circulated in human beings for at least 50 years. Soon after its discovery, hMPV was identified in patients with respiratory disease all over the world, including North America, Australia, Finland, and the UK. Although initially hMPV was mostly found in young children with acute respiratory infection, severe acute respiratory infection associated with hMPV was subsequently also found in elderly and immunocompromised patients. The emerging picture of clinical symptoms associated with hMPV infection appears to be similar to the disease caused by human respiratory syncytial virus (hRSV). Cough, sore throat, rhinitis, and high temperature are the most common symptoms associated with hMPV infection, with wheezing, dyspnoea, pneumonia, bronchitis, bronchiolitis, conjunctivitis, and otitis media diagnosed in 10–70% of patients depending on the study population. It is important to note that screening of 400 samples from infants without respiratory disease symptoms in the Netherlands by hMPV RT-PCR revealed no positive samples, indicating that asymptomatic or subclinical infections are very rare.

Stockton and colleagues show that community-acquired influenza-like illness seen by general practitioners in the UK may also be caused by hMPV infection. In a recent study in the Netherlands, hMPV was identified in 3% of individuals reporting with influenza-like illness or other acute respiratory infection to general practitioners but in none of 397 matched healthy controls (Berrill Wilbrink, personal communication; National Institute of Public Health and the Environment, Bilthoven, Netherlands). In the Dutch study, hMPV was detected less frequently in individuals with influenza-like illness compared with other acute respiratory infections, which could explain the difference in the prevalence of hMPV in the community in the UK and the Netherlands in the same winter.

The currently available diagnostic methods to identify hMPV infections are more or less restricted to RT-PCR assays with primer sequences, which can probably be improved. Virus isolation proved to be relatively difficult, hence the late discovery of the virus, but may be improved in the near future. Serological assays to quantify virus-specific serum IgA, IgM, and IgG levels and development of antibody preparations for use in (direct) immunofluorescence will complete the set of tools generally used in virus diagnostics. All such diagnostic assays should take into account the genetic variation between hMPV isolates. At least two genetic lineages that display differences in serological reactivity circulate simultaneously around the world. Each of these two genetic lineages may be subdivided into two sublineages. It is tempting to speculate that viruses belonging to different genetic lineages can cause multiple hMPV infections in human beings. Indications for repeated hMPV infection in the same individual first came from serological data, and repeat infection was then shown in an immunocompromised child.

The recently discovered hMPV is a ubiquitous and important human respiratory pathogen that, although being a different virus of a separate Pneumovirinae family, shares many features with hRSV. hMPV can cause severe acute respiratory infection in young children, elderly people, and the immunocompromised, having its main clinical impact in the winter months at least in countries with moderate climate zone (figure). The overall burden of disease caused by hMPV infections needs to be further elucidated.

Genomics—a global public good?

In October, 2002, scientists published the sequence of the parasites responsible for most of the world’s human malaria, Plasmodium falciparum and P. yoelii, as well as the mosquito that carries it, Anopheles gambiae. The knowledge of these genomes and of the human genome, will lead to new drug and vaccine targets against malaria. But how fully will new genomics knowledge be used to the benefit of developing countries?

The WHO Advisory Committee for Health Research recently emphasised the relevance of genomic knowledge for health improvement in developing countries. However, as evidenced by the enormous inequities in global health and global health-research, knowledge—including genomics knowledge—is not developed to the optimum or used for improving the health of people in developing countries. In a closely interconnected world, this growing “genomics divide”...
will have global repercussions, including increased illnesses and instability. Genomics has significant characteristics as a global public “good”, but these are not fully developed in developing countries—thus collective action is needed.

Goods can be defined along a spectrum from pure “private” goods to pure “public” ones. Most goods are private in nature, having clear property rights associated with them. For example, an apple is first with knowledge and its consumption can be withheld until a price is paid (ie, it is excludable). Eaten by one person, an apple cannot then be eaten by someone else (ie, it is rivalrous in consumption). By contrast, the benefits of public goods are enjoyed by all (non-excludable) and consumed by one individual does not deplete the good and thus does not restrict its consumption by others (non-rivalrous). For instance, the internet is typically open to all (non-excludable) and downloading information does not deplete the information (non-rivalrous). Global public goods are simply public goods that possess such properties of publicness across national boundaries.

Genomics is principally about knowledge, which is commonly conceived to be the archetypal public good. Genomics knowledge is non-rivalrous in consumption (not depleted by use), and is usually made public by genomics databases and internet research, as was the case with the malaria and mosquito genome. It is a global public good in the sense of the knowledge not being bound by national border, in discovery, transmission, or use. Further, the global public-good nature of genomics is reflected in the way in which the Human Genome Project was funded and undertaken.

Although the development of genomics knowledge has significant global public-good characteristics, its application, especially at the individual level, may have private good characteristics (excludable and rivalrous in consumption). For example, consumed by one individual, an antimalarial drug cannot also be consumed by another. However, the application of genomics at the population level—such as by genetically altering mosquitoes to block the cycle of parasite transmission—retains significant public-goods characteristics. The incidence of malaria infection will be reduced both in the region where the modification is done as well as in other regions to which the modified mosquitoes spread. The effects of these interventions are therefore non-excludable and non-rivalrous in consumption.

This analysis shows that genomics knowledge and its application have, in principle, considerable global public-good characteristics. However, in practice, genomics knowledge and its application do not always express these characteristics. Although knowledge is theoretically free to be disseminated, in practice constraints are often put on its use. To absorb and make use of scientific knowledge, considerable investment is required. For example, education and training, physical access to journals or the internet, research infrastructure, and the ability to establish the necessary production processes to turn genomic knowledge into a useful product, all challenge the ability to make practical use of genomics knowledge.

The international patent system can accentuate this problem for developing countries. Genomics is only a public good to those countries that have the capacity to exploit genomics knowledge and to conduct genomics research. Because of the need for these “access goods”, genomics becomes a “club good”, accessible mainly to industrialised countries.

The global public-good concept, applied to genomics, highlights three important issues. First, as with knowledge, the free-market does not have an incentive to produce a non-excludable good since a price cannot be charged, and thus different mechanisms for finance or production are required.

Second, in developing countries, because of the lack of access goods, genomics becomes a club good. Finally, to achieve the best global production and use of genomics, collective action is required.

Collective action will be required in many areas, including efforts to improve research infrastructure, education, and training to provide developing countries with the access goods they need. These steps will require a financial commitment on the part of industrialised country governments—as highlighted in the recent Commission on Macroeconomics and Health—and the sharing of relevant intellectual property by multinational corporations, for example through public-private partnerships such as the Malaria Vaccine Initiative and the Medicines for Malaria Venture. A global genomics initiative—in partnership with developing countries—would provide a suitable forum to discuss and develop these steps, and strengthen global genomics governance.

The global public-goods lens magnifies the failures of the global community to realise the full potential of genomics, and shines a light on needed collective actions to harness genomics to improve global health-equity.

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