Sharing data key to tackling major disease outbreaks

An EU-funded project has pioneered new techniques to detect and share information about infectious disease outbreaks. These methods will be used in the future to improve public health responses to pandemics. Already, some of the tools devised in the project are being further developed to specifically tackle the spread of COVID-19.

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As the world now knows only too well, a lack of preparedness and a sluggish response to a suspected disease outbreak can have devastating health consequences.

The global coronavirus pandemic has laid bare the fact that rapidly detecting the existence and spread of a disease outbreak – and sharing this information - is crucial to limiting its impact. In effect, this is the critical first step that public health bodies must take when dealing with a health crisis of this kind.

The COMPARE project was launched in 2014 to assess the potential of using next generation sequencing (NGS) data to survey, diagnose and detect disease outbreaks.

“NGS is a technique that enables scientists to rapidly determine a complete or a specific part of a genome (the complete genetic composition of an organism),” explains Prof Frank Aarestrup, Head of Research Group at the National Food Institute, Technical University of Denmark. “It also helps researchers to recognise pathogens (the agents responsible for diseases such as bacteria, viruses, etc.) via their genetic information.”

Although initiated years before the current pandemic, the project’s findings could have important implications for how we tackle this, as well as the next, disease outbreak.

Sharing outbreak data

Aarestrup and his team were interested in finding out if NGS technology could lead to more effective responses to a wide range of communicable disease threats. “Our aim was to develop a solution to collect, process and analyse sequence-based pathogen data,” he notes. “If this data was then combined with other clinical data, it could provide public health authorities with vital information. This could help them to decide if rapid action in response to a disease outbreak is required.”

The COMPARE project began by demonstrating how NGS technology could be used to sample, collect and sequence outbreak data. One interesting element was proving the usefulness of metagenomics. This is the study of genetic material recovered directly from environmental samples. Aarestrup and his team showed how antimicrobial resistance and viruses could be detected and analysed in sewage collected globally.

The team then sought to develop solutions to ensure that such data can be shared across the scientific community, among different countries and institutions.

“COMPARE is fully in line with the ambitions and principles of open science”, says Aarestrup. “We developed novel solutions for sharing sequencing data between countries and scientists. And we showed the value of NGS for detecting foodborne diseases, diagnosing clinical pathogens and identifying outbreaks.”

Ready for future outbreaks

The results of the COMPARE project are being sustained through a user-friendly data upload and analysis platform, made up of datahubs. This is where all NGS data can be shared in the public domain. The platform addresses issues such as the long-term storage of high-density data, and the need to make such data easier to find and re-use.

“This concept will be further developed through the H2020 projects RECODID and ECRAID,” says Aarestrup. “In the recently launched H2020 VEO project, core members of the COMPARE consortium will take the COMPARE results even further. A versatile forecasting and tracking system will be established.”

This will also serve as an interactive observatory to generate and distribute information for risk assessments and the monitoring of emerging infectious diseases. Many of the project’s activities are being expedited due to the current COVID-19 outbreak.

“COMPARE has changed the landscape of emerging infectious diseases, foodborne pathogens and clinical investigations,” says Aarestrup. “At the beginning of the project, combining different disciplines, such as focusing on specific pathogens or even specific species, was a challenge.”

Aarestrup believes that, at least in some cases, such barriers have been successfully broken down. This will help to ensure that important data is even more widely shared across multiple scientific disciplines. “Even though further work is still needed, this has also been a major success of the project,” he says.

Project details

- Project acronym: **COMPARE**
- Participants: Denmark (Coordinator), Belgium, France, Germany, Greece, Hungary, Italy, Netherlands, Spain, UK, Australia
- Project N°: 643476
- Total costs: EUR 20 847 771
- EU contribution: EUR 20 817 771
- Duration: December 2014 to November 2019

See also

More information about project COMPARE:
https://cordis.europa.eu/project/id/643476

View the article online:
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