Structural Characterization and Physical Chemistry Properties of the SIVA1 Protein

Dantas, L.E.¹; Cepeda, A.O.²; Ramos, C.H.²; Saad, S.T.¹

¹Centro de Hematologia e Hemoterapia, UNICAMP, SP; ²Departamento de Química Orgânica, Instituto de Química, UNICAMP, SP.

INTRODUCTION: Cell signaling is the mechanism by which cells communicate in internal processes, and with the environment. Therefore, understanding how this signaling works in a healthy cell provides support for evaluating the molecular basis of diseases. The participation of the SIVA1 protein in the signaling pathway of the tumor suppressor p53 has been reported in the literature; moreover, recent in vivo experimental data has reported that the function depends on oligomeric structure. In this context, we aim to characterize the structure and measure the physical chemical parameters of SIVA1, which has been proved to have a role suitable for the treatment of hematopoietic disorders.

MATERIAL AND METHODS: The protein sequence was analyzed by I-TASSER and SYMMDOCK softwares. Recombinant protein overexpression is currently being carried out in E. coli competent strains. The protein was then purified by standardized protocols in order to obtain the highest yield and purity possible.

RESULTS AND DISCUSSION: Preliminary results on structural modeling showed that the protein had a globin-like folding which was formed predominantly by alpha-helices. This model was used to predict soluble domains and specific deletion mutants were designed. Various E. coli strains, expression protocols, and lyses were tested to achieve soluble wild type and mutant proteins. So far, wild-type SIVA1 was produced as an insoluble aggregate, and refolding protocols are in test to obtain the protein from inclusion bodies. However, a deletion mutant containing the C-terminal domain was produced folded as a single species and its secondary structure is under investigation by Circular Dichroism spectroscopy.

CONCLUSIONS: Structural studies such as Circular Dichroism, Tryptophan Fluorescence, Dynamic Light Scattering will be used to characterize SIVA1 and the mutant. The results obtained will contribute to the scientific literature and will enable to further understand the mechanisms of signaling pathways in hematologic malignancies.

Word Keys: SIVA1, leukemia, protein structure
Supported by: FAPESP, CAPES, and CNPq.