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Shifting priorities in vector biology to improve control of vector-borne disease

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Summary Vector control remains the primary measure available to prevent pathogen transmission for the most devastating vector-borne diseases (VBDs): malaria, dengue, trypanosomiasis, filariasis, leishmaniasis, and Chagas disease. Current control strategies, however, are proving insufficient and the remarkable advances in the molecular biology of disease vectors over the last two decades have yet to result in tangible tools that effectively reduce VBD incidence. Here we argue that vector biologists must fundamentally shift their approach to VBD research. We propose an agenda highlighting the most critical avenues to improve the effectiveness of vector control. Research priorities must be diversified to support simultaneous development of multiple, alternative control strategies. Knowledge across relevant diseases and disciplines should be better integrated and disease prevention efforts extended beyond the academic sector to involve private industry, ministries of health, and local communities. To obtain information of more immediate significance to public health, the research focus must shift from laboratory models to natural pathogen-transmission systems. Identification and characterization of heterogeneities inherent to VBD systems should be prioritised to allow development of local, adaptive control strategies that efficiently make use of limited resources. Importantly, increased involvement of disease-endemic country (DEC) scientists, institutes, and communities will be key to enhance and sustain the fight against VBD.

keywords arthropod vectors, capacity building, heterogeneity, transdisciplinarity, vector biology, vector control, vector-borne disease

Introduction

Despite remarkable advances in vector biology over the last two decades, vector-borne diseases (VBDs) remain a significant threat to human health worldwide (Hill *et al.* 2005). Control of arthropod vectors is the primary available intervention for some of the most devastating VBDs, particularly those lacking vaccines such as malaria, dengue, trypanosomiasis, filariasis, leishmaniasis, and Chagas disease (Gubler 1998). History shows that vector control – when done properly – can effectively reduce disease transmission (Townson *et al.* 2005). However, current control strategies are ineffective or insufficient to contain VBD (re-)emergence (Gubler 1998), and breakthroughs in genomics and molecular entomology have yet to result in improved public health outcomes (Fish 2008). The aim of this essay is to highlight persistent gaps in vector biology that hinder translation of basic knowledge into effective prevention strategies and to present a research agenda for new investigators in the field. Specifically, we outline key priorities we feel will markedly advance the field of vector biology and lead to significant reductions in disease burden:

- greater diversification and integration of vector biology research,
- transition from laboratory-based research to studies of field systems and conditions, and
- understanding and accounting for the role of heterogeneities in VBD systems.

A crucial ingredient of this agenda, and overall success, is the enhanced involvement of disease-endemic country (DEC) scientists and institutes.

Diversify and integrate research efforts

Vector biology is the study of arthropod vectors and their role in pathogen transmission. This field encompasses

entomology, ecology, microbiology, and epidemiology, and merges approaches ranging from landscape ecology to functional genomics. The diverse and integrated nature of vector biology is, unfortunately, not reflected in current research priorities. Here we argue that diversification of research priorities, integration of research efforts across disciplines, and extension of disease control efforts beyond the academic and health sectors is necessary for improved vector control.

Translation of basic research into effective tools to combat VBDs is impeded by this field's narrow focus. Over the past two decades, scientists have increasingly concentrated their efforts on genetic strategies to suppress vector populations or render them incapable of transmitting pathogens (Aultman *et al.* 2001). Although vectors rendered pathogen-resistant by genetic manipulation (Ito *et al.* 2002) or carrying life-shortening bacterial symbionts (McMeniman *et al.* 2009) offer promise, formidable technical, logistical, and political barriers will limit their effective public health application in the foreseeable future (Scott *et al.* 2002; Fish 2008). This emphasis has shifted attention and funding away from research areas that could provide more immediate, cost-effective impact on disease transmission, such as vector ecology and population biology (Curtis 2002; Tabachnick 2003). For example, knowledge of *Aedes aegypti* larval development sites and indoor resting behaviour has led to the development of container covers and insecticide-treated window curtains for low-tech and low-cost prevention of dengue (Kroeger *et al.* 2006). Conversely, surprisingly little is known of sand fly larval habitats, even though such information would improve control of these vectors of leishmaniasis, bartonellosis, and phleboviruses (Feliciangeli 2004). Diversifying the vector biology research agenda to include the ecology, behaviour, and population biology of vectors is necessary not only to ensure the success of genetic control methods (Scott *et al.* 2002), but also to provide alternative disease control tools.

