Medical Xpress

Will genomics help prevent the next pandemic?

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This week, the Public Library of Science, an open-access publisher, presents the "Genomics of Emerging Infectious Disease," a collection of essays, perspectives, and reviews that explores how genomics—with all its associated tools and techniques—can provide insights into our understanding of emerging infectious disease.

As pandemic H1N1 2009 influenza (commonly referred to as swine flu) continues to spread around the globe, people want to know if this flu poses more of a threat than other seasonal flu strains, how fast it's spreading (and where), and what can be done to contain it. The increasing speed at which complete genome sequences and other genome-scale data can be generated provides tremendous opportunities to address these questions by identifying the molecular changes in disease agents such as influenza viruses that will enable us to track their spread and evolution and to generate the vaccines and drugs necessary to combat them. The "Genomics of Emerging Infectious Disease" collection discusses the challenges involved and how scientists and public health professionals might take advantage of these opportunities and advances to prevent the next pandemic.

Emerging infectious diseases are caused by a wide range of organisms, but they are perhaps best typified by zoonotic viral diseases, which cross from animal to human hosts and can have a devastating impact on human health. These zoonotic diseases include monkeypox, Hendra virus, Nipah virus, and severe acute respiratory syndrome coronavirus (SARS-CoV), in addition to influenza A and the lentiviruses (HIV) that

cause AIDS. As Albert Osterhaus and colleagues from the Erasmus Medical Center, Rotterdam, The Netherlands, point out in their article in the collection, the apparent increased transmission of pathogens from animals to humans over recent decades can be attributed to the unintended consequences of globalization as well as environmental factors and changes in agricultural practices.

Articles in the collection also shine a spotlight on specific pathogens, some familiar and widespread, such as the influenza A virus, some "reemerging," such as the Mycobacterium tuberculosis complex that causes tuberculosis, and some identified only relatively recently, such as the bacterium *Helicobacter pylori*, which is associated with peptic ulcers and gastric cancer. Others discuss the broader implications of genomics research in this area, such as what it means for researchers in developing countries or for our biosecurity. As Jacques Ravel and colleagues from the US University of Maryland School of Medicine note, genomics can and should be used proactively to build our preparedness for and responsiveness to biological threats.

The collection is a collaborative effort that combines financial support from Google.org [http://www.google.org/predict.html] with PLoS's editorial independence and rigor and the expert opinion of leading researchers from several different disciplines. Rajesh Gupta from Stanford University, and colleagues provide Google.org's perspective and vision for how systematic application of genomics, proteomics, and bioinformatics to infectious diseases could predict and prevent the next pandemic. To realize this vision, they urge the community to unite under an "Infectious Disease Genomics Project," analogous to the Human Genome Project.

Jonathan Eisen, a Professor at the University of California, whose laboratory is in the UC Davis Genome Center, is the Editor of this PLoS collection, which includes 14 articles—all publishing on 26 October

2009—from six different PLoS journals (*PLoS Biology*, *PLoS Medicine*, *PLoS Computational Biology*, *PLoS Genetics*, *PLoS Neglected Tropical Diseases*, and *PLoS Pathogens*), reflecting the multidisciplinary nature of the topic.

Many scientific journals produce special issues on a topic of interest for their audiences. However, open-access publishing, such as that done by the Public Library of Science, makes it possible to have such a large multidisciplinary cross-journal collection simultaneously available online for unrestricted reuse, regardless of venue. As outlined in the collection's editorial published in PLoS Biology, this collection will add to other "open science" activities that have helped provide insights into infectious disease more quickly than would have been thought feasible only a few years ago.

The faster, cheaper, and more openly we can distribute the discoveries of science, the better for scientific progress and public health. Managing the threat of novel, re-emerging, and longstanding infectious diseases is challenging enough even without barriers to scientific research.

More information: Link to the final online location of the Collection (active at 9AM Pacific on 26th October; please use this link in your coverage): ploscollections.org/emerginginfectiousdisease/

Source: Public Library of Science (news : web)

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