increased Zn levels in Aβ plaques in a mouse model of AD that overexpresses human presenilin and a chimeric amyloid precursor protein (PSAPP) [19]. Interestingly, PSAPP mice did not show an elevation of Fe or Cu in plaques while Fe was increased in the brain parenchyma. It was later shown that in mouse models presenting with severe neurodegeneration (5 × FAD and CVN), Cu but not Fe was increased in Aβ plaques [20]. The authors concluded that Cu accumulation in  $\mathsf{A}\beta$  plaques is correlated with the degree of neurodegeneration.

James et al. published a follow-up report in which they used the powerful Maia detector at the Australian synchrotron to analyze 49 plaques from 4 PSAPP animals for their metal content (previous studies analyzed <10 plaques). Instead of employing a correlative approach they used Compton scattering to identify plaques. Their findings mirrored those of Leskovjan et al. with Aβ plaques having less Fe compared to the surrounding neuropil, insignificant changes in Cu levels and increased Zn levels when concentrations were normalized to plaque density (i.e. proteinacous content) [21]. The authors concluded that concentrations of Cu and Zn within Aβ plaques is dependent on the levels of these metals in the surrounding neuropil. Having established that plaques may contain more Cu, it is now crucial to understand how Cu promotes the oligomerization of  $\mathbf{A}\beta$  peptides and the formation of β amyloid fibrils. Summers and colleagues took the first step towards this end by showing that the Cu(II) -  $\mathsf{AB}(1-42)$  coordination of monomeric  $\mathsf{AB}(1-42)$  in solution depends on pH and other stabilizing compounds added to the solution [22]. XANES and EXAFS investigations of the bulk material revealed a square planar  $O/N$  Cu(II) environment at pH 6.1 and 7.4, while the Cu(II) coordination changed to a square pyramidal geometry at pH 9.0. Based on their own work and that of others, the authors suggested that Cu(II) binding to Aβ peptides exists in several different confirmations in vivo and may include some unspecific binding. Future studies that employ time-resolved Cu k-edge EXAFS analysis of the oligomerization process and EXAFS analysis of β amyloid fibrils may shed further light on this issue.

#### **4. Current challenges and future developments**

With the highest sensitivity to date and resolutions approaching the low nanometer range, a new limitation of XFM has surfaced. The only information XFM provides is the elemental distribution, making it impossible to detect cellular or subcellular structures unless they exhibit significant differences in elemental concentrations (e.g. phosphorous in the nucleus). Thus, several laboratories are actively developing correlative approaches to directly detect trace element distribution in (sub)cellular structures. These include the parallel use of synchrotron-based ptychography, multipronged microscopy approaches and gene editing methods that incorporate an XFM-detectable tag into the desired gene of a model organism [\*\*23–26]. A particularly nice albeit extremely challenging example of a correlative approach using epifluorescence was provided by Carmona and colleagues who showed that feeding manganese (Mn) to HeLa cells lacking the wild-type Mn transporter SLC30A10 leads to Mn accumulation in the trans-Golgi network. RFP constructs were used to visualize the Golgi in HeLa cells alone or in those transfected with cDNAs encoding wild-type or disease-causing variants of SLC30A10. Once visualized by epifluorescence, HeLa cells

were flash frozen and scanned for their elemental distributions allowing for the overlay of Mn and SLC30A10 profiles [\*27].

Upgrades to 4th generation synchrotron sources are currently underway (ESRF) or planned (APS) and will improve brilliance, coherence and further decrease pulse duration of synchrotron x-rays by  $100 - 1000$ -fold. For users with biological or biomedical interests, these upgrades will greatly increase throughput (scan times will also be 100x −1000x faster) regardless of the resolution. Thus, collection of statistical data for biological replicates will be possible and 3D-tomography will become routine. The number of high-resolution studies is expected to increase and with correlative methods in place researchers will be able to ask new scientific questions. Direct co-localization of proteins and metals will provide further insights into metal homeostasis in complex biological specimens where bulk methods fail. For example, an important finding by the Lutsenko group described distinct distribution patterns of the Cu transporter Atp7b and Cu in the crypts of the small intestine, which may have important implications for Cu uptake into the lumen [28]. Once high-resolution and correlative methods are in hand it will be possible to simultaneously detect Cu and Atp7b in a single XFM scan.

