European Management Platform for Emerging and Re-emerging Infectious Disease Entities (EMPERIE)

Research Areas

- Tool Development
- Basic Research
- Data-Sharing Enabler

At a Glance

- Status: Completed Consortium
- Year Launched: 2007
- Initiating Organization: European Commission Sixth Framework Programme (FP6)
- Initiator Type: Government

Abstract

The European Management Platform for Emerging and Re-emerging Infectious Disease Entities (EMPERIE) consortium brings together international experts of different disciplines in an efficient and decisive collaborative network to coordinate the response and control of an emerging new disease.

Mission

The EMPERIE mission is “to contribute to effectively countering the potential public health threat caused by new and emerging infectious diseases in Europe by establishing a powerful network capable of structural and systematic prediction, identification, modelling and surveillance of infectious diseases health threats and pathogens.”

In pursuit of this mission, EMPERIE will establish and maintain three integrative platforms: (a) virus discovery and sequencing platform — using common tools, procedures, methods, and technology to rapidly isolate, identify, and characterize (novel) viruses in animal and human samples; (b) technology and knowledge development platform — developing the virus discovery and sequencing platform,
European Management Platform for Emerging and Re-emerging Infectious Disease Entities (EMPERIE)

Consortia-pedia

EMPERIE focuses on animal species that have previously shown to be an imminent health threat to humans: birds, bats, pigs, rodents, and arthropods, such as flies and mosquitoes.

Consortium History

May 2009: Program launched.

Financing

Funded by the European Seventh Framework Programme.

Impact/Accomplishment

EMPERIE started its activities in May 2009, at the start of the first influenza pandemic of the 21st century. This pandemic prompted EMPERIE to postpone a significant portion of its originally planned activities to focus on influenza A/H1N1v. Several studies on the epidemiology, antigenic and genetic characteristics, replication-kinetics, re-assortment potential, pathogenesis, and transmission of this novel pandemic virus were conducted by EMPERIE partners, providing valuable information for the development of risk assessment and containment strategies. In addition, novel serological assays, real-time reverse transcription (RT) polymerase chain reaction (PCR) methods specific to pan-influenza and influenza A/H1N1v, and indexed (multiplex) 454 whole influenza genome sequencing methods were developed.

In Year 2, EMPERIE shifted its main focus back to the originally planned deliverables. Since its start, EMPERIE has collected and analyzed a wide range of samples (e.g., blood, fecal, respiratory, cerebrospinal fluid) covering different viruses (e.g., influenza viruses, West Nile virus, coronaviruses, Bluetongue virus, and Crimean Congo Haemorrhagic Fever virus) and different reservoir species (e.g., bats, pigs, arthropods, birds, and humans) from different regions in Europe, Asia, and Africa. These
samples are used for virus discovery and for development and validation of EMPERIE’s technological platforms. Standard operations procedures (SOPs) for generic PCRs for adeno-, annello-, asfar-, astro-, corona-, flav-, herpes-, orthomyxo-, pappilloma-, paramyx-, picorna-, picornabirna-, polyoma-, pox-, reo-, and rhabdoviruses are available as well as different cell cultures and SOPs for ribonucleic acid (RNA) purification for rapid prescreening, characterization, and identification of (novel) (sub)types of viruses as well as for next-generation sequencing.

During EMPERIE’s first three years, more than a dozen novel viruses, or known viruses identified in certain host species for the first time, have been identified and characterized using the technologies established in EMPERIE. Examples include novel astroviruses and a novel orthobunya virus (Schmallenberg virus).

Important steps were made in the field of coronaviruses, with new findings on virus persistence and underlying mechanisms of host innate immunity, host tropism, and virulence. In Year 3 significant progress can also be reported in modeling work. Models for emerging or endemic vector-borne diseases, and analysis techniques for integrating multiple epidemiological data streams in pandemics and for inferring epidemic dynamics from sequence data, were published, and the work on optimizing syndromic surveillance for detecting case clusters is nearing completion.

Several papers on phylogenetic/antigenic methods for predicting pathogen emergence have been published that are foundational for the development of strategies to minimize antigenic evolution of an emerging pathogen — to be able to minimize antigenic evolution, one must (likely) first have to understand the potential variation.

Clinical microbiology training programs have been conducted at various sites in Indonesia, Nepal, and Ghana on Good Clinical Practice (GCP), quality assurance/quality control safety, ethics, database entry, and maintenance. Laboratories in Ha Noi, Vietnam, have been upgraded, and staff has been trained in the molecular diagnostic procedures.

**Links/Social Media Feed**

Homepage  
http://emperie.eu/

**Points of Contact**
Martine van Roode
Erasmus Medical Center, Viroscience Lab
phone: +31 (0)10 704 3665

Sponsors & Partners

Academic Medical Center
Consejo Superior de Investigaciones Científicas
Erasmus MC
Friedrich Loeffler Institut
Genome Research Ltd.
Imperial College
Institut Pasteur
Universitäts Klinikum Bonn
University of Cambridge
University of Hong Kong
University of Oxford
ViroClinics Biosciences

Updated: 04/15/2016