Advancements in individual disciplines within vector biology have not led to significant reductions in the VBD burden (Hill *et al.* 2005). Active collaboration, communication, and coordination across disciplines and vector–pathogen systems are necessary to develop meaningful disease control tools (Moore 2008). For example, infectious disease research and control has clearly benefited from integrating evolutionary biology and medical sciences (Restif 2009). Collaboration between disciplines is facilitated by integrative publication platforms, trans-disciplinary meetings, and multi-disciplinary institutions. While many scientific journals focus on a single aspect of pathogen transmission, journals such as *Ecohealth* address the sustainable health of humans, wildlife, and ecosystems as a whole (http://www.ecohealth.net). *Ecohealth* encourages trans-disciplinary approaches to solving health problems (Wilcox & Kueffer 2008) as exemplified by recently published studies integrating landscape ecology with West Nile virus epidemiology (Irwin *et al.* 2008). Trans-disciplinary meetings such as the *European Molecular Biology Organization* Workshop on the Molecular and Population Biology of Mosquitoes and other Disease Vectors (Schneider & James 2006) are other desirable venues for active collaboration between disciplines. Similarly, integrative institutions such as the *Consortium for Conservation Medicine* (http://www.conservationmedicine.org) or the *Center for Infectious Disease Dynamics* (http://www.cidd.psu.edu) promote collaborative scientific research across disciplines.

Translating knowledge into effective and sustainable disease control strategies requires collaboration between not only scientists and health professionals, but also among the different public and private sectors that impact VBD (WHO 2004). For example, development activities such as agricultural irrigation, dam construction, and forest clearance can greatly affect VBD transmission, but are often planned without public health consequences in mind. Coordinating control efforts between relevant sectors (including health, agriculture, water, construction, and waste disposal) as well as target communities is a tenet of Integrated Vector Management (IVM; Box 1). Cooperation between health and agricultural sectors in rice-growing regions of Asia, for example, has lead to promotion of intermittent irrigation and coordinated insecticide application as avenues to improve control of malaria and Japanese encephalitis (WHO 2004; van den Berg *et al.* 2007). Involvement of private stakeholders may be instrumental in the funding and implementation of VBD control, as demonstrated by the successful malaria control campaigns mounted in Zambia by copper-mining companies (Utzinger *et al.* 2002).

Ultimately, engaging and sharing the decision-making process with target communities is essential. The attitudes and actions of local communities affect disease transmission. For any control effort, a wide gap may exist between theoretical efficacy and community effectiveness, the realised benefit when applied at the community level (Vlassoff & Tanner 1992). In Uganda, anti-malarial drug efficacy ranged from 50% to 90% in clinical trials, but community effectiveness was estimated to be only 4–6% due to problems associated with inadequate coverage, delay of treatment, incorrect drug dosage, and failure to complete treatment (Nsungwa-Sabiiti *et al.* 2005). Engaging local communities to understand and plan how to improve uptake or compliance may lead to greater and more sustainable impact on disease transmission than merely

Box 1 Integrated Vector Management (IVM)

IVM is a comprehensive strategy to suppress vector populations in a cost-effective, ecologically sound, and sustainable manner (WHO 2004). IVM emphasises tailoring control measures to local epidemiology and ecology, as well as public health infrastructure. To maximize the effect of limited resources, IVM advocates combining interventions to achieve a synergistic effect. By encouraging planning and evidence-based decision-making at the local administrative level, IVM promotes a bottom-up approach to managing VBDs. VBD control cannot be maintained by the health sector alone, so IVM promotes collaboration among public and private organizations whose projects (e.g. forest clearance, housing construction, road building, and dam construction) affect transmission. Furthermore, IVM seeks to engage local communities to ensure sustainability of disease control efforts (WHO 2004).

