Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Open source clinical science for emerging infections

Emerging infections cause justifiable global concern. Current outbreaks of avian influenza A H7N9[1] and the Middle East respiratory syndrome (MERS)[2] raise troubling memories of pandemic influenza and severe acute respiratory syndrome (SARS). With few mutations,[3-5] these or other pathogens could evolve to cause widespread outbreaks.

When new threats emerge, well established public health systems rapidly identify cases and evaluate sources, clinicians provide early descriptive case reports, and laboratories develop diagnostics and characterise pathogens. Clinical science is markedly less agile. We lack the tools to answer key questions rapidly. Who is susceptible, and why? What are the mechanisms of disease? What are the sites and dynamics of pathogen replication? How can early cases be identified and stratified? What is the clinical utility of new diagnostics? What treatments might work?

Each emerging infection presents these fundamental questions. The method of answering them need not be reinvented from one infection to the next. If clinical scientists across the world were able to agree on methods and cooperate, the results of separate studies from diverse locations and conditions could be collated, allowing clinically useful conclusions to be reached from shared data.

The International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC)[6] grew from the recognition that we have to do things differently, in the light of our experience during the epidemics of SARS, H5N1, and the 2009–10 influenza pandemic, but also regional epidemics of enterovirus 71, dengue, viral haemorrhagic fevers, and even during the rapid emergence of drug resistant malaria.[7] We must motivate and equip individual investigators and networks around the world to work together to rapidly answer basic questions when new threats emerge. Academic credit and access to data and samples must be given to clinical investigators, who often recruit patients in extremely challenging circumstances. Unlike the existing model that prioritises independence, effective collaboration should be rewarded. The core materials needed to enrol patients must be freely available, making it as easy as possible for investigators at the front line.

For the **ISARIC protocol** see http://www.prognosis.org/isaric

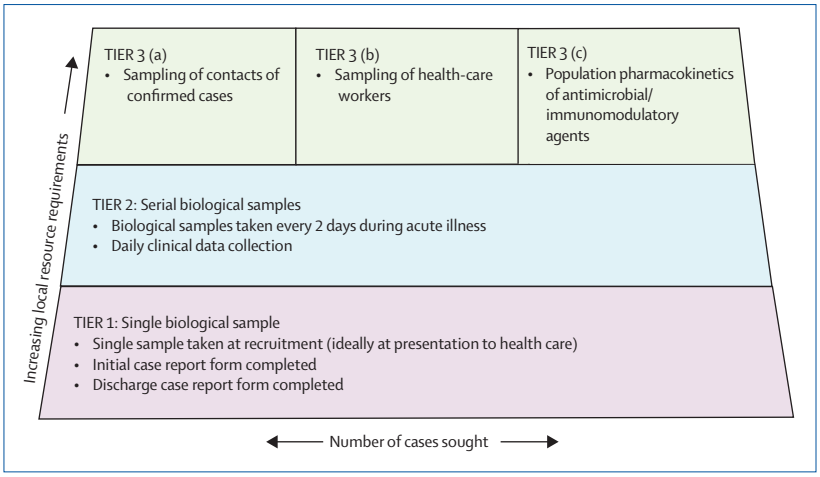

***Figure*: Stratified, modular framework of research studies enabling recruitment in a range of different conditions**

The core materials of clinical research—protocols, information sheets, consent forms, and case report forms—are analogous to the source code of computer software. In open-source software projects contributors receive recognition that builds their reputation within the software community. We propose a similar approach to clinical research, in parallel with the drive towards open access in academic publishing.[8] Although community projects have a long history in other fields, individual recognition is required for scientists to obtain funding and promotion; to succeed, academic institutions, funders, journals, the clinical science and public health communities, and the public need to be in full support.

To develop a consensus set of documentation, we engaged with investigators across countries and disciplines, in collaboration with WHO, in a systematic three-stage process: first, to agree criteria by which to prioritise and stratify studies; second, to identify important unanswered questions relating to pathogenesis, susceptibility, and pharmacology in severe infection; and to allocate studies within a globally scalable framework.

In the resulting protocol, research intensity is stratified according to the local costs incurred. The lowest tiers have a minimum requirement for staff and resources to recruit a case (figure), enabling adaptation for use in places with differing resource levels, and also in different phases of an outbreak. For example, early in an outbreak there are urgent questions that require

intensive study of a small number of cases; later, when larger numbers of cases present, it will be both more difficult and less important to obtain frequent serial samples.

ISARIC aims to reach a global consensus behind collection of harmonised clinical data linked with biological sampling protocols that are of value to anyone facing future outbreaks of any emerging infection. Importantly, our recommendations are not to be regarded as fixed and final, but an initial contribution to an evolving framework of research studies to which anyone, anywhere, may contribute and improve, and which will be openly shared in perpetuity.

We regard this consensus as essential but not sufficient. Here we lay the foundations for more challenging coordinated studies, including clinical trials of pathogen-specific therapies with pragmatic endpoints. We encourage clinicians everywhere to develop and share appropriate research protocols and seek approvals for clinical research that can begin immediately as soon as future epidemics threaten. Experience confirms that the time to act is now.

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See Online for appendix

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Vector control to eliminate artemisinin resistant malaria in the Greater Mekong subregion

The emergence of artemisinin resistance in the Greater Mekong subregion threatens to undermine global progress in malaria control.[1] Artemisinin derivatives are used in artemisinin-based combination therapy, the predominant first-line treatment for uncomplicated *Plasmodium falciparum* malaria.

Efforts to contain artemisinin resistance were launched in 2009 and have since been expanded.[2,3] The required intervention scale-up is substantial and costly; most of the funds were not available by early 2013. To accelerate progress, the Global Fund announced in February, 2013, that it would contribute US$100 million to help support the emergency response to artemisinin resistance.[4] Decisions on how best to allocate these resources are needed, including on how much to emphasise investments in vector control.[5,6]

The main vectors for malaria transmission are in the *Anopheles dirus* and *Anopheles minimus* complexes, occurring predominantly in forested areas. A third vector, *Anopheles epiroticus* (formerly known as *Anopheles sundaicus*), occurs mainly in coastal areas. These vectors exhibit substantial outdoor resting and feeding,[5,7] which could lead to the assumption that interventions used predominantly indoors, such as longlasting insecticidal nets and indoor residual