

ABSTRACT

Forkhead transcription factors are structurally similar molecules containing approximately 110-amino-acid-long DNA-binding domain known as a forkhead domain. Protein FOXO4 is a member of subgroup "O" of forkhead transcription factors. Members of this subgroup play a key role in many biologically important processes. For example, FOXO factors participate in metabolism control, cell-cycle control, apoptosis and oxidative stress resistance. The forkhead domain (DNA-binding domain) consists of three α -helices (H1, H2 and H3), three β -strands (S1, S2 and S3) and two flexible loops (called wings W1 and W2). The role of the wing W2 in FOXO binding to the target DNA is still elusive. Wing W2 probably interacts with the DNA in the region upstream of the core motif. It has been speculated that the FOXO DNA-binding affinity depends on A-T content (number of A-T pairs) in the region upstream of the core motif. In order to investigate this hypothesis, DNA-binding domain of the FOXO4 protein was expressed and purified and it was determined its binding affinity for three molecules of double stranded DNA containing different number of A-T pairs in the region upstream of the core motif using steady-state fluorescence anisotropy-based method. Our results show no significant differences between obtained FOXO4 binding affinities to tested DNA molecules.