The concept of IVM for VBD control is not new. From 1930 to 1950, integrated malaria control programs in the copper-mining regions of Northern Rhodesia (now Zambia) successfully reduced malaria morbidity and mortality. In an economic analysis of these programs, Utzinger *et al.* (2002) stress that successful control of malaria was achieved by simultaneous implementation of multiple interventions. These interventions interrupted transmission at several 'vulnerable points' and reduced reliance on any single control measure (e.g. anti-malarial drugs, insecticides) to control malaria.

Another hallmark of IVM is to simultaneously target multiple diseases. Malaria interventions have also reduced lymphatic filariasis incidence in areas of co-occurrence in Africa and South East Asia. Because the vectors often share the same habitats and behaviors, control measures such as indoor spraying of residual insecticides, use of insecticide-treated nets, environmental management, and larviciding have been used to combat both diseases concurrently (Manga 2002; Prasittisuk 2002). Consequently, WHO recommends coordination of control activities between the Roll Back Malaria campaign and the Global Programme to Eliminate Lymphatic Filariasis (WHO 2004).

increasing efficacy of interventions (Vlassoff & Tanner 1992; Bryan *et al.* 1994).

Nevertheless, without sufficient incentive or demand for an intervention (i.e. 'market pull'), any disease control gains are likely to be unsustainable. The 'Health in Your Hands' initiative relied on public–private partnerships to encourage the use of soap in poor nations. Much of the success of this program was attributed to professional marketers who understood how to identify and create demand in the target population (Curtis *et al.* 2007). Similarly, application of marketing principles was successful in changing attitudes and creating a 'bednet culture' for malaria control in Tanzania (Heierli & Lengeler 2008). These examples highlight that understanding individual behaviour is essential to the design and implementation of interventions (Grier & Bryant 2005; Curtis *et al.* 2007; Elder & Ballenger-Browning 2009). The RE-AIM model (Reach, Efficacy, Adoption, Implementation, and Maintenance) for assessing public health interventions 'provides a framework for determining what programs are worth sustained investment and for identifying those that work in real-world environments' (Glasgow *et al.* 1999). In this model, reach refers to the level of participation by individuals, while maintenance describes the degree to which an intervention becomes part of an individual's routine or regular way of life. Simply put, interventions that are less efficacious in laboratories or controlled trials, but likely to be delivered to and adopted by more people in the community, may have far greater public health impact.

Move from laboratory systems to reality

Useful advances in vector biology are most likely to arise from research focused on the natural systems and conditions involved in human disease propagation. While laboratory studies of biological model systems have provided valuable information, insights have proven difficult to translate into effective control measures (Hill *et al.* 2005). The usefulness of laboratory systems for enhancing basic understanding is irrefutable. To provide insights of more immediate relevance to disease control, however, a paradigm shift is necessary. Whereas progress has historically been based on laboratory findings later transplanted to field situations, we feel model systems should now play a complimentary role to research focused primarily on natural systems and conditions.

Arguably the most spectacular recent progress in vector biology has been in genetics. This was achieved through methodological advances in molecular biology and sequencing of the genomes of key vector species (Hill *et al.* 2005). The 'genomic era' for vector biology was heralded by publication of the genome sequence of the African malaria vector, *Anopheles gambiae,* in 2002 (Holt *et al.* 2002). The genome sequences of two other mosquitoes (*A. aegypti* and *Culex pipiens*) followed, three more vector species genomes are underway, and others will surely follow. Genomic data of invertebrate vectors of human

pathogens have been made easily available through the web-based bioinformatic resource center VectorBase (Lawson *et al.* 2009). Such breakthroughs and resources have revived interest in developing genetic manipulation strategies to replace or eliminate natural vector populations (Aultman *et al.* 2001), identifying new molecular targets for insecticide design (Hemingway *et al.* 2002), and developing olfaction-driven vector control strategies (Justice *et al.* 2003). Despite two decades of considerable effort (Beaty *et al.* 2009), it has become clear that converting genomic innovations into effective disease control strategies will require a radical departure from traditional practices in vector biology (Hill *et al.* 2005).

