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Health in Action

Developing Global Maps of the Dominant *Anopheles* Vectors of Human Malaria

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Introduction

Despite advances in mapping the geographical distribution and intensity of malaria transmission [1,2], the ability to provide strategic, evidence-based advice for malaria control programmes remains constrained by the lack of range maps of the dominant *Anopheles* vectors of human malaria. This is because appropriate vector control depends on knowing both the distribution and epidemiological significance of *Anopheles* vectors [3]. Substantial investments by major donors in the distribution of long-lasting insecticide-treated nets and indoor residual spraying campaigns [4] are, therefore, not always fully informed by the basic biology of local anophelines.

Recent attempts to delineate *Anopheles* distributions have been conducted in Africa [5–11], the Americas [12–16], Europe [17], Central and South East Asia [18–22], and at the global scale [23–26]. The mapping techniques used in these various studies range from those based on expert opinion and simple interpolations to those employing more sophisticated statistical methods. Consequently, these studies are difficult to compare and impossible to synthesize globally. In addition, whereas in some regions *Anopheles* species distributions and their contribution to human malaria transmission are well known, uncertainty arises when suites of vectors contribute to local transmission, when the margins of the species ranges are poorly defined, and/or when there is simply a lack of any, or

reliably identified, distribution records. Furthermore, as many regions attempt to maintain their malaria-free status against imported malaria [27] and others consider their prospects of malaria elimination [28,29], contemporary maps of anophelines that are competent vectors for malaria are important in assessing local receptivity to reintroduction [30].

To help address these needs, the Malaria Atlas Project (MAP, http://www.map.ox.ac.uk) [31] has extended its activities to collate anopheline occurrence data to map the contemporary geographic distributions of the dominant mosquito vectors of human malaria. The plans for, and progress of, this initiative are described here.

Defining the Dominant Anopheles Vectors of Human Malaria

There are 462 formally named *Anopheles* species, with a further 50 provisionally

designated and awaiting description [32–34]. Of these, approximately 70 have been shown to be competent vectors of human malaria [35] and from this set, 52 candidate dominant vector species (DVS) were initially chosen for inclusion in the MAP vector distribution mapping project. These DVS are species (or species complexes) that transmit the majority of human malaria parasites in an area by virtue of their abundance, their propensity for feeding on humans, their mean adult longevity (only old individuals incubate the parasite long enough to transmit the disease), or any combination of these and other factors that increase overall vectorial capacity [36]. The DVS were the inclusive set of those species identified as "main" [37,38], "dominant" [24], or "principal" [23,25] in major reviews of *Anopheles* distribution and biology. The list was then further refined by anopheline experts from the Americas, Europe, Africa, Asia, and the Pacific, who co-author this article, to

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Abbreviations: DVS, dominant vector species; MAP, Malaria Atlas Project; MODIS, Moderate Resolution Imaging Spectroradiometer.

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