Rendiconti
Accademia Nazionale delle Scienze detta dei XL.
Memorie di Scienze Fisiche e Naturali
98° (1979-80), Vol. IV, fasc. 13, pagg. 205-210.

MARIO COLUZZI (*)

Recent advances in the cytogenetic study of afrotropical malaria vectors (**)

SUMMARY. — The genetical approach to the study of vector species should be considered as an essential part of the epidemiological entomology. The estimation of vectorial capacity and of its reduction under the impact of vector control measures is really meaningful only when applied to genetically known vector species. Undetected genetical heterogeneities in the vector system can result in an incorrect evaluation of basic epidemiological parameters. The cytogenetic approach has been the field of vector genetics most extensively and successfully applied to malariological entomology. Reliable and practical cytotaxonomic identification is now possible for example in the Afrotropical complex *Anopheles gambiae* allowing the separation of epidemiological important specie from un important ones. Moreover, epidemiological important intraspecific variations have been revealed in some populations by the study of inversion polymorphism.

The conventional morphological approach to the study of vector species has shown important limits in the last few years. Although a correlation is generally observed between the amount of genetical differences and the probability of an expression of such differences at a morphological level, the available data in different groups of vectors (particularly mosquitoes and black flies) show that morphological divergences may be acquired more slowly than reproductive isolation resulting in sibling species virtually undetectable morphologically. Moreover, intraspecific genetical variations are known which can produce important biological heterogeneities without necessarily being expressed morphologically.

The genetical approach to the study of vector species should be considered as an essential part of epidemiological entomology. The estimation of vectorial capacity and of its reduction under the impact of vector control measures is really meaningful only when applied to genetically known vector species. Unde-

(*) Istituto di Parassitologia, Università di Roma.

(**) Intervento nella seduta promossa dall'Accademia delle Scienze detta dei XL: *Man and tropical insects*. Roma 20 marzo 1980.

ISSN 0370-3460

tected genetical heterogeneities in the vector system can result in an incorrect evaluation of basic parameters for the assessment of vectorial capacity, for example the rate of vector-vertebrate contact, the susceptibility to the parasite, the expectation of infective life, the host-choice habit, etc. Let us stress the relevance of this point by considering Macdonald's mathematical model which is commonly used to monitor the effect of vector control measures on malaria transmission. According to this model the effect of an insecticide is translated into an effect on transmission assuming a uniform reduction of longevity within the vector population. However a uniform reduction in longevity implies a uniform exposure to the insecticide, i.e. a random distribution of the vector population in respect to the insecticide sprayed surfaces. This would clearly not be compatible with the finding of an association between resting behaviour and genetic variation.

Crossing experiments, cytogenetics and biochemical genetics are the three main genetical methodologies so far applied to the study of vector species and populations. Ideally these methodologies should be combined in an integrated genetical approach but only the techniques of biochemical genetics are in fact widely applicable. The electrophoretic study of isozymes has been already successfully applied in the detection of sibling species in various vector groups and in the evaluation of genetic divergences both at the interspecific and intraspecific level. There is no doubt about the tremendous potential of this approach in detecting genetical heterogeneities in the vector system as well as in the parasite and in the vertebrate host. Hybridization studies can provide and have provided data of fundamental importance in the knowledge of species complexes, particularly in revealing hybrid sterility. Even when expressed by slight abnormalities in the spermiogenesis, hybrid sterility represents a highly reliable guide to specific distinctness although absence of sterility is not necessarily indicative of conspecificity. An important limiting factor in the testing of reproductive compatibility experienced with certain vector groups (e.g. *Simulium*) is the difficulty in laboratory handling and breeding. The cytogenetic approach, with which we are dealing in detail, has been up to now the field of vector genetics most extensively and successfully applied to epidemiological entomology. Reliable and practical cytotaxonomic identification is now possible for various complexes of sibling species allowing the separation of epidemiologically important species from unimportant ones. Moreover, epidemiologically important intraspecific variations have been revealed in vector populations by the study of inversion polymorphism (Coluzzi and Dunnar, 1978).

The value of vector cytogenetics has been fully tested in the Afrotropical complex *Anopheles gambiae*. Cytotaxonomic characters due to fixed paracentric inversions are routinely used to identify the six sibling species of the complex. Distinctive morphological characters can be used for the separation of the two salt water members of the complex *An. melas* and *An. merus* while the reliable identification of the remaining four species depends essentially on chromosomal characters. A few possibly discriminant isozymes were recently found but their taxonomic use is of little practical value since excellent polytene chromosomes