Because findings from studies of laboratory systems do not necessarily translate to the field (Randolph & Nuttall 1994), it is crucial to move toward human disease systems. Focusing on field-collected samples of naturally co-evolved vector–pathogen systems will ensure the applicability of insights to natural settings. For example, knocking out genes in *A. gambiae* found critical for the development of parasites in a rodent malaria model had no significant effect on transmission of the deadliest human malaria parasite, *Plasmodium falciparum* (Cohuet *et al.* 2006; Michel *et al.* 2006). Using laboratory vector colonies introduces bias into genomic studies that may substantially reduce the relevance of results because adaptation to artificial conditions can cause rapid, significant reduction in genetic diversity (Norris *et al.* 2001). A single colony can differentially respond to strains of the same pathogen (Armstrong & Rico-Hesse 2001; Lambrechts *et al.* 2005), and independent colonies of the same vector may display distinct phenotypes even at the gene expression level (Aguilar *et al.* 2005).

When vector–pathogen systems cannot be studied directly in the field, genetically representative populations should be studied in an artificial environment that closely emulates natural conditions. Because environment can significantly influence not only overall fitness but also vector–pathogen interactions (Thomas & Blanford 2003; Lambrechts *et al.* 2006; Vaidyanathan *et al.* 2008), the impact of laboratory conditions on phenotypes should be compared to natural situations (e.g. food *ad libitum vs.* food limitation, regulated *vs.* variable temperature and humidity), especially for analysis of genetic expression profiles (Feder & Mitchell-Olds 2003; Gibson 2008). Such studies will identify environmental factors critical to the design of experiments and control interventions (e.g. Huho *et al.* 2007). Ultimately, field readiness of strategies should be demonstrated in contained, semi-field experimental environments that simulate natural ecosystems, such as giant outdoor cages (e.g. Ferguson *et al.* 2008).

Finally, translating novel ideas from basic biology into effective control strategies will occur only by promoting mutually beneficial interactions between laboratory and field research (Knols & Louis 2006). For example, rendering a vector population refractory to pathogen transmission by genetic manipulation in the laboratory assumes most wild vectors are susceptible. Frequent segregation of naturally occurring resistance alleles in anopheline populations (Riehle *et al.* 2006) indicates that we could manipulate or leverage these natural genes rather than introduce artificial transgenes. Additionally, field monitoring and periodic evaluation of control programs are necessary to identify potential deficiencies critical to the success of interventions, such as changes in vector behaviour or development of insecticide resistance. Thus, disease control programs must be adaptive, with periodic evaluation through surveillance and appropriate modification of interventions to sustain efficacy (WHO 2004).

Understand and account for heterogeneities

Heterogeneity can dramatically influence the dynamics of natural systems. This is particularly true for VBD systems, where heterogeneity may take many forms, with numerous consequences for disease dynamics and control interventions (Box 2). For instance, variation in vector–host contact can greatly amplify transmission as well as influence the individuals and locations where risk of pathogen transmission is greatest, with significant implications for VBD control (Woolhouse *et al.* 1997; Galvani & May 2005; Stoddard *et al.* 2009). Understanding natural heterogeneity and its relative importance in the transmission of pathogens or control of vectors will improve control strategies by identifying key variation undermining existing control efforts and targets for focused interventions.

