Chromosomal studies in *Aedes* (Finlaya) *niveus*, a vector for filariasis

The genus *Aedes*, belonging to the tribe Aedini, subfamily Culicinae of the family Culicidae[1] comprises over 30 species widely distributed in Southeast Asia and the South Pacific[2–4]. Many of the species are endemic to single islands geographically isolated by natural barriers. Therefore, this complex is of importance for the study from the speciation point of view. Among the 2960 species of mosquitoes[5], karyotype of about 100 species has been described so far. The limitations of the conventional cytological techniques for separation of different species of mosquitoes might have been one of the reasons. Relatively little information is available on the type and extent of chromosomal variations among different aedine species. Since the polytene chromosomes of *Aedes* are unsuitable for cytogenetic studies[6], only the somatic and meiotic chromosomes have been the subject of analysis in studying the cytogenetic relationship among aedinine species[7] and the karyotypic evolution among this group[8–10].

The larvae of *Aedes niveus*, a vector of filariasis, was collected from tree holes of Chowra island in the Nancowrey group of islands, Nicobar district (8.5–9.5°N and 93–94°E) in the Andaman and Nicobar island, India. This species of aedine mosquito is a vector for diurnally subperiodic filariasis[11,12]. The Chowra island with an area of 2.8 mile^2 and a Nicobari population of 1212, has microfilaria rate[13] of 25%. The larvae were transported to Malaria Research Centre Field Station Laboratory located at Malacca, Car Nicobar island. The larvae were reared in an enamel tray and fed a mixture of dog biscuits and yeast powder in a ratio of 3 : 2 in the insectory, maintained at 28 ± 2°C and 70–80% RH. Larva and pupa from this culture were selected for the present chromosomal study. Since the species is of importance from the point of view of medical entomology and as no work has been carried out on its cytology, it was considered worthwhile to study the chromosomes of the species and their behaviour during cell division.

Mitosis was studied from the neuroblast cells of third instar larvae and early fourth instar larvae, and meiosis from the testes of early pupae. The tissue was dissected in Shen's physiological saline, fixed in 1 : 3 acetic acid : methanol and stained and squashed in lacto-aceto-orcein[8]. The somatic metaphases contained six metacentric chromosomes ($2n = 6$). During prophase, the chromosomes started condensing and appeared like a network of coiled threads (Figure 1 *a*). During metaphase, the chromosomes were maximally condensed with smoother surfaces arranged on the equator (Figure 1 *b*). During the onset of anaphase, the chromosomes repelled each other and progressed synchronously towards the opposite poles (Figure 1 *c*). Since the repulsion seems to be initiated at the centromeric region, the separation appeared V-shaped.

The first recognizable stage during meiosis is zygotene (Figure 1 *d*). Similar reports are available in different species of aedine mosquitoes[14–17]. The lack of leptotene stage is probably due to the presence of somatic pairing. During this stage, pairing was clearly observed as the homologous chromosomes undergo gradual condensation. During pachytene, the formation of chiasma was well observed (Figure 1 *e*). The homologues undergo further condensation as they enter diplo-

