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Thermodynamics and kinetics of single stranded DNA (ssDNA) binding proteins NABIN KANDEL, UTB Graduate Student, AMHED TOUHAMI, UTB Faculty, AMHED TOUHAMI TEAM, NABIN KANDEL TEAM — The aim of the present research project is to probe the thermodynamics and binding kinetics of bacteriophage T7 gene protein, gp2.5, and its deletion mutant lacking 26 C-terminal residues, gp2.5-26C. Single-stranded DNA binding proteins which stabilize ssDNA relative to dsDNA are essential for DNA replication in all living systems. Bacteriophage T7 gene 2.5 protein (gp2.5), encoded by gene 2.5 of the bacteriophage T7, is a single-stranded DNA binding protein that binds to and stabilizes transiently formed regions of ssDNA. The factor gp2.5 physically interacts with both T7 DNA polymerase and with T7 helicase/primase and plays multiple roles in T7 DNA replication and recombination in phage-infected cells. It forms a stable homodimer in solution and has a core that is well adapted for interactions with ssDNA and a highly acidic C-terminal tail. This tail is required for dimer formation and for interactions with other replication proteins of the bacteriophage T7 replication system. Its deletion mutant, lacking the C-terminal 26 residues, gp2.5-26C, binds ssDNA more tightly than the full length protein. To this end, force-extension relations at the overstretching transition of dsDNA in the presence of gp2.5 and gp2.5-26C are conducted using optical tweezers microscopy.

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