On the Quaternary Structure of The C-Type Lectin From *Bothrops jararacussu* Venom- BJ-32 (Bjcul)

De-Simone, S.G.[1,2], Alexandre, G.M.C[1], Ramos, C.[3] & Silva-Jr, F.P.[1]

[1]*Lab. Bioquímica de Proteínas e Peptídeos, Instituto Oswaldo Cruz, Fiocruz, Rio de Janeiro,RJ, Brazil;*
[2]*Dep. Biologia Celular e Molecular, Ins. Biologia, Universidade Federal Fluminense, Niterói, RJ, Brazil;*
[3]*Instituto de Química, Universidade Estadual de Campinas, UNICAMP, Campinas, SP, Brazil.*

Lectins comprise a group of proteins of non-immune origin with one or more sugar-binding site per subunit that bind specifically and reversibly to carbohydrates, particularly the sugar moiety of glycoconjugates, resulting in cell agglutination and precipitation of polysaccharides, glycoconjugates and glycolipids bearing specific sugars, thus acting also as cell recognizers. They are ubiquitously distributed in nature, being found in plants, microorganisms (fungi, viruses, and bacteria), and insects as well as vertebrate and invertebrate animals. Presently, the biochemical and structural studies on this class of proteins are well advanced. The C-type lectins are widely distributed and display various functions. Typically, these proteins bind calcium and sugar (generally galactose), presents stereo specificity and has apparently a common sequence motif of 115-130 amino acid residues, referred to as the carbohydrate recognition domain (CRD).

BJ-32 (also known as Bjcul) is a C1-type lectin from the venom of *Bothrops jararacussu* with specificity for ß-galactosides and a remarkable ability to bind in different tumor cells and agglutinate several species of trypanosomatids. To achieve further insights into the structure-function relationship, we have studied the oligomerization state of native BJ-32 by using different biophysical and computational methods. Small-angle X-ray light scattering (SAXS) experiments disclosed a compact, globular protein with a radius of gyration of 36.72±0.04 A and molecular weight calculated as 147.5±2.0 kDa. From analytical ultracentrifugation analysis, it was determined that the BJ-32 sedimentation profile fits nicely to a decamer model. The analysis of the intrinsic emitted fluorescence spectra for BJ-32 solutions indicated that association of subunits in the decamer is accompanied by changes in the environment of Tryptophan residues. Both *ab initio* and comparative models of BJ-32 supported the resemblance of the decamer in the crystallographic structure from a close homologue, the rattlesnake venom lectin (RSL) from *Crotalus atrox*.

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