

Palestra a ser apresentada em sessão oral (CE-MS)

CE-ESI-MS: a versatile tool for the characterization and quantification of protein hydrolysates from different sources

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In recent years, capillary electrophoresis (CE) has been strongly considered in the determination of amino acids and peptides from protein hydrolysates. The coupling of capillary electrophoresis with mass spectrometry (CE-MS) has become increasingly used since its first report in 1987. Because MS is a universal and sensitive detector it has been considered for many applications, although its use has not become customary in many laboratories yet. In addition, the second dimension offered by the MS detection (molecular mass and structural information) aids identification of solutes when migration time variation or comigration occurs. Therefore, coupling CE to MS is a very attractive choice for protein hydrolysate characterization since it combines the high efficiency and velocity of the former technique to the high selectivity and analyte information of the latter.¹

The determination of the total amino acids contents after protein hydrolysis is a classical procedure for protein characterization. The literature reports four different hydrolysis methods: hydrolysis under highly acidic conditions; basic hydrolysis; and enzymatic hydrolysis. An interesting alternative to acid hydrolysis is a milder procedure based on the catalytic cleavage of peptide bonds by H⁺ ions adsorbed on a strong cation exchanger resin. Depending on the mildness of the hydrolysis method, amino acids or peptides may be obtained in the final hydrolysates.

This lecture will show the applicability of CE-ESI-MS for the characterization and quantification of protein hydrolysates from two different sources, such as food and cosmetics. The former application is related to the development of a method for the quantification of amino acids in Brazil nuts samples, after adequate hydrolysis procedure.² For this purpose, different hydrolysis methods were evaluated with BSA protein and the resulting products were analyzed by CE-MS. Afterwards, amino acids quantification has been carried out using hydroxy-proline as internal standard, presenting acceptable linearity ($r > 0.99$) in the linear range from 3 to 80 mg L⁻¹ and good detectability (16 – 172 μmol L⁻¹). The second application was the characterization of milk, soy and rice protein hydrolysates used as cosmetic raw materials. Such samples are composed by peptides, since a milder method of hydrolysis was used in the manufacturing. After background electrolyte and sheath liquid compositions optimization, the peptides have been *de novo* sequenced, showing their suitability for the moisturizing and substantivity properties in the cosmetic final product.

[1] Assunção, N. A.; Bechara, E. J. H.; Simionato, A. V. C.; Tavares, M. F. M.; Carrilho, E. *Quim. Nova* **2008**, *31*, 2124-2133.

[2] Simionato, A. V. C.; Moraes, E. P.; Carrilho, E.; Tavares, M. F. M.; Kenndler, E. *Electrophoresis* **2008**, *29*, 2051-2058.