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Species Complex in Anopheline Vectors of Malaria

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Sibling species appear to be common in Anophelines which include many of the malarial vectors. Sibling species of a complex are reproductively isolated and differ from each other much more genetically and biologically than morphologically.

The practical application of such a study will clarify epidemiological information in disease transmission and improve the proficiency of vector control techniques.

Key Words: Anophalines, Malaria, Sibling species, Vector Control

The practical importance of species complex in malariology emphasizes the accurate identification of vector species in order to clarify epidemiological information and to improve the efficiency of vector control. Bates (1940) first recognised, that the European malarial mosquito *Anopheles maculipennis* consisted of different races, and afterwards as cytotaxonomic studies progressed, many of the Anopheles turned out to be complex of sibling species; e.g. *A. maculipennis*, *A. minimus*, *A. funestus*, *A. gambiae*, *A. barbirostris*, etc.

Sibling species in a complex are reproductively isolated and ecologically distinct, having minimal morphological differences and differ much more genetically and biologically (Reid 1968). Sibling species are characterized by being exclusively sympatric; and the morphological variations, if any, are not sufficient to discriminate the taxa without genetical evidence to substantiate.

Even though identification could depend on minor morphological characteristics, non-morphological methods such as crossing experiments chromosome patterns, and biochemical determinations are more reliable in identifying and defining anopheline sibling species. Chromosomally, Frizzi (1953) recognised 6 taxa in the *A. maculipennis* complex. Similarly six of the *A. gambiae* complex were identified through the polytene chromosome pattern (Kitzmiller 1967, Coluzzi & Sabatini 1968).

The usual indicators of species complex are the different factors in the biology of a supposed single species and with well developed field studies (Service 1976), it is rather easy to detect in what ways each puzzling vector species differs. The important variations between sibling species concern their host preferences, resting places, vectorial capacity and response to insecticides. The marked ecological and behavioural diversity of *A. gambiae* divulged that this species consisted of 3 fresh water, 2 salt water and 1 mineral water forms, one was zoophilic and the others were probable vectors of human malaria and filariasis but with wide variation in their levels of vectorial efficiency (White 1974, Highton et al. 1979). Similarly, Frizzi (1952) reported that 3 out of 6 *A. maculipennis* sibling groups were efficient malarial vectors in Eurasia—others being more zoophagic and less important medically (White 1977).

In the majority of cases where sibling anophelines have been detected, their reproductive incompatibility has been domonstrated in the laboratory. As with species in general, the members of a sibling species complex are all likely to show clonal variation, seasonal modification, subspecific differentiation and individual polymorphism.

Coming to the Indian situation where nine vector species *A. culicifacies*, *A. stephensi*, *A. minimus*, *A. sundaicus*, *A. jeya poriensis*, *A. philipiensis*, *A. fluviatilis*, *A. varuna* and *A. annularis* are responsible for the transmission of malaria the need to find out whether each one is a single species or a complex has become evident. Only then control measures could be devised separately for each.

A. stephensi, one of the primary vectors of malaria has been considered to have two races based on egg measurements by Sweet and Rao (1938) and this has to be confirmed cytologically. Rutledge et al. (1970) discussed the absence of species complex in this species because of conspecificity of the population. But De Zulueta et al. (1968) reports that such evidence is not conclusive and species status should be determined from evidence of positive assortative mating in nature. Additional importance is caused by genetic polymorphism (Coluzzi et al. 1973) and according to the arrangement of floating chromosome inversions, the behaviour pattern is altered.

The biological behaviour of *A. fluviatilis* which either occurs at high density and zoophilic or low density and anthrophilic needs further analysis cytogenetically (Bhombora et al. 1956, Chowdiah & Seetharaman 1975). *A. philipiensis* is a vector in deltaic Bengal but not in Assam (Krishnan 1961). *A. sundaicus* known to transmit malaria in Andaman and Nicobar islands, South-east India and Java is a coastal vector species. Crossing experiments and cytogenetic examination should be carried out in order to revise the taxonomic status of this species. Even though *A. varuna* is a vector of minor importance the extent of variation in this species which closely resembles *minimus*, is not clear. Highly zoophilic vector population in the midst of continued malaria transmission has led several workers to propose the concept of genetically separated but sympatric races in *A. culicifacies*. Recent cytogenetic studies indicates the possibility of species complex and this malarial vector needs further study.

A. subpictus is not considered as a malaria vector throughout most of its distribution although transmission in selected endemic areas in Indonesia has been attributed to this species (Reid 1970). In India it is highly zoophilic and rarely infected with malaria parasites (Reisein & Boreham 1979). But in the coastal areas of Tamil Nadu and Pondicherry subpictus breeds profusely and is suspected as a vector because in some of these areas no known vector species are breeding. Therefore the need for mapping the distribution of *A. subpictus* along the coastal land and mapping the polytene karyotype is essential.

Once cytogenetically the vector species are analysed their studies should be made as to their degree of attractiveness to man versus animals, susceptibility to malaria parasites, adult and larval habits with the ultimate aim of finding means to control the potential vectors of human malaria.

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