SMALL-ANGLE X-RAY SCATTERING (SAXS) STUDIES OF A BASIC LEUCINE ZIPER (bZIP) SCF5 TRANSCRIPTION FACTOR FROM SUGARCANE

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Basic leucine zipper proteins are important regulators of several processes of signaling in plants, such as light response, hormone signaling or pathogen defense. bZIPs are characterized by a basic domain, responsible for sequence-specific DNA binding, and an adjacent heptad leucine repeat, the leucine zipper. The ZIP domains form two parallel α-helices, arranged as coiled coils, enabling dimerization of bZIP proteins, which, in turn, orient the basic DNA-binding domains within the major groove of the DNA. Protocols for cloning, expression and purification of a sugarcane bZIP SCF5 were previously reported (Schlögl, P. S. *et al.*, 2004, *Plant Sci.* **167**:583-595). In this work, we present a first structural characterization of SCF5 bounded to DNA. Data were collected in the SAXS beamline at LNLS and processed with the programs TRAT1D, PRIMUS, GNOM and GASBOR. The low-resolution model recovered for the SCF5/DNA complex has an elongated form. Our results seems to indicate that SCF5/DNA is a homodimer in solution, as judged by structural comparisons to available bZIPs crystallographic structures. We gratefully acknowledge the SAXS beamline staff at LNLS and FAPESP for financial support.