

Analytical assay development to study metal-binding proteins in plants

Aleksandra Polatajko¹, Ingo Feldmann¹ and Norbert Jakubowski¹

¹ Institute for Analytical Sciences, Bunsen-Kirchoff-Str. 11
44139 Dortmund, Germany, polatajko@isas.de

Trace elements play an important role in biochemical processes. Metabolism of the trace elements, in particular their binding to proteins in a biological system is of great importance in biochemical, toxicological and pharmacological studies. The knowledge of the specific binding mechanisms of metals within the soil, water and plants has significant implications for delineating potential bioavailability and/or release of metals. The identification of metal complexes is important to improve understanding of the tolerance and transport mechanisms in plants, which are for instance essential to phytoremediation of the heavy-metal contaminated soil as well as for risk assessment of contaminated foodstuffs.

Cadmium is one of the most widespread metals which is highly toxic to plants and animals. The concentration of Cd in foods depends on many parameters such as ability of the specie to absorb and accumulate Cd, the availability of Cd in the soil, which is itself influenced by soil characteristics (pH, cation exchange capacity). Some leafy crops like spinach are able to accumulate more than other food plants. Furthermore, non-nutritional species such as *Arabidopsis halleri* can hyperaccumulate Cd and can be used to clean up the contaminated soil by using the phytoremediation method.

The objective of this work was to develop (i) a suitable sample preparation method for the provision of high yields of intact metal-binding proteins; (ii) an analytical method suitable for characterization of metal containing proteins. In this research we have elaborated a new strategy for screening of cadmium containing proteins which consists of the extraction of proteins by application of an ultrasonic homogenizer, separation of the metal-binding proteins by use of native PAGE and size exclusion chromatography and their detection by ICP-MS.