GENERAL INTRODUCTION
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Insects represent a major life form on earth. Nearly 900,000 insect species have been described by now, comprising 75% of all the recorded animal species. They are found in almost all ecosystems including deserts as well as in the Antarctic. This truly demonstrates the immense ecological adaptation of insects and their extraordinarily adaptable life forms in diverse environments where other animals cannot survive. This biological success is attributed to the enormous diversity of their size and body structure, mating strategies and the remarkable adaptive abilities in feeding and behaviour. Such diversity imposes a delicate relationship between insects and human life. The evolutionary history of insects stretches back at least to the Devonian period, i.e., about 450 million years ago. Diptera, the insect order to which flies and mosquitoes belong, might have first appeared not later than the Triassic period, about 200 million years ago (Service, 1978). Mosquitoes probably arose later in this same period, but the first fossil specimens recognizable as such are associated with the Eocene epoch of the quaternary period (40-60 million years ago). Some of those specimens look remarkably similar to the present day Culex species (Edwards, 1932). Insects are beneficial as they pollinate crops, act as natural enemies of damaging pests and produce useful products such as honey, silk and wax for humans. At the same time, these are major pests of our food crops, act as vectors for transmitting deadly epidemic/pandemic diseases and sometimes interfere in our international trade, commerce and economic affairs. Thus, very often one wonders what makes insects so diverged and how the genes and genetic make-up of insects contribute to their adaptations and life forms and most importantly, how they affect human
life either directly or indirectly. Insect populations even within a species vary in their behaviour and morphology that attributes to their complex interaction with the environment (Dempster & McLean 1999). Thus, the study of insect ecology and genetics at different foci is important to understand their evolution and diversification and their influence on the functional and trophic links between different components of associated habitats (Speight et al. 2005).

Mosquitoes are the most primitive dipterans being closely related to midges, gnats and crane flies. Three quarters of all mosquito species live in the humid tropics and subtropics where the warm moist climate has favoured the existence of diversity of habitats permitting the evolution of many species. The family Culicidae is separated in to two medically important subfamilies, the Anophelinae and Culicinae. The former being the smaller group includes the vectors of human malaria (Genus: Anopheles) and the later consists of vectors of filarial and viral diseases such as filariasis, Japanese encephalitis, dengue, chikungunya, yellow fever etc. (Genera: Aedes, Culex and Mansonion). In terms of public health importance, over 300 species of mosquitoes in the world play important roles due to their vectorial capacity.

Mosquitoes have been the focus of investigations since the time the first human disease was linked to them. Compared to other insects, they cause more human suffering, serving a cyclic or mechanical but exclusive vectors of 5 important diseases of man namely malaria, dengue, yellow fever, filariasis and encephalitis. Among the mosquito genera, Anopheles, Aedes and Culex are very important as they include the principal vectors of malaria, dengue, chikungunya, yellow fever and most of the encephalitis causing arboviruses. More than fourteen
mosquito genera are known to harbour arboviruses (arthropod borne viruses) [Mattingly, 1973].

Among different mosquito borne diseases, dengue vectored by *Aedes aegypti* and *Aedes albopictus* attracted the attention of the health care workers with the emergence of more critical forms, dengue haemorrhagic fever (DHF) and dengue shock syndrome (DSS), which are the most important re-emergent arboviral diseases of the human beings (McBride and Ohmann, 2000). It is the second most important mosquito borne disease in the world next to malaria. Due to the severe pain caused in the joints and muscles, it is commonly called the ‘brake-bone’ disease. There are four serotypes namely DEN1, DEN2, DEN3 and DEN4 viruses belonging to the family Flaviviridae. Infection with one serotype confers life long immunity to that particular virus (Gubler and Clark, 1995). There is very strong evidence that, the risk of DHF is substantially greater among persons suffering a second dengue infection with different serotypes. These unique characteristics of dengue viruses make vaccine development, disease surveillance and laboratory diagnosis exceptionally challenging. Dengue has been known clinically since many years and the fatality rate in case of this disease is nil whereas in DHF, it may exceed 13% in some areas (Gubler, 1997).

