EDITORIAL

DISTRIBUTION OF THE AFRICAN MALARIA VECTORS OF THE ANOPHELES GAMBIAE COMPLEX

MAUREEN COETZEE

Vector Control Reference Unit, National Institute for Communicable Diseases, Johannesburg, South Africa

The Anopheles gambiae complex contains what many consider to be the most efficient malaria vector mosquito species in the world: A. gambiae s.s. There are currently six named and one unnamed species recognized within the complex\(^1\) and excellent evidence for at least three species within A. gambiae itself in west Africa.\(^2\)

The identification of the species and concomitant distribution records are not simply of academic interest, but are vital to effective malaria control. With species identification comes the associated knowledge of the biology of that species which, in turn, dictates appropriate control measures. For example, in Zimbabwe in 1977 a malaria outbreak occurred in the southeastern lowveld areas and members of the A. gambiae complex were collected inside benzene hexachloride (BHC) (organochlorine)—sprayed dwellings. Species identification showed that all survivors on World Health Organization susceptibility tests were A. arabiensis, while most of those that died were the non-vector species A. quadriannulatus. The realization that A. arabiensis, a major vector in southern Africa, was resistant to the insecticide used for house spraying led to a change in policy and BHC was replaced with DDT, to good effect.\(^3\) A similar situation arose in South Africa where DDT was replaced by pyrethroids in 1996 because of environmental concerns, objections by the community to DDT residues on the walls of their houses, and increased bed bug biting activity. Unbeknown to the control program authorities, populations of the very efficient vector A. funestus across the border in southern Mozambique had developed resistance to pyrethroids. Four years after stopping DDT spraying, South Africa experienced the worst malaria epidemic since house spraying was first introduced in the 1950s.\(^4,5\) Appropriate trapping techniques and species identification confirmed the presence of A. funestus inside pyrethroid-sprayed houses and enzyme-linked immunosorbent assays showed a Plasmodium falciparum infectivity rate of 5.4% in these samples.\(^6\) Current research is aimed at determining the extent and distribution of resistant populations.

Insecticide resistance is now a major problem facing malaria vector control programs in most African countries with all three important vector species, A. gambiae, A. arabiensis (of the A. gambiae complex), and A. funestus, showing resistance to one or more of the insecticide classes used in vector control. There is obvious concern regarding the spread of the resistance and gene flow studies and distribution predictive modeling provide valuable data for use in control programs.

Early distribution maps\(^6,7\) reflected the distribution of entomologists rather than mosquito species and this has long been recognized as a limitation of these maps. More recent studies have also not adequately addressed this issue. Coetzee and others\(^8\) did not attempt to predict species distribution beyond actual collection points, but simply overlaid the collection data with temperature data. Lindsay and others\(^9\) used climatic and distributional data to predict species occurrence, but this resulted in maps with limitations that were obvious at the periphery of the species distributions, for example, A. arabiensis in South Africa was predicted to occur in areas of semi-desert with no rivers and extending down the southern coast to Cape Town. Discrepancies in such predictive models are obvious at the distributional limits of a species, but variation in species composition would not be easily detected in areas with large numbers of mosquitoes without real data to support the models.

The paper by Levine and others\(^10\) in this issue is an improvement on previous studies using spatial imaging. However, again there is a discrepancy between the predictions and reality, particularly obvious when A. quadriannulatus is considered. From what is currently known about A. quadriannulatus species A and B, it would appear that the former is restricted to southern Africa, south of the Zambezi River, while the latter is known only from the highlands of Ethiopia. Records from the islands of Zanzibar and Pemba are historical and it is doubtful whether the taxon still occurs there, if it ever did. However, the maps presented by Levine and others show that suitable habitats for these species occur widely throughout southern, eastern, and central Africa. The investigators’ suggestion that unknown biological species requirements determine distribution seems logical at first, considering that known climatic factors are not sensitive enough to correlate precisely with actual collection data. However, in southern Africa, much of central Botswana is semi-desert, unsuitable for A. quadriannulatus breeding and yet the predictive models do not detect this. It illustrates the limitation of computer modeling for species distribution, particularly where breeding sites in arid areas are highly localized at permanent springs, river edges, or irrigational projects, and are not affected by local rainfall.

There is no doubt that geographic information systems and distribution modeling are useful components of an efficient malaria control program where models are based on verified distributional data. They are best used at the regional level (www.malaria.org) for practical program management rather than on a continent-wide scale where resolution is coarse and applicability limited.

The extrapolation of African data to South America (Levine and others\(^10\)) to predict in retrospect which member of the A. gambiae complex was imported into Brazil during the 1930s was very interesting. Most African malariologists have always assumed that it was A. gambiae s.s. because of the ferocity of the epidemic. This is confirmed by the predictive model of Levine and others, and the consequences had Soper failed to eradicate the species, aptly summarized.

Author’s address: Maureen Coetzee, Vector Control Reference Unit, National Institute for Communicable Diseases, PO Box 1038, Johannesburg 2000, South Africa, E-mail: Maureen.coetzee@nhls.ac.za.
REFERENCES