Folding and Stability Studies on Naturally Truncated Form of C-Phycoerythrin from Cyanobacterium *Phormidium tenue*

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The conformational changes during folding/unfolding process of biliproteins (BPs) are of great importance because of its potential role in energy transfer in photosynthesis. The phycoerythrin of *Phormidium tenue* is hexameric protein $(\alpha\beta)_6$, and its alpha-subunit consists of 164 amino acids (19kDa). The multimeric protein assembly forms stable arrangement however, undergoes degradation in the starved condition and releasing a truncated α-subunit of 133 amino acid residues only (devoid of 31 N-terminal residues). Recently, this naturally truncated form of alpha-subunit discovered and its crystal structure was determined successfully. Here we performed the denaturation studies using GdmCl, urea and weak salt like LiCl, using UV-visible absorbance, CD and fluorescence spectroscopy on both wild type and truncated C-PE. These denaturation studies suggest that a minor difference in the ΔG_D° (~1.0 kcal mol^{-1}) and *Cm* (~0.25 in M GdmCl) of full length and truncated proteins. Furthermore, GdmCl-induced denaturation is reversible in both the cases. The transition curves of different probes are precisely overlapping on f_d plot, suggests that GdmCl-induced denaturation is a two-step process in truncated as well as in full length C-PE. The difference in the ΔG_D° value of both the proteins is quite less, indicates that both proteins are approximately equally stable and the deletion of does not alters its function.