Dakar to Douala

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Malaria is an infectious disease that accounts for some 300,000 deaths every year in Africa. Whilst significant efforts over the last 20 years mean that this number is around half of what it was in the year 2000, it is still the biggest single disease killer across the breadth of Africa. The main contributors to the reduced death toll have been the widespread use of insecticide treated bednets, which stop infected mosquitoes from biting people and therefore infecting them, and the better use of drugs to treat disease. It is with renewed confidence then, that the global community has articulated a grand plan to eradicate malaria by 2040.

However, there are at least two challenges to this ambitious proposal. Just as we are starting to make real gains, the parasite is beginning to fight back. The progress that has been made is in danger of being reversed because the parasite is evolving resistance to our drugs and this resistance is spreading. Therefore a crucial part of the global strategy for malaria control is to monitor the spread of antimalarial drug resistance, and identify and contain drug resistant strains when they're found.

The second challenge relates to the changing nature of malaria transmission. As parasite prevalence drops, fewer people are infected. So malaria changes from being an endemic disease, where most people are infected most of the time, to an epidemic disease where new infections can arise in isolated groups of previously uninfected people. In such cases, it is not clear whether these new infections represent the recrudescence of local parasites or whether they are due to the importation of new parasites from elsewhere. Local malaria control strategies will differ greatly depending on which of these two scenarios best explains new infections.

Fortunately, there is an approach that can provide both up-to-date information about which drugs a parasite is resistant to and which populations it is related to: DNA sequencing. Drug resistance manifests itself as mutations in the parasite genome, and by comparing an unknown parasite genome to a reference database, we can understand where it comes from. Traditionally, genome sequencing has been expensive and lab-based, and global parasite reference datasets have been unavailable. But not any more.

Côte kwa pwani is a bold and innovative scientific expedition that will take the very latest mobile genetic sequencing technology into remote malarial regions of Africa and perform realtime genetic analysis of parasite DNA in the field. For the first time, this will allow scientists on the ground to test new malarial infections for the presence of drug resistance and to understand where they have come from. Côte kwa pwani is a collaboration between British and African scientists and a major ambition for the expedition is to raise awareness for the need for scientific training and infrastructure investment in Africa so that future African scientists can perform similar analyses to those undertaken during the expedition.

Deaths from infectious diseases are disproportionately concentrated in developing countries

The Global Burden of Diseases, Injuries, and Risk Factors Study (GBD) is a now annual analysis of the global, regional, and national trends in life, death and disability (Murray and Lopez, 2017). The GBD is a mammoth effort involving thousands of researchers and provides an incredibly useful window into the changing nature of life expectancy. Encouragingly, the most recent incarnation shows that mortality rates across all age groups have decreased over the last five years, meaning that people are generally living longer, healthier lives than they have done in the past. Despite this heartening news some 10.5 million deaths, or just under 20% of all globally were due to communicable, maternal, and neonatal causes (Abajobir et al., 2017). Nevertheless, roughly 50% fewer people died from HIV in 2016 than in 2006, with numbers for TB dropping by 20% and malaria by 25% over the same time period (Abajobir et al., 2017). Unfortunately, deaths from the most common infectious diseases, like HIV, TB, and malaria disproportionately effect those in the developing world.

Data on health outcomes is worse in developing countries

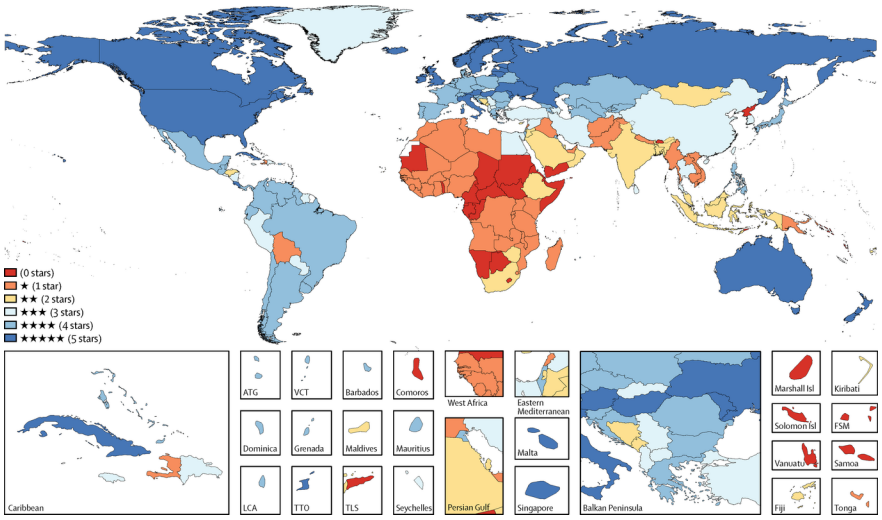

Figure 1: Classification of national time series of vital registration and verbal autopsy data, 1980–2016, on the basis of the fraction of deaths well certified and assigned to a detailed GBD cause (from (Abajobir et al., 2017)). This maps shows that poor quality data on the certification of death (0-2 stars) is concentrated in the developing world.

Building global data infrastructure to control infectious disease in the developing world

To achieve sustainable reduction of the large endemic burden of infectious disease in the developing world, it is necessary to have timely, relevant and actionable data - to understand what interventions are likely to be effective, to target available resources for maximum impact, to monitor whether or not interventions are having the desired effect, and to alert control programmes when new problems emerge, e.g. new strains of drug resistant or virulent pathogens. Recent technological and scientific advances provide many opportunities to tackle these problems, e.g. with mobile data collection, genomic pathogen surveillance, cloud data platforms, novel statistical and machine learning methodologies, sophisticated mathematical models for decision support. The benefits of these recent advances are already being realised in rich countries, e.g. in the National Health Service.

In many ways the need for such systems is greatest in the developing world, because infectious diseases are so deeply entrenched, and because the resources to tackle disease are limited, making it all the more important that effective interventions are chosen and that resources are allocated for maximum impact. However there are many practical roadblocks to putting such information systems in place. There is lack of local capacity, both for data generation and for data analysis. There is a lack of clarity about use cases for data, i.e. what are the practical decisions that need to be made in disease control, and precisely what data are needed to make these decisions? There is a need for tools and infrastructure that are suitable for resource-poor settings, e.g. for mobile data collection, pathogen genome sequencing, data integration and analysis. Data are highly fragmented, both within and between countries, and also between different infectious diseases.

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