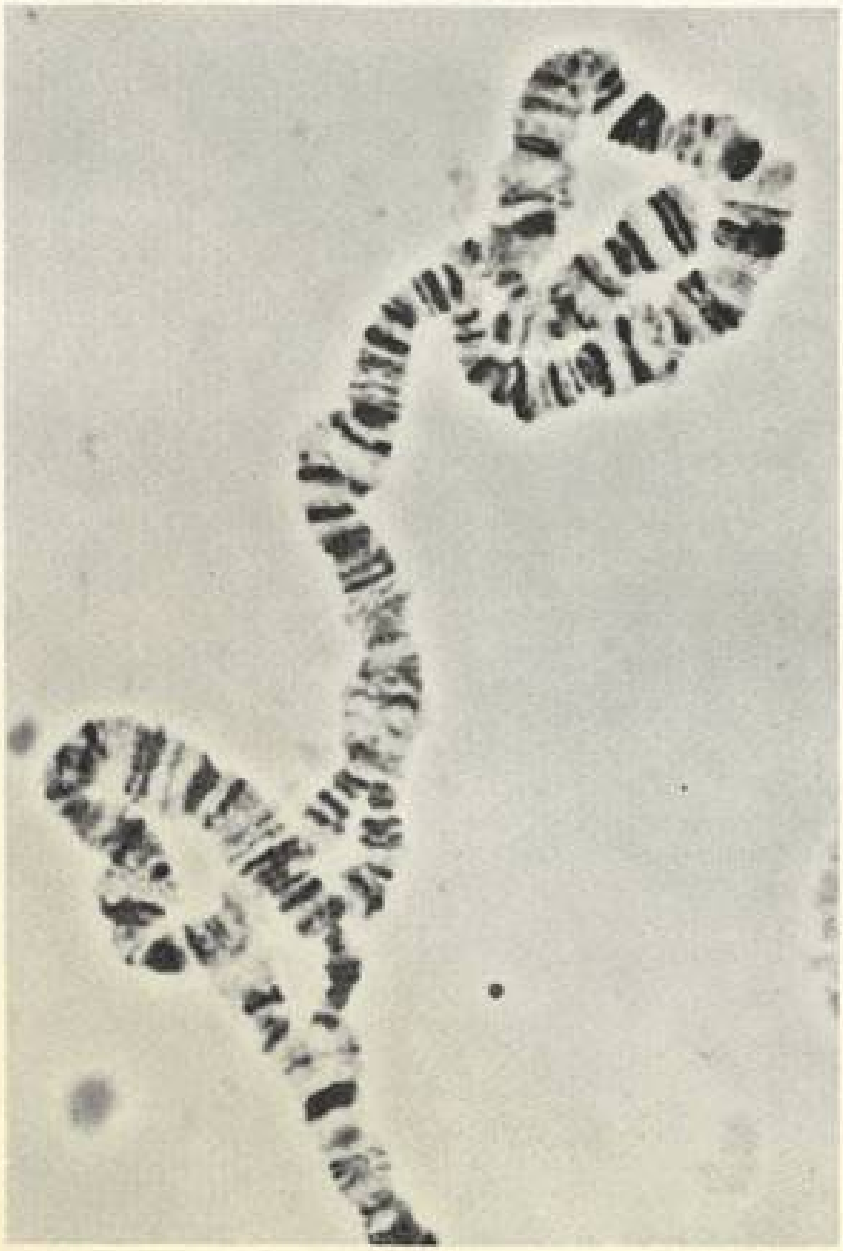

Fig. 1. — Chromosome 2R from ovarian nurse cell polytene complement of adult *Anopheles arabiensis* showing two heterozygous inversions.

are available not only in the larva but also in the female adult. As noted by Kitzmiller (1976) in his recent review the possibility of accurately determining distribution, proportions and biology of these taxa has far-reaching implications in the epidemiological studies of malaria and bancroftian filariasis, and in the planning and monitoring of control operations.

Recent advances in the study of the *gambiae* complex have been made particularly on the two main malaria vectors *An. gambiae* and *An. arabiensis*. The latter which has been found up to now prevailing in the Sahel and the Sudan Savannas was recorded for the first time in the West African forest zone. However it was shown that *An. arabiensis* is successfully established only in forest towns where it was probably introduced and where it is the main vector responsible for urban malaria (Coluzzi *et al.*, 1979). The demonstration that this vector species is largely isolated in forest urban areas should open new perspectives for its control by chemical as well as by biological and genetical means.

Cytogenetic studies carried out on *An. gambiae* and *An. arabiensis* also demonstrated in both sibling species chromosomal variations due to paracentric inversions. Some of the inversions show seasonal and geographical changes in frequency with obvious correlations with climatic conditions and vegetation zones. When studying polymorphic populations in the Nigerian Savanna zones various cases of microgeographical variations of inversion frequencies were recorded which appear to be related to man-made environmental contrasts. Parallel indoor/outdoor collections of *An. arabiensis* and *An. gambiae* showed that the adult mosquito carriers of certain inversion karyotypes do not distribute at random in relation to the human environment they being significantly more frequent in outdoor samples or vice versa. The practical significance of this phenomenon is obvious when it is considered that intraspecific variations in house resting behaviour could be expected to produce differences in vectorial capacity and, more important, in the response to house spraying with residual insecticides. The assumption, commonly made, of identical probability of contact with the sprayed surfaces for all mosquitoes of the vector population, is invalid for such polymorphic populations of *An. gambiae* and *An. arabiensis* and this could explain the mediocrity of the results of past efforts to control malaria with residual insecticides in the African savannas (Coluzzi *et al.*, 1977, 1979).

References

Coluzzi M. and Dunbar R. W. (1978) - *Cytogenetics of vector-hosts*. Proc. 4th Int. Congr. Parasit., Warsaw 1978, Workshop G1.

Coluzzi M., Sabatini A., Petrarca V. and Di Deco M. A. (1977) - *Behavioural divergences between mosquitoes with different inversion karyotypes in polymorphic population of the* Anopheles gambiae *complex*, « Nature », *266*, 832-833.

Coluzzi M., Sabatini A., Petrarca V. and Di Deco M. A. (1979) - *Chromosomal differentiation and adaptation to human environments in the* Anopheles gambiae *complex*, « Trans. R. Soc. trop. Medic. Hyg. », *73*, 483-497 .

Kitzmiller J. (1976) - *Genetics, cytogenetics and evolution of mosquitoes*, « Advances in Genetics », *18*, 315-433.