In summary, XFM is a reliable tool to solve scientific questions that involve trace metals. Progress in technique development that is expected over the next decade will further enhance the capabilities and transform XFM into a routine analysis tool.

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# **Abbreviations**



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a) A typical experimental setup for XFM is shown utilizing an undulator as a source for xrays and a double crystal monochromator to tune the energy of the x-ray. A sample is scanned in x-y through the focused x-rays and fluorescence photons are collected by an energy dispersive detector. The spectra are fitted at each point and converted into area concentrations via calibration. b) Phosphorus (P, red) and Cu (green) co-localization maps of a saggital mouse brain section (left, 25 μm spot size), lateral ventricle of a coronal mouse brain section (middle, 2 μm spot size) and mouse embryonic fibroblast (right, 200 nm spot size). Elemental maps were created with the program MAPS [1]. Elemental concentration ranges are represented by false coloring from darkest (lowest concentration) to lightest (highest concentration). Mouse brain were provided by Dr. S. Hayflick (Oregon Health and Science University) and Dr. M. Knutson (University of Florida). Mouse embryonic fibroblasts were provided by Dr. M Petris (University of Missouri). Unpublished results.



#### **Figure 2. Age-dependent Cu accumulation into CSVs.**

H&E images, elemental maps for potassium (K) and Cu, and 3D overlays for Cu (green) onto the K (red) maps are shown in brain at 16 days (D16), 12 weeks, 19 weeks and 51 weeks of age. Cu CSVs become more abundant and expand more into the brain parenchyma with age. Area concentration ranges for Cu in 3D maps were adjusted to maximize visualization (D16 0 -> 0.28  $\mu$ g/cm<sup>2</sup>, 12 weeks 0->1  $\mu$ g/cm<sup>2</sup>, 19 weeks 0->1.8  $\mu$ g/cm<sup>2</sup>, 51 weeks  $0 \rightarrow 3.5 \text{ µg/cm}^2$ ). Elemental Maps were created with MAPS [1] and 3D overlays were created with the ImageJ 3D plugin [8]. Elemental concentration ranges are represented by false coloring from darkest (lowest concentration) to lightest (highest concentration). Mouse brains were provided by Dr. S. Hayflick (Oregon Health & Science University). Unpublished results.

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#### **Figure 3. Possible models of CSV formation.**

a) Model 1: Imported Cu (blue) is bound by chaperones or high affinity peptides (beige) delivered to target proteins or stored by MTs (red ovals). CSVs may be formed as a consequence of autophagy that initiates Cu release from MT and subsequent import into CSVs resembling what was described for MT3 [13]. Export is blocked because no Ctr2 is present. b) Model 2: In contrast to a) CSVs are populated by Cu from Cu chaperones or Cubound peptides. c) CSV formation in MT knockout brains. Model 2 can explain our XFM observations: MT knockouts reduce the cellular Cu storage capacity and signal for reduced Ctr1 expression at the plasma membrane. CSVs are populated with Cu as described in b).



#### **Figure 4. XFM maps and overlays for brains of different MT knockout mouse models.**

H&E images, K (red), Cu (green) and overlay maps are shown for saggital sections depicting the lateral ventricle of 6-week old MT1/2<sup>-/-</sup> (upper) and MT3<sup>-/-</sup> (lower) brains Elemental concentration ranges are represented by false coloring from darkest (lowest concentration) to lightest (highest concentration). Values are shown below the individual elemental maps. Scale bars are shown in the overlay. Elemental Maps were created with MAPS [1]. Mice were provided by Dr. M Petris (University of Missouri). Unpublished results.