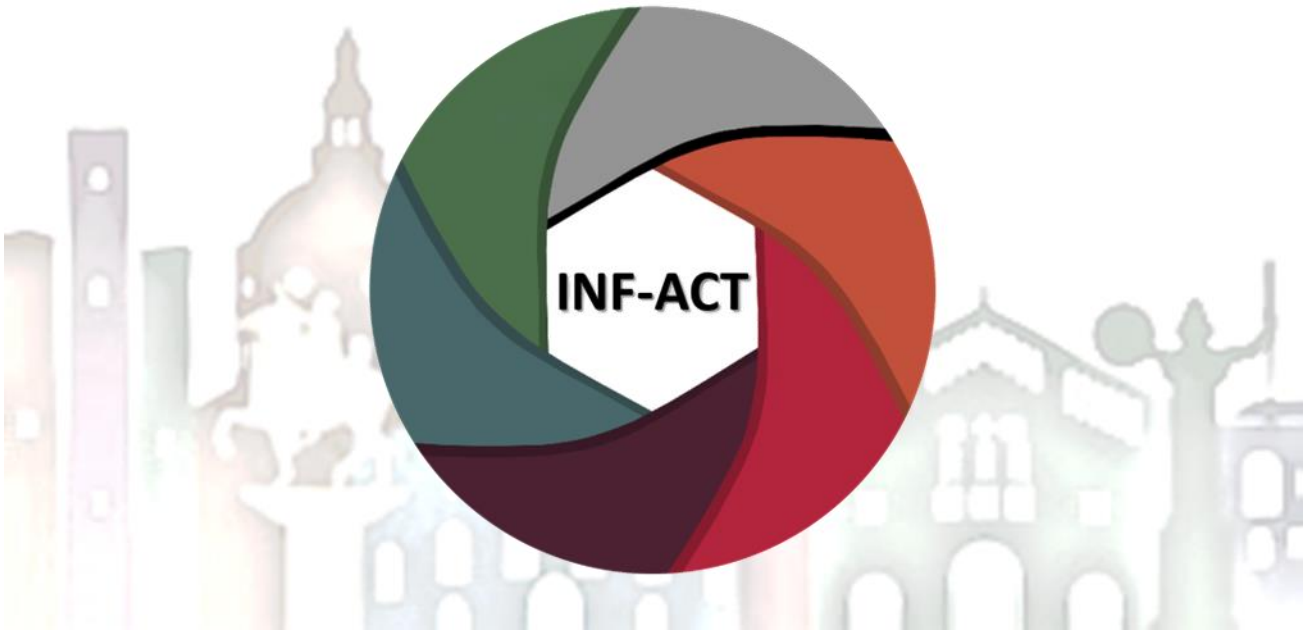
Finanziato dall'Unione europea NextGenerationEU
Ministero dell'Università e della Ricerca
Italiadomani PIANO NAZIONALE DI RIPRESA E RESILIENZA

INF-ACT MEETING 2024

11-12 SEPTEMBER 2024, PAVIA (ITALY)



ABSTRACT BOOK

of monitoring AMR trends in pediatric hospital settings, to identify emerging threats, tailor treatment guidelines, and promote antimicrobial stewardship programs.

Keywords: Paediatrics, multidrug resistance, trend

P92. Full genome characterization of the first Oropouche virus isolate imported in Europe from Cuba

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On May 27, 2024, the Cuban Ministry of Public Health reported the first Oropouche fever outbreak on the island. Oropouche virus, the etiologic agent, is a poorly studied arbovirus, responsible for several outbreaks since the early 1960s and represents a public health burden to various countries in Latin America. Analysis of Oropouche virus genomes can reveal the evolutionary forces that shape its genetic diversity. We report full genome characterization of a viral isolate from a returning traveller presenting Oropouche fever. Viral isolates were obtained from serum, and full genome sequencing was performed by Illumina sequencing. A subsequent phylogenetic analysis, coupled with genetic variability studies, was conducted to confirm the virus' origins and evolution. whole-genome sequence phylogenetic analysis showed that the most closely related sequence was from French Guiana 2020 outbreak. Interestingly, the sequence of our isolate was included in a highly supported monophyletic clade containing recent cases (Brazil 2015 - Colombia 2021) that clearly separated from the clusters of the other four previously known genotypes, suggesting a possible new genotype. These findings suggest these cases derive from the viral strain that is sustaining the present outbreak in Cuba and could reflect the genetic characteristics of the viral strain involved in the outbreak ongoing in Latin America. Additional studies are needed to understand if Oropouche virus is evolving towards the development of traits that favour its geographical spread through the adaptation to new environments, development of new characteristics including arthropod-vectors tropism, and availability of different amplifying host(s).

