Tomato yellow leaf curl disease is one of serious diseases causing yield loss in cultivated tomatoes. The causative agent was identified to be Tomato yellow leaf curl geminivirus (TYLCV). The virus is classified into genus Begomovirus family Geminiviridae. TYLCV isolated from Israel, Sardinia and Australia has a single genomic component while the isolate found in Thailand has a bipartite genome designated DNA A and DNA B. The DNA A of TYLCV – Thai isolate contains six open reading frames, one of which is AVI gene encoding for coat protein (CP). The CP was shown to be essential for systemic infection and insect transmission by whitefly Bemisia tabaci. Previously, it was reported that TYLCV-CP was able to bind single – stranded DNA (ssDNA) to form a CP-viral nucleic acid complex and translocates the complex to plant nucleus during infection process. To identify DNA binding domain on TYLCV CP, a wild type and two truncated CPs were overexpressed in E. coli. The wild type CP consists of 257 amino acids. A truncated protein named CPΔ1-62 has a deletion of 62 residues from the N – terminus. The other protein named CPΔ126-257 could produce N – terminally 125 residues. South western analysis (SW) and electrophoretic mobility shift assay (EMSA) were employed to investigate the DNA binding activity of these proteins. Results showed that wild type CP and CPΔ126-257 were able to bind both ssDNA and dsDNA, with a preference to ssDNA. The CPΔ1-62 did not bind both ssDNA and dsDNA. This suggested that DNA binding domain may resides in the residue 1 – 62 of the N – terminal region and the residues 63 – 125 may also play an important role in DNA binding.