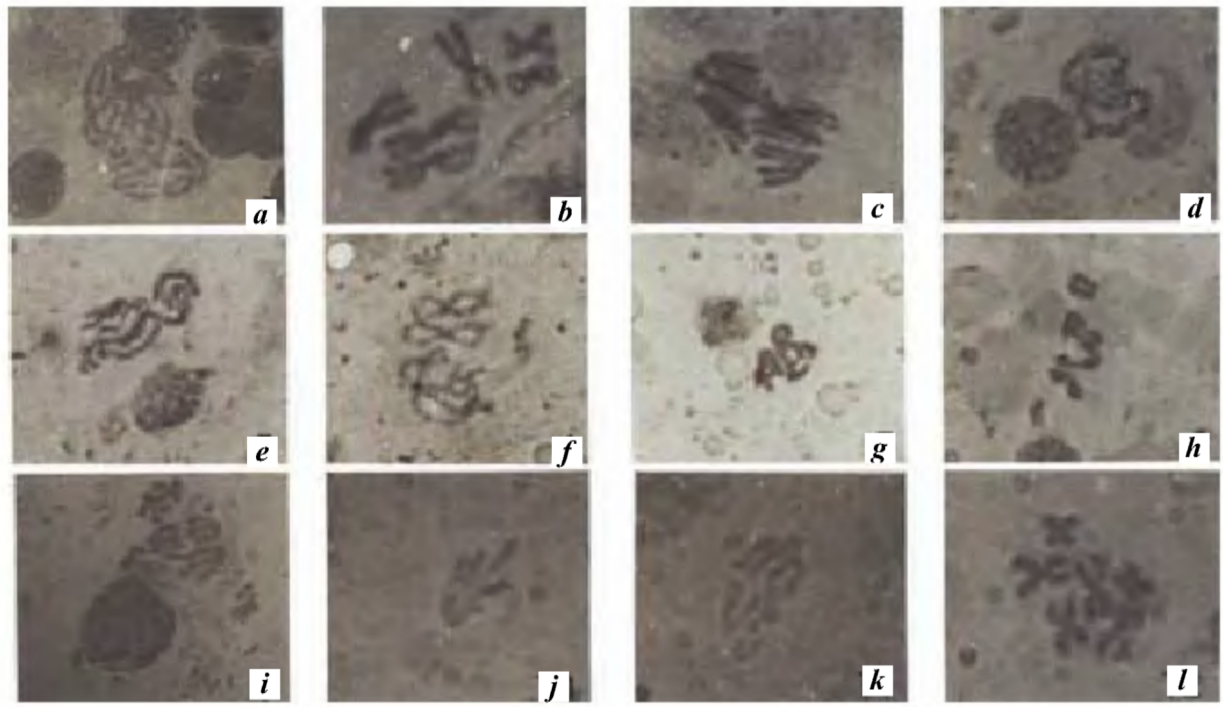

Figure 1. ***a***, Mitotic prophase of *Aedes niveus*; ***b***, Mitotic metaphase; ***c***, Mitotic anaphase; ***d***, Zygotene; ***e***, Pachytene; ***f***, Diplotene; ***g***, Diakinensis; ***h***, Metaphase I; ***i***, Anaphase I; ***j***, Metaphase II; ***k***, Anaphase II; ***l***, Spermatogonial metaphase.

tene (Figure 1*f*). Here, possibly due to centric repulsion, the homologous chromosomes started separating from each other, excepting the points of crossing over. As the cell entered diakinesis, the bivalents were further condensed and the chiasmata had almost terminalized (Figure 1*g*). Each bivalent bears a pair of chiasmata, which appeared to have originated interstitially. As in most other species, terminalization was incomplete at metaphase I (Figure 1*h*). As polarization is initiated, the two homologues free themselves and enter into the anaphase I (Figure 1*i*). The chromosomes appeared to move synchronously to the opposite poles. In metaphase II, the chromosomes had arranged themselves at the equator (Figure 1*j*) and the chromatids appeared to proceed synchronously to the opposite poles at anaphase II (Figure 1*k*).

The diploid number of chromosomes in all mosquito species studied so far[18] is $2n = 6$ except for the genus *Corethra*[19], where $2n = 8$. Since fairly uniform karyotypes have been observed in different genera of mosquitoes like *Anopheles*, *Culex* and *Aedes*, it may be argued that the mosquitoes have a primitive modal number of 6, with originally biarmed chromosomes. Although the mosquitoes exhibit conservation with respect to the number of chromosomes, their morphology varies in different species. Typically, the three pairs of chromosomes are metacentric with minor variations in all species of mosquitoes. The two larger pairs are almost of equal size and chromosome 1 is the smallest[20].

Although Craig *et al.*[21] and Hickey and Craig[22,23] have reported the presence of heteromorphic sex pair *X* and *Y*, this has been disproved by Patnaik *et al.*[24]. In *A. niveus* also, no heteromorphic sex chromosomes could be identified in the present study. Probably the sex in different species of *Aedes* is determined by a small segment of chromosome by a block of genes, as proposed by Motara[25]. According to Rai[26], the different species of genus *Aedes*, viz. *A. albopictus*, *A. mascarensis*, *A. polynesiensis* and *A. vittatus* contain three pairs of metacentric chromosomes, although in *A. aegypti*, one out of three pairs is submetacentric in morphology. In the present study, however, it has been observed that *A. niveus* has three pairs of metacentric chromosomes. The uniformity in karyotype in majority of aedine species hints at the possibility of gene mutations as the basis of speciation.

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ACKNOWLEDGEMENTS. We thank Dayal Chand and Uttam Singh for technical assistance. Financial support by Indian Council of Medical Research is acknowledged.

Received 3 February 2004; revised accepted 14 June 2004

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Preconcentration and determination of mercury in natural waters using immobilized biosorbent of *Aspergillus niger*

Mercury is one of the most toxic heavy metal ions to all living organisms. The toxicity of mercury increases drastically on transformation to its organic forms, such as methyl mercury via biomethylation through bacterial intervention in the environment[1]. Mercury is released into the atmosphere by a variety of natural and anthropogenic sources[2]. Elevated levels of mercury in waters remote from anthropogenic emission sources have also been documented, indicating that the atmospheric transport and deposition is an important source of contamination[3]. The speciation and chemical transformations of mercury in the atmosphere strongly influence its transport mechanism and global cycling. Thus, it is of great importance to regularly monitor and recover all the species of mercury from the environment, so that the decontamination process can be undertaken. WHO prescribes a limit of 1 ppb for total Hg in potable waters. The same limit has been adopted