Keywords: Oropouche virus, phylogenesis, surveillance, sequencing

P93. COVID-19 cases and monthly all-cause, cancer, CVD and diabetes mortality in 16 countries, 2020-2021

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Background: The COVID-19 pandemic has been associated with increased mortality from various chronic diseases. This study evaluates the monthly excess mortality from all causes, cancer, cardiovascular disease (CVD), and diabetes during 2020 and 2021, examining its correlation with COVID-19 cases.
Methods: Monthly cause-specific mortality data were obtained from national statistical offices' public repositories or obtained directly from them upon request. Population data were obtained from the United Nations archives. Excess deaths were calculated as the difference between observed and expected deaths, with expected deaths for 2020 and 2021 estimated using a quasi-

Poisson regression model fitted on 2010-2019 data (or a shorter available period). The correlation between COVID-19 cases and monthly excess mortality was quantified using Spearman's correlation coefficient (r).
Results: The study included 16 countries (Argentina, Austria, Brazil, Switzerland, Chile, Czech Republic, Germany, Georgia, Hungary, Italy, Latvia, Lithuania, Mexico, Serbia, Slovakia, and the USA). A positive correlation between COVID-19 cases and monthly excess mortality was observed for all causes in all countries (r: 0.61 to 0.91), for CVD in 11 countries (r: 0.45 to 0.85), and for diabetes in 13 countries (r: 0.42 to 0.79). Excess mortality above 5% was identified for all causes in 14 countries in both 2020 and 2021, for CVD in seven countries in 2020 and nine in 2021, and for diabetes in 10 countries in 2020 and 11 in 2021. No significant excess cancer mortality was observed.
Conclusions: Excess mortality from CVD and diabetes persisted through 2021 in several countries, aligning with COVID-19 peaks and indicating a short-term impact of the pandemic on mortality from vascular and metabolic diseases but not cancer.

Keywords: COVID-19; excess mortality; cancer; cardiovascular diseases; diabetes.

P94. Development of a safe viral vector-based neutralization assay platform for arboviruses

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Background: The impact on public health of emerging and re-emerging arthropod transmissible viruses (arboviruses), has dramatically increased in the past decades. Insect vectors and associated arboviruses, such as Dengue (DENV), Zika (ZIKV), West Nile (WNV) and Chikungunya (CHIKV) viruses, have been spreading into new tropical, subtropical, and temperate areas, including Italy. Virus neutralization is the gold standard for determining antibody efficacy against viral infections, and bioassays to measure serum neutralizing antibodies (nAbs) are crucial tools for serological monitoring of arboviral infections. However, neutralization tests are generally performed using infectious virus in appropriate laboratory containments (BSL-3 or 4), involving important safety and technical issues. Our goal is to develop and optimize a high-throughput and safe pseudovirus-based platform for the safe evaluation in BSL-2 laboratories of nAbs present in sera of humans and animals infected with arboviruses, thus avoiding the use of replication competent infectious viruses in BSL-3 laboratories. The platform employs a Yellow Fever Virus (YFV)-based vector expressing luciferase to produce non-replicating single-round infectious particles (SRIP-Luc) pseudotyped with homologous and heterologous prME glycoproteins (SRIP-Luc/prME) from representative Flaviviruses, including YFV, ZIKV, DENV, WNV and Japanese encephalitis virus (JEV).
Methods: SRIP-Luc/prME were produced on 293T cells by using a YF-based replicon plasmid expressing the nanoluciferase, a plasmid codifying the YF capsid and the prME-plasmids. Infectivity and titres of SRIP-Luc/prME pseudoviruses were evaluated on VERO cells using serial 2-fold dilutions of each preparation. Luciferase activity was measured at 72 hrs using a Victor Nivo luminometer (Perkin Elmer).
Results: SRIP-Luc/prME for each flavivirus were generated and titrated and all produced prME pseudotyped SRIPs were infectious. The pseudovirus preparations will be used to evaluate the presence of nAbs in sera from Flavivirus infected individuals previously characterized by molecular and serological assays. Following optimization, this platform will enable rapid, safe and versatile quantification of antiviral nAbs.

Keywords: Flavivirus, Arbovirus, pseudovirus, neutralization assay, neutralizing antibodies