and designed to produce VLPs in vaccinated individuals, for the construction of a Zika virus (ZIKV) vaccine.

**Methods & Materials:** Two MVA-VLP vaccine candidates have been developed from ZIKV strain Suriname 2015 sequences: one expressing pre-Membrane and Envelope (prME) genes, and the other expressing prME + Non-Structural protein 1 (NS1) genes. These antigens were chosen based on documented evidence that flavivirus prME and NS1 proteins are sufficient to elicit protective immune responses.

**Results:** The production of ZIKV prME VLPs was demonstrated by EM in after infections of DF1 cells with MVA-PrME virus. VLP were produced at high concentrations in production cell lines. ZIKV-specific antibodies detected both E (54 kD) and NS1 (40 kD) proteins in cell lysate and supernatant (only E) of infected cells. Research stocks were made from sucrose gradient purified MVA-VLP viruses at titeres of >10e8 TCID50/ml and being used for immunizations of various strians of mice at our collaborators' laboratories at CDC and University of Georgia.

**Conclusion:** This is the first report that a viral vector (replication competent or replication deficient) has produced a vaccine candidate for Zika that forms VLPs in vivo. Induction of VLPs in the host cells of the vaccine recipients not only eliminates the need for VLP purifications during manufacturing, but also generates a potent single dose vaccine (as shown with our MVA-VLP Ebola vaccine) that induces strong humoral and cellular immune responses similar to that of a natural Zika virus. Being tested safely in more than 120,000 subjects, including immunodeficient individuals, MVA based vaccines will be appropriate to be used in women of child bearing age, elderly or infant population. A potential single dose MVA-VLP Zika vaccine can be used for stockpiling by governments as well as for an immediate response to an ongoing epidemic.

### http://dx.doi.org/10.1016/j.ijid.2016.11.046

#### 09.001

# Cross border infection surveillance in mobile European population—GeoSentinel and more

#### P. Schlagenhauf

# University of Zürich, WHO Collaborating Centre for Travellers' Health, Zurich/CH

The flow of migrants and refugees throughout Europe is governed by complex geopolitical and social factors. More than 800,000 asylum applications have been filed and numbers are growing. Some processes are in place for screening migrants for infectious disease (ID) at the point of arrival but on-going, cross border ID surveillance remains an important challenge. This presentation proposes a matrix approach to sustained surveillance of migration related infection. It suggests the use of existing surveillance systems such as GeoSentinel and the European subnetwork of GeoSentinel sites, EuroTravNet. Here clinicians at 22 sites in Europe provide surveillance data on diagnoses in travellers who present at one of the network's tropical and travel medicine specialist sites. To be eligible for inclusion in the database, the patient must have crossed an international border before presentation and the diagnosis must be considered to be travel/migration related. A strength of this approach is that the infection data are linked to country of origin, travel/migration route and possible area of illness acquisition. Other surveillance approaches include analyses of existing systems such as ProMED-mail, a rapid reporting system of emerging diseases in humans and HealthMap, a service that uses web-crawling to find information on disease outbreaks and place it in a detailed Google map. Systematic reviews (according to PRISMA guidelines) can also be pivotal in identifying illness profiles in specific migrant groups and guiding screening and care guidelines. Migrants themselves, using mobile devices and novel tech, such as ITIT, may soon contribute to the surveillance of travel related infections. Cross border infection surveillance of migrants within Europe necessitates a mosaic approach, using available resources and innovation for new approaches.

## http://dx.doi.org/10.1016/j.ijid.2016.11.047

## 09.002

## German experience with screening and healthcare in refugee and asylum seeker reception camps

#### W. Kern

# University Hospital & Medical Center, Division of Infectious Diseases, Freiburg/DE

The burden of disease among refugees and asylum seekers (refgs) has been in three areas: chronic preexisting non-communicable diseases (diabetes etc.), infections (preexisting/latent - depending on geographic/socioeconomic origin, and acute - depending on transmission risks during migration and in reception/transit camps [cmps]) as well as mental illness and psychosocial disorders. All three types may be highly relevant for healthcare organization (HCO) during migration, at arrival in cmps and thereafter. In addition two groups merit special consideration: unaccompanied or separated children/minors (UASC) and pregnant women. Screening upon arrival can identify only a part of these diseases and needs to take into account the dynamics of the risks associated with the different periods of flight/migration. Major limitations have included communication/language problems, registration processes disconnected to housing/accommodation capacities and with asynchronous health screening. Germany's experience in the phase of the overwhelming influx of refgs in 2015 (0.9-1.0 million, most from Syria) and in (first half of) 2016 (0.2-0.3) has clearly pointed to a strong need for integrated HCO with on-the spot or camp-near health units and early access to primary care as well as specialized care. The demand for special woman&child and UASC care was unexpectedly high as was the need for counselling, psychosocial support and mental healthcare which tended to increase rather than decrease after arrival. Apart from initial X-ray screening for pulmonary tuberculosis among adults there has been no uniform infectious disease screening in Germany states and counties. Also, vaccination coverage within the first 4 weeks after arrival has been highly variable. Surveillance and monitoring has shown that there were several outbreaks of chickenpox and measles in cmps and a clear increase in the number of tuberculosis cases in the country so far restricted to the refgs population. Other complex/complicated infections were sporadic and not a major part of disease burden.

# http://dx.doi.org/10.1016/j.ijid.2016.11.048

### 09.003

# Tracing antibiotic resistance genes along the migration pathways

### G. Cornaglia

University of Verona, Pathology and Diagnostics, Verona/IT

no abstract received by submitter

http://dx.doi.org/10.1016/j.ijid.2016.11.049





