1. Introduction
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Mosquitoes transmit a number of important animal and human diseases in the tropical and sub-tropical countries. Human malaria, caused primarily by the protozoans *Plasmodium falciparum* and *Plasmodium vivax*, affects nearly 500 million people and is responsible for 1.1 to 2.7 million deaths annually (WHO, 2005). The filarial nematodes, *Wuchereria bancrofti* and *Brugia malayi* are the major parasitic agents of human lymphatic filariasis, causing morbidity in over 100 million individuals world wide and the total population at risk is estimated to be 1.3 million (Bockarie *et al.*, 1998; WHO, 2007). The filariasis most widely prevalent in India is the bancroftian filariasis, caused by nocturnally periodic *Wuchereria bancrofti* (Cobbold). It is transmitted by the vector mosquito *Culex quinquefasciatus* Say.

The maintenance/development/multiplication and transmission of the parasites/pathogens that cause malaria, lymphatic filariasis, and numerous viral infections, by mosquitoes are dependent upon both the susceptibility of the host vector and compatibility of the parasite/pathogen, as dictated by their genomes. The genetic control of vector competence can operate at different developmental stages of the parasites/pathogens and in different tissue sites within the mosquito. Encounters of different stages of the parasites/pathogens with different tissues of the host mosquito create specific opportunities that determine whether the association is compatible. In short, numerous physical as well as physiological factors determine the susceptibility of a particular mosquito species to parasite infection and the efficiency with which the mosquito may function as a disease vector (Warburg and Miller, 1991). Another plausible factor is the performance of the insect's immune defense system, which can afford protection against prokaryotic and eukaryotic parasites/pathogens (Hoffmann, 1995; Lackie, 1998). In insects, including vectors that transmit parasites/pathogens causing diseases, immunity has been described as the germ line-encoded anti-infection response of the host organism. In this process, immune peptides are produced *de novo*, usually in the fat body or haemocytes, or are activated from precursors and released into the haemolymph or delivered to other tissues. This response generally lacks immunologic memory and the discrete specificity of the antigen-antibody
response components of classical immunology (Boman, 1998). The performance of the vector immune system upon parasite challenge has not been evaluated adequately, because until very recently, molecular characterization of immune effectors and regulatory factors was largely confined to model insects of no obvious medical importance (Richman et al., 1996; Koutsos et al., 2007).

Mosquito control still remains the primary strategy for controlling mosquito-borne diseases. Insecticide resistance of mosquitoes, drug resistance of parasites, cost of new drug development, limitations of vaccines, and environmental hazards of pesticide application, all necessitate the need for development of novel disease control strategies. The decreasing efficacy of traditional methods of vector-borne disease control has provided the impetus to explore host-pathogen interactions at the molecular level with the aim of designing novel control methods (Bartholomay et al., 2004). Innate immune responsiveness is of particular interest in such explorations, because vector mosquitoes and mosquito cell lines have been demonstrated to produce robust humoral and cellular immune responses against invading parasites/pathogens. The molecules that are involved in these immune systems, several anti-parasitic proteins, are known to be induced and secreted into the haemolymph by the fat body and the circulating haemocytes (Ham et al., 1995). Also, identification of molecules that might influence parasite development, and the isolation of the genes that code for these molecules, is an approach to clarify the mechanisms controlling mosquito vector competence. Investigations into anti-microbial gene expression in mosquitoes have been limited to the genera Anopheles and Aedes. With respect to the genus Culex, despite their importance as human disease vectors, information on immune system peptide activation or synthesis is relatively little.

Development of the early larval stages of filarial parasite takes place within the mosquito, after ingestion of the microfilariae (mf) along with a blood meal. The parasite has to pass through various tissues of the mosquito before being transmitted to human hosts. The tissues involved are the midgut epithelium, the haemocoel (and fat body), the indirect flight muscles, and the salivary glands. Determining the genes that are transcriptionally up- or down-regulated in each of
these tissues, in response to infection by filarial worms, will be an important milestone in tracing the genetic and biochemical consequences of parasite development. Information on the genes and their products that regulate parasite development could lead to identification of susceptibility markers as well as xenodiagnosis of infection. Hence, the present study was carried out with the following objectives:

- *To identify the immune molecules up-regulated/produced in Culex quinquefasciatus as a consequence of infection and development of Wuchereria bancrofti,*

- *To characterize the transcripts corresponding to the up-regulated/produced immune molecules in Culex quinquefasciatus upon infection with Wuchereria bancrofti.*