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DEVELOPMENT OF A RAPID CAPILLARY ZONE ELECTROPHORESIS METHOD FOR THE QUANTIFICATION OF C18:2 N-6 AND C18:3 N-3 FATTY ACIDS IN FORAGE SAMPLES

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Forages are the major components of ruminant diets, representing the primary source of energy and nutrients for milk and meat production. Among the fatty acids found in forages, two (C18:2 n-6 and C18:3 n-3) have received particular attention due to their roles as precursors for the synthesis of conjugated linoleic acid (CLA), a class of health enhancing compounds predominantly found in dairy products. Thus, the quantification of C18:2 n-6 and C18:3 n-3 fatty acids in forages has been considered an indicator of their potential for increasing milk CLA content. Gas chromatography (GC) is the reference method for fatty acids quantification in feed samples,

but this analytical technique is cumbersome and time consuming as it requires fatty acid methylation and long runs to separate individual fatty acid methyl esters. The objective of this study was to develop an alternative and rapid method for the quantification of C18:2 n-6 and C18:3 n-3 fatty acids in forages samples using capillary electrophoresis (CE). *Brachiaria ruzizienses* was used as the reference forage. A preliminary test was performed to compare the most traditional fat extraction methods used in biological samples, with Hara and Radin's method showing the best overall results when compared to both Micro Folch and Bligh and Dyer. The

analytical procedure involved CE with direct detection zone in the UV at 200 nm and capillary external coating of Teflon. The electrolyte background consisted of 12.0 mmol/L tetraborate buffer (pH 9.2) mixed with 12.0 mmol/L Brij 35, 17% acetonitrile (ACN) and 33% methanol (MeOH) [1]. Under these conditions, both C18:2 n-6 and C18:3 n-3 fatty acids in the forage samples were quantified in about 4 min. Thus, the new CE method proposed herein could be an interesting alternative for the quantification of C18:2 n-6 and C18:3 n-3 in forage samples due to analytical advantages (less time consuming and no methylation step required).

References:

1. Porto BSL, Souza MVN, Oliveira MAL. Anal Sci 2011, 27, 541-546.

Acknowledgements:

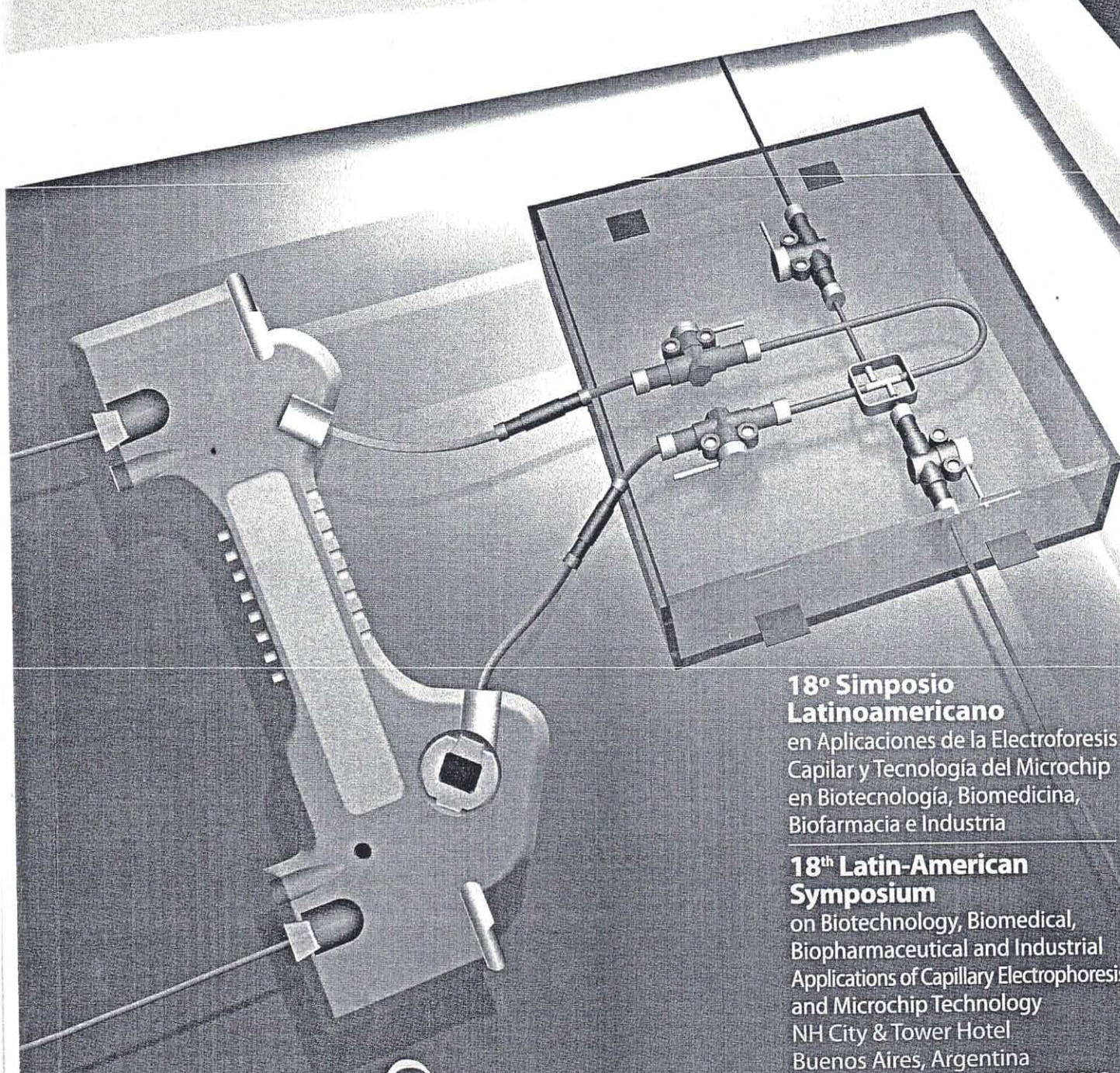
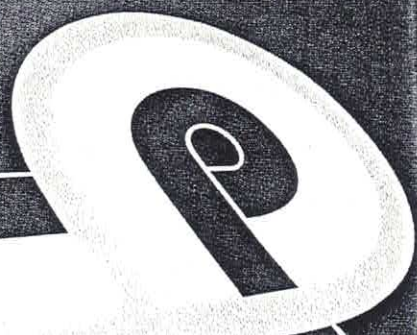
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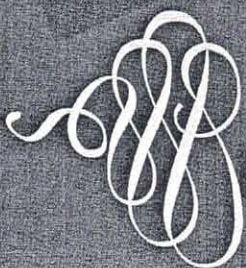
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