NMR STUDIES ON THE STRUCTURE OF THE C-TERMINAL DOMAIN FROM A MULTIPROTEIN BRIDGING FACTOR (TRMBF1) FROM *TRICHODERMA REESEI*

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Multiprotein bridging factor 1 (MBF1) is a transcriptional coactivator, which mediates the interaction of TATA binding protein (TBP), in the preinitiation complex, with gene-specific activators. By using PolyHis-Tagged Pull-Down assay we have shown that TrTBP interacts specifically with the whole TrMBF1. In order to get more insight into the functions of MBF1 in the filamentous fungus *Trichoderma reseei* (TrMBF1), we are studying its solution structure by high resolution NMR. However the whole protein was shown to be very unstable when expressed in *E coli.* Removing the N-terminal segment, which shows less conservation within different organisms, and does not participate in binding to TBP, increased the stability. The isolated the C-terminal domain of TrMBF1 (CTD-TrMBF1; AA 56-151) shows a good dispersion of H^N cross peaks in the ^{15}N HSQC spectrum, indicating that it forms a well folded domain in solution. Sequential assignment of backbone resonances of CTD-TrMBF1 is nearly complete, and the assignment of side-chain resonances is in progress. Analysis of ^{13}C chemical shifts data shows that the central part of the protein contains four alpha-helices, while the N-terminal and C-terminal portions are largely unstructured. The folding of CTD-TrMBF1 could be similar to a homologous domain in the human EDF1 whose structure was solved by NMR (PDB 1X57, http://www.rcsb.org/pdb).
Supported: FAPESP/CAPES