An experimental and Molecular Approach of the Anticancer Action of RGD-Peptide Lunasin

Geórgia Maria Amaral Junqueira[a], Maria Jose Valenzuela Bell[a], Blanca Hernández-Ledesma[b], Pedro Indiano-Romacho[b], Lourdes Amigo[b] and Virgílio Carvalho dos Anjos[a]

[a] *Physics Department, Federal University of Juiz de Fora, Juiz de Fora 36036-900, Brazil*
[b] *Instituto de Investigación en Ciencias de la Alimentación (CIAL, CSIC-UAM), Nicolás Cabrera 9, Madrid 28049, Spain*
georgia@fisica.ufjf.br

Lunasin is a cancer-preventive peptide isolated from soybean, wheat, barley and other seeds. This compound contains 43 amino acid residues with a cell adhesion motif constituted by arginine-glycine-aspartic acid (RGD) and a carboxylic acid tail of nine aspartic (D) acids [1]. The conformational profile of lunasin has been theoretically studied by means of molecular dynamics [2]. Here, our main objective was to get insights about adhesion of lunasin to cancer cells. Both experimental and computational analyses were carried out to study chemical and physical interactions between lunasin and integrins. Different cancer cell (gastric, colon, and hepatocarcinoma) lines were used to evaluate the lunasin's capacity to adhere cells. First results demonstrated that this ability was dependent on the cell line that could be due to the different level of integrin expression. Computational analysis was carried out with lunasin (model) and other RGD-peptides. Once RGD sequence serves as the primary integrin recognition, its structure and electronic properties has have been studied (Figure1). The calculations were performed at $\mathrm{CAM-B3LYP/6-31+G(d,p)}$ level of theory in the gas phase and in solution using GAUSSIAN09 program [3]. Besides, theoretical models of RGD-water-aspartic acid are being proposed. The next step is to obtain structural and energetic data that allow understanding the lunasin-integrin interactions. Changes of properties like temperature, pressure, concentration and solvent during the process are being evaluated.

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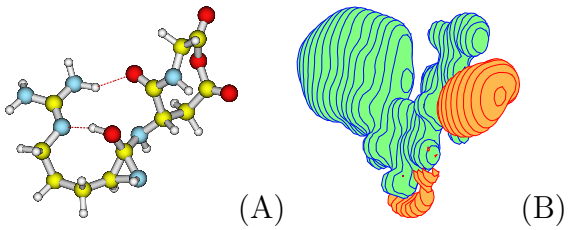

Figure 1: RGD sequence. (A) Optimized geometry and (B) electrostatic potential energy map at $\mathrm{CAM-B3LYP/6-31+G(d,p)}$.

References

1. B. Hernández-Ledesma *et al. Protein & Peptide Letters*, **20** (2013), 424.
2. P. Singh and K. Bisetty, *S. Afr. J. Chem.*, **65** (2012), 115.
3. M.J. Frisch *et al.*, *Gaussian09 Revision* E.01, *GaussianInc. Wallingford CT* 2009.