The global dengue pandemic has intensified during the past two decades and now affects all continents except Antartica. It has become a major international and debilitating health problem affecting the tropical and subtropical regions of the world. The conditions responsible for dengue epidemics continue to mount and the global population at risk is estimated to range from 2.5 to 3 billion. World Health Organisation (WHO) currently estimates approximately 50 to 100 million cases of DHF every year spread to over 100 countries belonging
to America, Africa, Eastern Mediterranean, South-east Asia and the Western Pacific, the latter two being seriously affected (WHO, 2002). Formerly thought to be strictly urban, dengue is now recognized as being of significance in rural areas as well in South-east Asia. Since the end of II world war, 38 out of 46 countries of the Asian continent and islands of pacific have experienced dengue and dengue haemorrhagic fever (DHF) epidemics. All the four serotypes are virtually present in every country of the region. Recent dengue epidemics have occurred in India, Srilanka, Pakistan, Myanmar, China, Thailand, Indonesia, Philippines, Maldives, Cambodia, Laos, Vietnam, Malaysia, Singapore and many islands of the Pacific. Dengue is the leading cause of hospitalization and death in children of many countries in Asia and the pacific nations. In the year 2003, 70,959 cases of dengue were reported from Asia, out of which maximum number of cases were from Thailand (24,004), followed by Indonesia (18,797) and India with 4720 cases stood fifth in the list. In addition, the same Aedes vectors are transmitting chikungunya in epidemic form in many countries including India.

In India, dengue has been known for over a century. Seasonal and cyclic epidemic pattern of dengue is a recent phenomenon observed in India and Srilanka, identical to the problem detected in Philippines, Thailand and Indonesia (Gubler and Clark, 1995). This new dengue paradigm has now screened a firm foothold and has emerged as a major health problem in many parts of the country. Endemicity of DF, DHF and dengue shock syndrome (DSS) has been recognized for the past several years as the leading cause of death in children. The number of dengue cases ranges from 7 to 16 thousand per annum in India. A maximum of 21,79,996 cases were recorded in 1986. Dengue outbreak occur annually in India, with most cases are reported from Western and Southern states and the risk of
dengue is round the year. In northern states it primarily occurs from April through November. DHF was first recorded in the metropolitan city of Culcutta during 1963, so also chikungunya. Subsequent outbreaks of dengue fever occurred in cities on the east coast as well as the central, northern and southern parts of the country including an epidemic in Chennai during 1989 and 1990. A fairly recent and severe epidemic of DHF/DSS occurred in Delhi and adjoining areas from August through November 1996. A total of about 10000 cases were reported with a death rate of 4.2%. In addition, New Delhi experienced outbreaks of different magnitude due to different viral serotypes in 1967, 1970, 1982, 1996, 2003 and very recently (2006). All these outbreaks occurred during the monsoons (August – November) and subsided with onset of winter. However, an episode of dengue fever occur in Jalore town, southwest of Rajasthan state in April and May 1985. This was the first reported outbreak of dengue in the arid zone of west Rajasthan during dry season in contrast to other parts of India where the outbreak follow heavy rains.

After the 1996 episode, there was a decline in the incidence of dengue. With outbreaks in the state of Rajasthan (1452 cases and 35 deaths), Tamilnadu (816 cases and 8 deaths), Haryana (260 cases and 5 deaths) and Karnataka (220 cases and no death) during 2001, there was an increase in the number of cases and deaths (41%) was noticed during 2002, as compared to 2001. However, during 2003, cases and deaths increased to the tune of 62.7% and 60% respectively have been recorded. And this rising number is still growing with outbreaks in 2006 in National capital (cases 3225 and deaths 64) as on 19-11-2006 (http://namp.gov.in/dengueC&D.html). The disease has been spread at an alarming magnitude in the southern state as well with Kerala state registering 880
cases and 5 deaths. Karnataka state where the present study spot is situated with 92 cases and 7 deaths during 2006. The total number of cases and deaths recorded in India during 2003 was 4720 and 78 respectively. According to WHO (SEARO) in India number of Dengue cases were above 12000 in 2005 with CFR (Case Fatality Rate) nearly 1.4% (www.searo.who.intLinkFilesDengue_India_DC_CFR_1991_2005.pdf).

