

D5

## Cloning and sequence analysis of a full-length cDNA encoding *Cyclophilin A* from *Bombyx mori*

Sung-Wan Kim<sup>1,2</sup>, Tae-Won Goo<sup>2</sup>, Eun-Young Yun<sup>2</sup>, Kwang-Ho Choi<sup>2</sup>,  
Seok-Woo Kang<sup>2</sup>, O-Yu Kwon<sup>3</sup> and Si-Kab Nho<sup>1</sup>

<sup>1</sup>College of Agriculture and Life Sciences, Kyungpook National University, Daegu 1370, Korea, <sup>2</sup>Department of Agricultural Biology, The National Institute of Agricultural Science and Technology, RDA, Suwon 441-100, Korea and <sup>3</sup>Department of Anatomy, College of Medicine, Chungnam National University, Taejon 301-131, Korea.

Cyclophilins (Cyps) are a family of proteins that bind the immunosuppressive agent cyclosporin A (CsA) with high-affinity and belong to one of the three superfamilies of peptidyl prolyl *cis-trans* isomerases (PPIase) which catalyse the *cis-trans* isomerisation of peptide bonds N-terminal to proline residues in polypeptide chains. We report the characterization of a novel Cyclophilin A (bCyp A) isolated from *Bombyx mori*. To obtain bCyp A gene from *B. mori*, we have constructed the subtracted library which was screened by hybridization using T (Bm5 cell treated with tunicamycin) and D (normal Bm5 cell) cDNA mixture as probes, respectively. A total of 459 subtractive clones were randomly selected. Among these clones, we have isolated bCyp A gene showing similarity with Cyclophilin of Rotamase. A full-length cDNA sequence of bCyp A comprised 498bp with 166 amino acid residues. The sequence analysis of Cyp A indicates that the enzyme active site and the binding site for CsA are identical and well conserved in 13 residues that constitute the CsA-binding site, including the Trp residue essential for binding. As the above results, we suggest that bCyp A is a family of cyclophilin A.