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A global map of dominant malaria vectors

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Abstract

Background: Global maps, in particular those based on vector distributions, have long been used to help visualise the global extent of malaria. Few, however, have been created with the support of a comprehensive and extensive evidence-based approach.

Methods: Here we describe the generation of a global map of the dominant vector species (DVS) of malaria that makes use of predicted distribution maps for individual species or species complexes.

Results: Our global map highlights the spatial variability in the complexity of the vector situation. In Africa, *An. gambiae*, *An. arabiensis* and *An. funestus* are co-dominant across much of the continent, whereas in the Asian-Pacific region there is a highly complex situation with multi-species coexistence and variable species dominance.

Conclusions: The competence of the mapping methodology to accurately portray DVS distributions is discussed. The comprehensive and contemporary database of species-specific spatial occurrence (currently available on request) will be made directly available via the Malaria Atlas Project (MAP) website from early 2012.

Background

Global malaria vector maps, by necessity, must simplify a complex diversity of numerous interacting and sympatric anopheline species. Such simplification refines the information down to a minimum, indicating only the primary vector(s) at each location and provides users, such as public health officials, modellers and opinion formers, with a global and regional picture that is easy to digest and utilise for scientific, operational and advocacy purposes.

Global maps have long been used to aid in visualising the malaria problem. These include the vector species map of May [1] and the 12 zones of malaria epidemiology described by Macdonald [2], determined using broad climatic ranges and physical land features, as well as consideration of the known distribution of the major anopheline vectors at the time. More recently Mouchet *et al.* [3] updated Macdonald's map, reassigning the 12 zones into more conventional biogeographical regions. This history of malaria vector (or vector-associated) visualisation indicates a past appetite for such maps,

continuing more recently with Kiszewski *et al.* [4] publishing a global distribution map for the major malaria vectors in 2004. Their map was created to aid the authors in the development of a malaria transmission 'stability' map, but has since been adopted widely within the malaria research community and reproduced in many publications (their paper is listed as being cited 81 times in Web of Science and 37 times in PubMed). There is, therefore, a substantial and continuing demand for global maps of the major vectors of malaria.

Human malarial protozoa are transmitted by mosquitoes of the genus *Anopheles*, which includes 465 formally recognised species and more than 50 unnamed members of species complexes [5]. Approximately 70 of these species have the capacity to transmit human malaria parasites [6] and 41 are considered here to be dominant vector species/species complexes (DVS), capable of transmitting malaria at a level of major concern to public health [7].

A comprehensive database of contemporary occurrence data for the 41 DVS was compiled over two years, beginning in January 2008 [7-10]. Using these and other data (see methods), distribution maps were produced for each species or species complex, which have been made available for download via the Malaria Atlas Project

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