All the four serotypes of dengue virus are transmitted through the bites of the infective female mosquito of the genus, Aedes (Gubler, 1988), which has been known since 1903. By 1926, investigations had incriminated Ae. albopictus was also as dengue vector. Since then, over 20 species of mosquitoes, all belonging to the genus Aedes have either been proved or suspected as the vector of dengue virus, by isolating the virus in nature and/or by experimental studies. Ae. aegypti has been found to be the most important vector in epidemics worldwide and is the principal vector of DF and DHF in southeast Asia (WHO, 1999). Ae. albopictus is the secondary vector, important in the maintenance of dengue viruses in Asia and Americas (WHO, 1999; Pant and Self, 1999). Ae. scutellaris, Ae. africanus, Ae. luteocephalus and Ae. polynesensis are the other species of mosquitoes incriminated as secondary vectors in Pacific Nations and Africa. Even though excellent hosts of dengue viruses, they are less efficient epidemic vectors than Ae. aegypti. In Australia, Ae. aegypti, Ae. scutellaris and Ae. katherinensis are the vectors. Species of the subgenus Finlaya (Asia) and Diceromyia (Africa) appear to be important mosquito hosts involved in dengue maintenance cycles in the forest. Two other species, Ae. mediovittatus shown to be excellent experimental hosts of dengue viruses.

In India, Ae. aegypti is the most competent primary vector in epidemic outbreaks and Ae. albopictus, Ae. vittatus and Ae. w-albus are the other potential
vectors. *Ae. aegypti* has high anthropophilic index and their population density fluctuate with rainfall and water storage habitats. Urbanization and migration of people have increased the habitats suitable for *Ae. aegypti* over the years. This breeds in natural and artificial container such as tree holes, pots, discarded tyres, plastic containers, open tanks, air coolers etc.

*Ae. albopictus*, known as the ‘Asian tiger’ mosquito, is a species that originated from the tropical forests of Southeast Asia (Pant and Self, 1999). Basically a sylvatic species, it creates serious public health problem because of its vectorial capacity in transmission of several arboviruses, which may be even greater than that of *Ae. aegypti* (Mitchell, 1995). Secondly, this species has the capacity to transmit the serotypes 2 and 3 of dengue virus vertically. Additionally, *Ae. albopictus* shows aggressive anthropophilic behaviour and greater adaptability to different habitats (Miller and Ballenger, 1988; Rodhain, 1995). It breeds in tree holes, coconut shells, axils of leaves, artificial containers like plastic jars, broken pots, discarded tyres etc.

The mosquitoes, *Aedes aegypti* and *Aedes albopictus* are also vectors of another arboviral disease ‘Chikungunya’. The disease resembles dengue fever and is characterized by severe, sometimes persistent, joint pain, as well as fever and rashes. It is rarely life-threatening. Nevertheless widespread occurrence of diseases causes substantial morbidity and economic loss. Till 10th October 2006, 151 districts of eight states of India have been affected by chikungunya fever. The affected states are Andhra Pradesh, Andaman & Nicobar Islands, Tamil Nadu, Karnataka, Maharashtra, Gujarat, Madhya Pradesh, Kerala and Delhi. More than 1.25 million cases have been reported from the country with 7,52,245 cases from
Karnataka and 2,58,998 from Maharashtra provinces. In some areas attack rates have reached up to 45% (http://www.who.int/csr/don/2006_10_17/en/index.html).

In the light of the said information and the existing endemicity of several mosquito borne disease and in particular dengue and chikungunya in Karnataka state, India, study of diversity of mosquitoes of forest and rural habitats with respect to differential ecology was choosen. Detailed studies were undertaken in particular on *Ae. aegypti* and *Ae. albopictus*, from forest and rural areas of Karnataka with respect to systematics, insecticide bioassay, biochemical and molecular differentiation. As dengue and chikungunya are endemic in local situation the present investigation will add more knowledge on adaptability of mosquitoes to changing environment.