

PREPARE

Platform foR European Preparedness Against (Re-)emerging Epidemics



What is PREPARE?

PREPARE is a clinical research network established with support of European Union funding running from 1 February 2014 to 31 January 2019. The challenge of **PREPARE** is to build Europe's capacity for harmonised large-scale clinical research studies on infectious diseases (ID), prepared to rapidly respond to any severe ID outbreak and providing real-time evidence for clinical management of patients and for informing public health responses.

Main Achievements of PREPARE

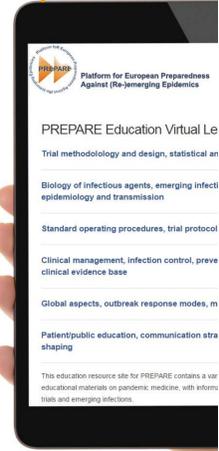
WP1 EARL: Ethical, Administrative and Logistical solutions



The EARL Workpackage (WP1) aims to identify bottlenecks and barriers to the rapid set up and conduct of clinical trials in Europe in response to severe infectious disease outbreaks, and provide solutions to overcome these hurdles. A report on ethical, administrative, regulatory, logistical and clinical bottlenecks that prevent rapid clinical research responses in EU Member States was completed.

WP9 CREATE: Clinical Research Education And Training in Europe

The Education and Training Workpackage - CREATE (WP9) aims to be an unique on-line open access and face-to-face education and training curriculum that comprehensively addresses the issues relevant to empower or ensure the incorporation of laboratory and clinical research and the results thereof, in the response to emerging epidemics. In conjunction with ERS WP9 has created the PREPARE Virtual Learning Centre (VLC).



WP3 PRACTICE A: MERMAIDS

The Workpackage PRACTICE A (WP3) aims to deliver a large-scale prospective observational study of infections with epidemic potential in Europe.

WP4 PRACTICE B: ALIC⁴E

The Workpackage PRACTICE B (WP4) aims to design and deliver the largest-ever pragmatic, publically funded randomised trial of antivirals for influenza-like-illness in primary care.

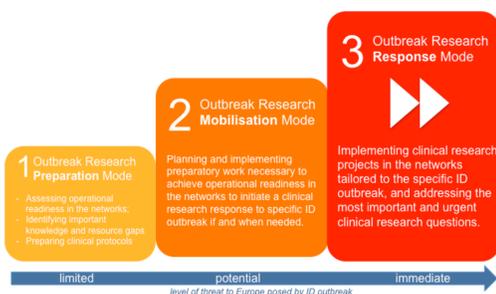
WP5 PRACTICE C: AD-SCAPE

The Workpackage PRACTICE C (WP5) aims to evaluate different treatment options for patients with community acquired pneumonia (CAP), who require invasive mechanical ventilation, and are admitted to the ICU.

The protocols for the "inter-epidemic" large scale observational MERMAIDS studies on (1) Arboviral infections affecting the central nervous system, (2) undifferentiated fever in infants, (3) pathogenesis of acute respiratory infections are in a final stage of development. Both adaptive trials, one in Primary Care sites (ALIC⁴E), and one in Intensive Care Units (AD-SCAPE) of three arms – antibiotics, steroids and a ventilator strategy, will start very soon.

The protocols for the observational and intervention studies were prepared in close collaboration with the pathogenesis, diagnostic and IT workpackages, and training of the sites will be provided with support of the workpackage on Education and Training.

Outbreak Response Modes



In addition to the 'inter-epidemic' activities, PREPARE can initiate ad-hoc activities in response to infectious disease outbreaks of concern. When responding to an actual ID outbreak, the scope and scale of the outbreak response of PREPARE can vary with each specific ID outbreak. PREPARE therefore distinguishes between three Outbreak Modes as described in the figure. For the Ebola Virus Disease (PREPARE outbreak mode 1), a web-based survey identified gaps in preparedness in European hospitals to assess and manage the risk of possible spread of Ebola Virus Disease and the results were published in Euro Surveillance.

PREPARE publications

1. de Jong et al. Preparedness for admission of patients with suspected Ebola virus disease in European hospitals: a survey, August - September 2014. Euro Surveill. 2014; 19(48): pii=20980. and a response to correspondence concerning this article was published in Euro Surveill. 2014; 19(50): pii=20990.
2. Sabirova et al. Whole genome mapping as a fast-track tool to assess genomic stability of sequenced Staphylococcus aureus strains. BMC Research Notes 2014; 7:704.
3. Sabirova et al. Complete genome sequences of two prolific biofilm-forming Staphylococcus aureus isolates belonging to USA300 and EMRSA-15 clonal lineages. Genome Announc. 2014; 2(3). Pii:e00610-14.
4. Xavier et al. Employing whole genome mapping for optimal de novo assembly of bacterial genomes. BMC Research Notes 2014; 7:484.
5. Koel BF et. al. Identification of amino acid substitutions supporting antigenic change of influenza A(H1N1)pdm09 viruses. J Virol 2015; 89:3763–3775. doi:10.1128/JVI.02962-14.

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