

3-4-7. Molecular cloning and characterization of a cDNA encoding the arylphorin-like hexameric storage protein2 from the mulberry longicorn beetle, *Apriona germari*

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We describe here the cloning and characterization of a cDNA encoding the arylphorin-like hexameric storage protein2 from the mulberry longicorn beetle, *Apriona germari* (Coleoptera, Cerambycidae). The complete cDNA sequence of *A. germari* hexamerin2 (AgeHex2) comprised of 2,088 bp with 696 amino acid residues. The AgeHex2 gene had four potential N-glycosylation sites. The deduced protein sequence of AgeHex2 showed high homology with AgeHex1 (51% amino acid identity), *Tenebrio molitor* hexamerin2 (49%), *T. molitor* early-staged encapsulation inducing protein (43%) and *Leptinotarsa decemlineata* diapause protein1 (43%). The AgeHex2 also contained the highly conserved two larval storage protein signature motifs. Hydropathy analysis suggested the profile of AgeHex2 was similar to known coleopteran hexamerins. Phylogenetic analysis further confirmed the AgeHex2 is more closely related to the coleopteran hexamerin genes than to the other insect storage proteins. The amino acid composition of AgeHex2 with high aromatic amino acids was similar to arylphorins. Northern blot analysis confirmed the AgeHex2 gene showed fat body-specific expression pattern at the transcriptional level.