The Oligomeric State of the SurE Protein from *Xylella fastidiosa*: a Study by Small-Angle X-ray Scattering

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Xylella fastidiosa is a phytophatogen that causes, among other diseases, the Citrus Variegated Chlorosis (CVC), a major concern to citrus in Brazil, particularly in the state of Sao Paulo, the largest domestic producer of orange and derivatives. The general function of 220 genes in the *Xylella* genome has been predicted so far. Among them, the orf XF0703 encodes a stationary phase survival protein E (EC 3.1.3.5). A construct of this enzyme comprising 270 amino acids (XfSurE; 29.5 kDa) has been expressed in *E. coli* and purified to homogeneity. In this work, we report the low resolution structure of XfSurE determined by Small-Angle X-ray Scattering (SAXS). The *ab initio* shape restoration of the envelope function from the scattering curve indicated that XfSurE is correctly folded, forming a tetramer in solution with a molecular weight of 108 kDa as estimated from the SAXS data, in good agreement within experimental error with the expected value of 118 kDa. The envelope has a radii of gyration R_g=32.7 Å and a maximum intramolecular distance D_{max}=100 Å. This is the first structural characterization of a SurE from a phytopathogen and, to our knowledge, the first structural study of this enzyme in solution. This work was supported by FAPESP and CNPq. We gratefully acknowledge the SAXS beam line staff and LNLS for beam line time.

Keywords: survival protein E (SurE), *Xylella fastidiosa*, Small angle X-ray scattering, oligomeric state.