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Methodological advances for selenium speciation analysis in yeast

Jorge Ruiz Encinar, Magdalena Śliwka-Kaszyńska[1], Aleksandra Połatajko, Véronique Vacchina, Joanna Szpunar*

Equipe de Chimie Bio-Inorganique Analytique, CNRS UMR 5034, Hélioparc, 2, av. Pr. Angot, 64053 Pau, France

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Abstract

Advances in analytical methodology for speciation of selenium in selenized-yeast food supplements were discussed on the basis of the recent developments in the authors' laboratory. Particular attention was given to the sample preparation with regard to the fractionation of selenium into different classes of chemical species, the high resolution fractionation of selenium from yeast water extracts by size-exclusion chromatography and characterization of the water soluble protein fraction by combined matrix-assisted laser desorption ionization (MALDI)-time-of-flight mass spectrometry (TOF MS) and electrospray quadrupole-TOF tandem MS. The true speciation of protein-incorporated selenium (down to individual proteins characterized by a unique aminoacid sequence) was discussed using an example of a family of selenium-containing proteins formed in yeast by the substitution of methionine residues by selenomethionine in a salt stress-induced protein.

Keywords: Selenium; Yeast; Selenium-containing protein; Speciation; HPLC-ICP MS; Mass spectrometry

1. Introduction

Selenium is a major nutrient element which also shows cancer preventive properties [1–3]. One of the most economic sources of organic forms of Se is yeast grown in quantity in selenium-enriched media [4]. In the course of this process the inorganic (low bioavailability, potentially toxic) selenite is converted to safer highly bioactive species with improved nutritional properties [5]. The correlation of the bioavailability and the toxicity of Se with its chemical form triggered interest in selenium speciation in selenized-yeast food supplements.

The development of analytical methodologies for selenium speciation has been gaining momentum since the study of Clark et al. indicating the putative role of selenized yeast in cancer prevention [1]. Despite a number of works that were recently reviewed [6,7], information available on the identity of the molecules incorporating or binding selenium in yeast is still scarce because of the complexity of the system and the lack of analytical approaches allowing the standardless identification of selenocompounds. This concerns in particular selenium-containing proteins for which virtually no data regarding their identity (sequence information) is available.

Selenoproteins incorporate the amino acid selenocysteine, a cysteine analog in which a selenium atom

* Corresponding author. Tel.: +33-55-980-6884; fax: +33-55-980-6885.
E-mail address: joanna.szpunar@univ-pau.fr (J. Szpunar).
[1] On leave from Department of Chemistry, Technical University of Gdansk, ul. G. Narutowicza 11/12, 80-952 Gdansk, Poland.

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