Heterogeneity potentially complicates efforts to control vector populations and pathogen transmission when variation key to the dynamics of a VBD is not accounted for. Control efforts focused on larval development sites prove ineffective in the long term if highly productive sites are missed (Barrera *et al.* 2008). Spatial and temporal variation in vector densities makes vector control difficult, leading to inadequate control and subsequent reinfestation (Tarleton *et al.* 2007). Failure to protect individuals contributing the most to transmission, even if only a small group, can undermine large-scale vaccination campaigns (Anderson & May 1991) or bednet use (Smith *et al.* 2005). Even where effective, disease interventions can introduce heterogeneity and lower epidemic thresholds, increasing the potential for outbreaks (Smith 2005). The importance of heterogeneity is especially acute when resources are

Box 2 Heterogeneities and the dynamics of vector-borne diseases

Heterogeneity-variation in biological and environmental factors – potentially influences the population dynamics of vectors, hosts, and pathogens as well as interactions between them, with key implications for transmission and control (Smith *et al.* 2004). Frameworks for categorizing sources of heterogeneity abound (e.g. Anderson & May 1991; Smith 2005; Bansal *et al.* 2007; Real & Biek 2007), all generally distinguishing between 'endogenous' heterogeneity (e.g. variation in fecundity or other vital rates) and 'exogenous' heterogeneity (e.g. landscape structure). Importantly, heterogeneities may exist at any level of biological organization or spatio-temporal scale that influences population-level patterns (Anderson & May 1991; Lloyd-Smith *et al.* 2005; Bansal *et al.* 2007).

Why is heterogeneity or variation *per se* important and why can averages fail to provide accurate estimate of natural phenomena? Simply because natural systems are non-linear. This is illustrated by Jensen's inequality, which states that for any non-linear function, the function of the mean is not equal to the mean of the function, $f(\bar{x}) \neq \overline{f(x)}$ (Ruel & Ayres 1999). We can use the equation for vectorial capacity to illustrate the impact of heterogeneity (Dye 1986):

$$C = ma\frac{P}{F}\exp(\frac{-n}{E})E \qquad (1)$$

Here, vectorial capacity, C, describes the potential for transmission based on contact between hosts and infective vectors, where m *is the* vector density, a *the* daily biting rate, P/F the human biting rate (where P is the human biting index and F the interval between meals in days), n *the* extrinsic incubation period, and E vector longevity (note for this example, we ignore vector competence, which can also vary considerably among vector populations). Consider a scenario where there is slight variation in day-biting rate and in vector longevity among sites, plausible on the basis of variable environmental conditions within a region (Figure 1). If C is estimated from average parameter values across sites (triangle), it will be lower than the actual mean (diamond). Similarly, estimating local C from average parameter values (solid line) over- or under-estimates actual C significantly. Control efforts based on calculations using overall averages will likely be insufficient except in locations where vector densities are already low; locally-tailored control based on average parameter values will either be too little to effect desired reductions in transmission or will result in excessive and inefficient use of resources. This emphasises the importance of understanding the spatial scale at which key parameter values vary in order to properly target control interventions (Moore 2008).

Box 2 (*Continued*)

limited. Disease control programs often face the challenge of allocating scarce resources to suppress transmission, and control success is generally required to ensure ongoing provision of resources. Not understanding and/or not accounting for heterogeneity threatens the effectiveness and sustainability of control programs both in the short and long term.

On the other hand, heterogeneity can present an 'Achilles' heel' for VBDs. Identifying and understanding the most important sources of variation underlying disease or vector dynamics facilitates targeted control. For instance, larviciding campaigns focusing on the most productive larval development sites may lead to dramatic and cost-effective disease reductions (Gu *et al.* 2008). Control of the triatomine vectors of Chagas disease in South America became effective after recognizing that spatial variation in vector densities coupled with inadequate control and vector dispersal was driving reinfestations (Tarleton *et al.* 2007). Historic successes of IVM can partially be attributed to using combined interventions to address heterogeneities (Box 1). Successful targeted control requires identifying the sources of heterogeneity most relevant to disease transmission and most tenable to control. Variation in vector densities, for instance, has less relevance than heterogeneity in biting rates or vector population age structure (Box 2). Also, understanding the underlying mechanisms may be necessary for targeted control. For example, increased risk in one age group of the host population could be due to biting preference or to where that age group spends their time.

