

Structural characterization of a small heat-shock protein from *Xylella fastidiosa*

Susely Ferraz de Siqueira Tada^a, Francisco Javier Medrano^b, Beatriz Gomes Guimarães^b, Cristiano Luís Pintode Oliveira, Iris Torriani^b, Anete Pereirade Souza^a, ^aCBMEG, *State University of Campinas, Brazil*. ^bLNLS-Brazilian Synchrotron Light Laboratory, *Campinas, Brazil*. E-mail: susy_fs@yahoo.com.br

The small heat shock proteins (smHSP's) belongs to a family of proteins that function as molecular chaperones by preventing protein aggregation, and are also known to contain a conserved region termed alpha-crystallin domain. The chaperonin smHSP17,9 kDa from the orange phytopathogen *Xylella fastidiosa* was partially characterized in respect to your assembly and structure. This protein was overexpressed in *E. coli* BL21(DE3) strain and after your purification (by affinity chromatography), crystallization tests were performed and a single crystal was obtained, which diffracted at low resolution. At this moment, refinement tests are in progress in different crystallization conditions, in order to obtain a greater crystal. Parallel this, SAXS (Small Angle X-Ray Scattering) measures revealed us that this protein tends to aggregate in oligomeric complexes, fact that is known in the chaperonins family.

An estimate of the molecular weight showed that the formed complexes possess 12 ± 1 monomers. The obtained radius of gyration was about $50,5 \pm 0,5$ Å with a maximum dimension of 157 Å. It was also verified that the protein has a spherical globular conformation and its tertiary structure is rigid, without flexible domains, what it corroborates some inherent structural characteristics of this protein family.

Keywords: protein structural analysis, bacterial pathogenesis, chaperonins