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The Value of Mosquito Taxonomy to the Study of Mosquito-Borne Diseases and Their Control

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Medical entomology and mosquito taxonomy are not mutually exclusive disciplines. There are substantial areas of both which have little relevance to one another, but there is also a significant interface between the two which results in a dependency of medical entomologists upon mosquito taxonomists for help in the solution of problems concerning mosquito-borne diseases and their control. In this regard, 3 situations come to mind:

1. Studies involving mosquito vectors which are either undescribed or inadequately described. This may apply to some or all of the life cycle stages.

2. Studies involving groups of sibling or incipient mosquito species which are morphologically similar, if not indistinguishable, and which differ significantly in behavior, physiology, or vector competence.

3. Studies involving mosquito populations which differ morphologically from other populations of the same species, but where such morphological differences may or may not be correlated with differences in behavior, physiology, or vector competence.

Medical entomologists commonly refer to taxonomic literature for information on geographic distribution, ecological observations, and phylogenetic affinities. Most taxonomic problems facing a medical entomologist, however, concern attempts to match a sample of a population of insects to a published description, and knowing whether all such samples which do match are conspecific with the species described, and if samples which do not are contraspecific.

The number of undescribed or poorly described mosquito species worldwide is undoubtedly considerable. The taxonomic literature of the past decade shows no evidence that the rate of new species descriptions is slowing, and the trend should continue as comprehensive reviews of mosquito faunae are completed.

Most studies of species complexes and of polytypic species in the Culicidae have been in the genus Anopheles and in the subgenus Stegomyia of Aedes. McClelland (1967) points out that many more examples of polytypy and sibling species would be discovered if more genetical information were available. Until recently, however, little such information was available except for the Anopheles maculipennis, A. gambiae, and Aedes scutellaris species groups.

Recently, Bryan (1973a, b, c) published a comprehensive study of the Anopheles punctulatus complex of the Australo-Papuan Region, and included data on the morphology, hybridization, and mating behavior of F_1 hybrids of member species. This complex includes the malaria vectors A. punctulatus, A. koliensis, and A. farauti. Bryan concludes that populations previously identified as A. farauti comprise 2 species, and that both are malaria vectors.

An enormous body of information is now available on the species comprising the *Anopheles gambiae* complex. In the decade since Davidson (1964) reported that the complex consisted of 5 distinct, but morphologically similar species, intensive studies have been carried out on the genetics, behavior, physiology, ecology, distribution, morphology, and vector competence of the various forms. The species are separable on the basis of cross mating with known laboratory colonies and by direct observation of polytene chromosomes. Recently, a sixth species has been discovered in the complex and tentatively designated species D. (Davidson and White 1972; White, 1973). Of particular epidemiological interest have been the studies showing differences among species in sporozoite infection rates (Davidson, et al., 1967), insecticide susceptibility (Haridi, 1972) and host preference (White et al., 1972).

There are other species groups of anophelines awaiting study which contain primary malaria vectors. In Southeast Asia, the entire subgenus *Cellia*, containing the *Anopheles minimus* and *A. leucosphyrus* species groups, is of particular medical importance and is in need of a thorough review. In Africa, there are species groups in addition to *Anopheles gambiae* which contain malaria vectors and are in need of clarification (Gillies and deMeillon, 1968).

In the Neotropical region, variation in behavior and morphology among populations of *Anopheles albimanus* is well known. Although genetically controlled morphological variation has been documented (Rozeboom, 1963), evidence of the existence of a complex of sibling species is lacking. Keppler and Kitzmiller (1969) found reciprocal fertility among samples of 5 populations of this species from Costa Rica, Guatemala, Nicaragua, Mexico, and a colonized strain from John Hopkins University. Furthermore, Keppler et al. (1973) found no individuals heterozygous for an inversion among 1000 slides of salivary gland chromosomes from these 5 strains.

The subgenus *Stegomyia* is in medical importance second only to the genus *Anopheles*. Because of its importance in the transmission of dengue, yellow fever and other virus diseases, and filariasis, it has been studied extensively. The *Aedes scutellaris* group has received comprehensive reviews for the South Pacific fauna (Belkin, 1962) and Southeast Asian fauna (Huang, 1972).

The African fauna of *Stegomyia* has not had a modern, thorough taxonomic treatment. In West Africa, the known fauna consists of only 11 described species. Biological and distributional data are relatively abundant for these species (Mattingly, 1952). In South and East Africa, however, over 30 known species occur, and little is known of many of these (Mattingly,

1953). No less than 9 African species of *Stegomyia* have been associated with yellow fever transmission to one degree or another (Muspratt, 1956).

Although differences in thoracic scaling patterns among African Stegomyia appear very distinctive and constant, many of the species are very closely related to one another. Laboratory hybridization studies have emphasized these affinities (McClelland, 1961, 1967; McClelland and Mamet, 1962; Hartberg, 1972; Hartberg and Craig, 1973). Two species described from morphologically distinct adults, Aedes (S.) vinsoni and A. (S.) mascarensis have been synonomyzed based on subsequent genetical studies. Hartberg and Craig (1970) suggest specific status for A. mascarensis, however, based on hybrid breakdown of aegypti x mascarensis crosses.

This entire subgenus certainly needs taxonomic treatment, although many of the affinities within the subgenus will be determined only by additional genetical studies (Mattingly, 1952).

In certain respects, the study of mosquito-borne disease transmission and mosquito control may be considered, along with mosquito taxonomy, a subfield of mosquito biosystematics. Modern taxonomists realize that studies of morphological variation are often inadequate to describe and delimit biological species. Most factors controlling vector status are also under genetic control. Susceptibility of a mosquito population to infection by a vertebrate pathogen may be, in fact, under the control of a single gene. This has been demonstrated for filariasis (McDonald, 1962) and malaria (Ward, 1963; Kilama and Craig, 1969). Genetic polymorphism may also exist for behavioral characteristics having epidemiological significance, such as host preference (Gillies, 1964).

Understanding of a given mosquito-borne disease situation necessary for its effective control is dependent upon a thorough understanding of the taxonomy of the vectors, which is dependent upon a thorough understanding of the genetics of the vector populations. It is not advantageous to use these approaches independently. This is the crux of the gradual acceptance of the term biosystematics. Thus mosquito taxonomy and the study of mosquito-borne disease are closely-linked endeavors and must always remain so.

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