

SPECIATION OF VANADIUM IN HUMAN SERUM PROTEINS BY HIGH LIQUID CHROMATOGRAPHY WITH INDUCTIVELY COUPLED PLASMA MASS SPECTROMETRIC DETECTION

Kelly G. Fernandes^{a,c}, Maria Montes Bayón^b, Elisa Blanco González^b, Ana Rita A. Nogueira^{a,c}, Joaquim A. Nóbrega^a and Alfredo Sanz-Medel^b

^aGrupo de Análise Instrumental Aplicada, Departamento de Química, Universidade Federal de São Carlos, P. O. Box 676, 13560 -970, São Carlos SP, Brazil

^bDepartment of Physical and Analytical Chemistry, University of Oviedo. 33006 Oviedo.

^cEmbrapa Pecuária Sudeste, São Carlos SP, Brazil

E-mail: asm@uniovi.es

Medication based on vanadium (V) is nowadays very promising, since some species of this element exhibit insulin-like properties with the big advantage that these molecules or, at least, their active centres are stable in gastric juice, allowing oral administration. However, vanadium compounds are potentially toxic and this toxicity depends on the transport mechanism and the target organ. Additionally, the valence states of the species of vanadium are prone to inter-conversion.¹ Some studies have shown that certain V oxidation states are distributed into the living systems through their coordination complexes with some serum proteins such as transferrin but a lot of work is still necessary to clarify biochemical and physiological functions of this element in higher organisms. In this regard, elemental speciation studies by hyphenated techniques (e.g. liquid chromatography coupled to inductively coupled plasma mass spectrometry, ICP-MS) can be a valuable tool to obtain information about possible biomolecules involved in vanadium transport and storage in body fluids and tissue.²

Separation techniques such as size-exclusion or ion exchange chromatography have been preferred for the determination of these vanadium-complexes. However, Size Exclusion exhibits poor selectivity among species of similar molecular weights and therefore, Ion Exchange in the Anion Exchange mode is better to allow complexes separation.³ On the other hand, vanadium detection by ICP-MS is affected by polyatomic interferences in the major isotope (⁵¹V, 99.75% abundance) when using chlorinated solvent due to the formation of ³⁵Cl¹⁶O⁺. Therefore, the use of Double Focusing instruments or Collision Cell is required in order to overcome such interferences.

In the present study, we investigated the coupling of Fast Liquid Chromatography (FPLC) with ICP-MS (Quadrupole and Collision Cell) for studying vanadium association to proteins present in human serum. Separation of human serum proteins is achieved on a MonoQ (HR5/5) anion-exchange column using an ammonium acetate gradient at the physiological pH of 7.4 with [Tris (hydroxymethyl)-aminomethane]-acetic acid buffer. A comparison of different ICP-MS detectors in order to evaluate V detection capabilities will be also illustrated. The experimental conditions and analytical performance characteristics will be presented.

(1) C.C. Chéry, K. De Cremer, R. Cornelis, F. Vanhaecke and L. Moens, *J. Anal. Anal. Spectrom.*, **18**, 2003, 1113.

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(3) A. Sanz-Medel, M. Montes Bayón and M. L. Fernández Sánchez, *Anal. Bioanal. Chem.*, **377**, 2003, 236.