## Purification and Biochemical Characterization of Pupal Major Haemolymph Protein of the Chinese Oak Silkmoth, *Antheraea* pernyi

## Sang Bong Park<sup>1</sup>, Jeong Wha Kim<sup>2</sup>, Soohyun Kim<sup>3</sup>, Nam Sook Park<sup>4</sup>, Hung Dae Sohn<sup>4</sup>, Byung Rae Jin<sup>4</sup>, and Sang Mong Lee<sup>1</sup>

Department of Sericultural and Entomological Biology, Faculty of Agriculture, Miryang National University, Miryang 627-702, Korea, Department of Agri-Biology, College of Agriculture, Chungbuk National University Cheongju 361-763, Korea, Biomolecule Research Team, Korea Basic Science Institute, Taejon 305-333, Korea and College of Natural Resources and Life Science, Dong-A University, Busan 604-714, Korea

A pupal major haemolymph protein of the wild silkmoth, the Chinese oak silkworm Antheraea pernyi (AMHP), purified and identified. The protein AMHP was purified by a simple preparative polyacrylamide gel electrophoresis (PAGE) and diffusive elution. The preparation was shown to be homogeneous by 7.5% native-PAGE. The native molecular weight of the AMHP was 450 kDa with a 80 kDa single subunit, suggesting hexamer. The protein contained high amounts (18.3%) of aromatic amino acids, phenylalanine (9.7%) and tyrosine (8.6%). Therefore, the protein was identified as a kind of a storage protein referred to as an arylphorin. The protein was stained by Schiff's reagent, suggesting a glycoprotein. The protein contained 4.9% (w/w) sugar and mannose and N-acetylglucosamine were major components. Also, degradation of protein was begun by heat treatment at 90°C for 20 minutes. From these results, it was concluded that the AMHP is a storage protein referred to as arylphorin which is purified from the pupal haemolymph of the wild silkmoth, A. pernyi.