How do we begin to identify relevant heterogeneities? We suggest a combination of approaches. Analytical methods can identify factors that will alter transmission. Simple approaches (e.g. Box 2) can be very informative. More sophisticated methods such as individual-based and network models will be necessary to truly evaluate the importance of fine scale variation, such as individual differences in host movement patterns or vector biting preference (Bansal *et al.* 2007; Real & Biek 2007). Studies should be spatially explicit and take advantage of GIS/GPS and remote sensing technologies (Kitron 1998; Kalluri *et al.* 2007). Environmental heterogeneity must then

Site	m	a	N	E
1	9	0.1	12	20
2	75	0.05	12	15
3	78	0.2	12	25
4	23	0.15	12	20
5	91	0.25	12	20
6	24	0.15	12	25
7	50	0.1	12	20
8	33	0.2	12	20
9	96	0.15	12	25
Mean	53.2	0.2	12.0	21.1

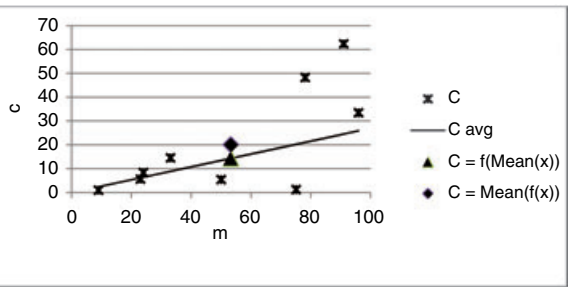

Figure 1 Example of heterogeneity affecting estimates of vectorial capacity, *C*. Vector densities, *m*, are estimated for nine sites and *C* estimated based on actual parameter values for each site or using an average for parameter values (line). Overall estimates for *C* were calculate either from average values across sites, $C = f(\bar{x})$, or from an average of *C* calculated for each site, $C = \overline{f(x)}$. Note that calculating *C* from mean parameter values will always be an underestimate in this instance because the relationships between *C* and *a* and *E*, respectively, are concave up (Ruel & Ayres 1999).

be assessed for structure, i.e. spatial and temporal autocorrelation, which is known to affect population dynamics (e.g. Hanski & Simberloff 1997; Roy *et al.* 2005). Quantification of fine-scale variation and movement among individual vectors or hosts is made possible by advances in genomics (e.g. Cohuet *et al.* 2008; Wong *et al.* 2008). Similarly, cohort-based methods promise to shine new light on the age structure of field populations (Carey *et al.* 2008). Finally, more research combining experimental with longitudinal studies of both entomology and epidemiology are needed to evaluate the effects of heterogeneities and the utility of targeted control efforts on the principal variable of interest: disease incidence (Scott & Morrison 2008).

The potential influence of heterogeneities on disease dynamics must be recognised even when they cannot be effectively characterised. Broad guidelines and uniform control are not effective and should be replaced by local, adaptive programs. An important challenge lies in identifying the right scale at which to focus and coordinate control (Box 2). Furthermore, while local, adaptive control programs promise to be more effective if well-informed (Box 1), they must be coordinated at a regional scale to avoid reintroduction of vectors and/or pathogens (Gurtler *et al.* 2007). Finally, because of the inherent variation in ecological, sociological, and epidemiological factors across disease endemic sites (Ellis & Wilcox 2009), there is great need for control programs to actively evaluate alternative interventions and share what they learn in a coordinated manner (*sensu* Sutherland *et al.* 2004).

