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Molecular cloning and partial characterization of Apolipophorin-III from *Anopheles gambiae*

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Pattern recognition proteins play a pivotal role in innate immune response of both vertebrates and invertebrates. Over the last couple years, attention has been given to apolipophorin-III (ApoLp3) that are known to be involved in LPS detoxification, phagocytosis and recognition protein. In this study we have partially characterized an mosquito ApoLp-III which is homologous to mammalian apolipoprotein, apoE. The genomic organization, cDNA and deduced amino acid sequence of an AgApoLp-III from the human malaria vector, *Anopheles gambiae*, is presented. Analysis of genome sequences indicates that there is a single intron (89 bp) between exon1 (155 bp) and exon2 (634 bp). The 789 bp sequence has a 633 bp protein-coding region with 56 bp of putative 5' untranslated region and with 100 bp of 3' untranslated region. On the other hand, the deduced amino acid sequence begins with a methionine codon at position 19 and extends to position 211, encompassing a polypeptide of 193 amino acids. It has some identity (19~25%) to a apolipophorin-III from various insects such as *Acheta domesticus*, *Manduca sexta*, *Bombyx mori*, *Bombyx mandarina*, *Galleria mellonella*, *Agrius convolvuli*, *Derobrachus germinatus*, *Epiphyas postvittana*. Expression patterns of AgApoLp-III was examined during the developemental stages, and also during the vitellogenic stages after blood feeding. Interestingly, RT-PCR analysis showed that AgApoLp-III was strongly induced in midgut in response to malaria parasite, *Plasmodium berghei*. The potential involvement of AgApoLp-III in midgut innate immunity and apoptosis remains to be elucidated.