A vision for vector biology

Our agenda acknowledges the complexity inherent in VBD systems and the implications for both research and operational control. Detailed understanding of VBDs and evaluation of a diverse array of control strategies must be promoted in areas where disease occurs. Doing so will require the local human and institutional capacity to conduct research and apply interventions. Sustainability is a principal issue for VBD control, and investing in human capacity is 'one of the most powerful, cost-effective, and sustainable means of advancing health' (White 2002). Not only are there too few vector biologists in academia in the developed world (Weller 1979; Reeves 1989; Fish 2001; Cuisance & Antoine Rioux 2004), but the capacity to study and manage VBDs is particularly weak in resource-poor DECs. Training opportunities in vector biology are limited because of the uncertainty of funding and the complicated nature of the field. Funding for DEC scientists is predominantly provided by multinational or foreign organizations (Nantulya *et al.* 2007), while for those in developed nations it often depends on the emergence of new diseases (e.g. West Nile fever in the USA or chikungunya in Europe). DEC scientists trained with the intention to return to work in local ministries of health or research institutes frequently do not, instead finding better job opportunities elsewhere. Curricula in vector biology are complicated by the multidisciplinary nature of the field, almost necessitating trans-disciplinary courses (e.g. the defunct Biology of Disease Vectors Workshop; see Beaty *et al.* 2009) and specialised courses in research method (Bates *et al.* 2006). Regional centers for tropical disease research would benefit both DEC and non-DEC scientists (TDR 2007). This would lead to productive collaborations such as those that led to breakthroughs in natural vector population genomics in Mali (Niaré *et al.* 2002; Riehle *et al.* 2006).

Research and implementation in disease-endemic areas should be conducted by local scientists. These individuals

need support from the broader scientific community. Not only do DEC researchers deal with limited local funding opportunities, but their science is often overlooked or not given due respect. Developing improved DEC capacity is not just an issue for funding agencies. Vector biologists can do more to foster growth and education in DECs, from providing informative and constructive manuscript reviews to cultivating knowledgeable scientists in DECs. Moreover, inclusion of in-country scientists in the development and evaluation of technologies will facilitate problem-ownership and technology transfer (Weatherall 2003), and will increase the use of technologies by the target community where these are considered risky (Knols & Louis 2006; Knols *et al.* 2007).

Improved access to scientific and medical knowledge is a fundamental requirement for the development of DEC research capacity (Cockerill & Knols 2008). While reference databases such as PubMed (http://www.ncbi.nlm.nih.gov/sites/entrez) and Google Scholar (http://www.scholar.google.com) permit easy access to abstracts of relevant literature, online open-access to full-text articles is necessary for DEC scientists to participate in the global debate on health issues, strengthen their collaboration with scientists in the developed world, and ensure local visibility of their own research. The knowledge management portal TropIKA (http://www.tropika.net) is one example of an initiative to make information more accessible. Most importantly, potential authors should strongly consider publishing in journals with open-access options such as the Public Library of Science (http://www.plos.org/journals) and BioMed Central journals (http://www.biomedcentral.com/browse/journals), and those participating in the HINARI network (such as this journal) established by the WHO (http://www.who.int/hinari/en/), which provides open-access to biomedical and health literature for individuals in developing nations.

Conclusion

VBDs are a global problem; their solution, however, begins locally. We reiterate that substantive reductions in VBD burden require modification of the current agenda in vector biology: diversify, integrate, and rebalance research effort among many research directions, refocus on systems of true relevance to human health, and consider the impact of natural heterogeneity to both research outcomes and operational control. Critically, realizing our vision for vector biology requires cultivation of local and independent capacity to conduct research and implement new control interventions in disease-endemic areas. Although our agenda includes issues long discussed in vector biology, these have not been adequately addressed. Overcoming these challenges will require not only the commitment of individual researchers, but also support from funding agencies and institutions. Our hope is to encourage new scientists in the field to tackle these problems, old and new, to ultimately reduce and control VBDs.

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