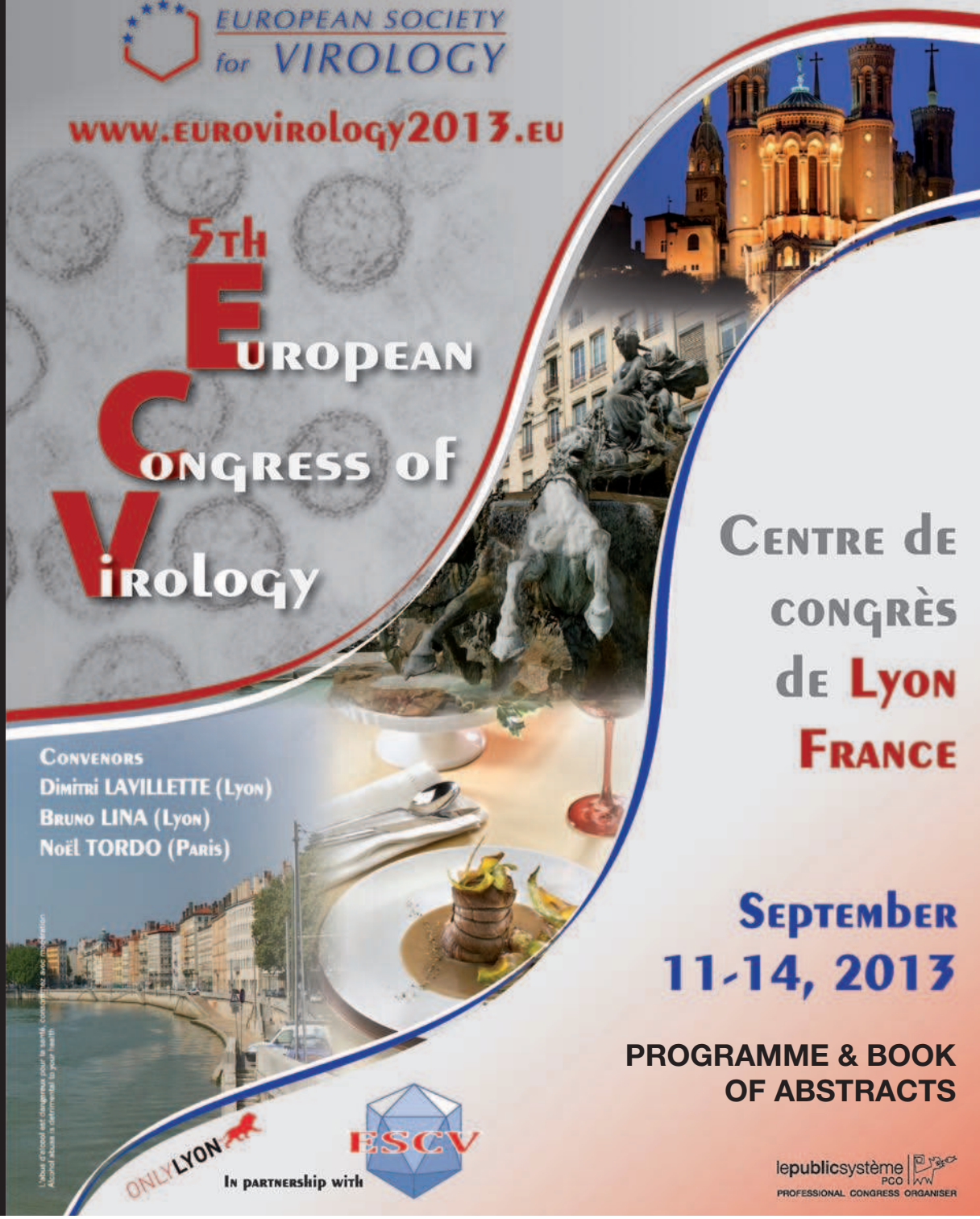
Virologie

Vol. 17
supplément,
Septembre 2013

EUROPEAN SOCIETY for VIROLOGY

www.eurovirology2013.eu

5th European Congress of Virology



Centre de congrès de Lyon France

Convenors
Dimitri LAVILLETTE (Lyon)
Bruno LINA (Lyon)
Noël TORDO (Paris)

September 11-14, 2013

PROGRAMME & BOOK OF ABSTRACTS

ONLYLYON

In partnership with ESCV

lepublicsystème PCO
PROFESSIONAL CONGRESS ORGANISER

SFM

Avec le parrainage
de la Société Française
de Microbiologie

www.jle.com

John Libbey EUROTEXT

ISSN n° 1267-8694

Thursday 12th September 2013, 8h30 – 10h30

WORKSHOP 17: "VECTOR BORNE VIRAL INFECTIONS"

Partnership with the FP7-EU programs
EuroWN, Vectorie & Wings
Chairpersons: Luiza BARZON (Padova, ITALY)
& Nathalie PARDIGON (Paris, FRANCE)
Room Gratte Ciel 1, 2, 3

KEYNOTES:

Epidemiology of WN in the Mediterranean region: towards better diagnostics and surveillance

Miguel-Angel JIMENEZ
INIA, Cisa, Madrid, SPAIN
<majimenez@inia.es>

West Nile virus (WNV) is one of the most relevant emerging pathogens of the World. Public health authorities worldwide have incorporated this pathogen as one of their priorities in their agendas and road maps. This means surveillance, preparedness and contingency plans at National and International levels, to tackle with the challenge of monitoring West Nile virus circulation in vast geographic areas, enabling capabilities to detect and diagnose efficiently every case of WNV infection.
WNV cycle involves different birds as vertebrate hosts and different types of mosquitoes as vectors. Spillover from this cycle may affect other vertebrate hosts, such as horses and humans. Understanding the risk of spillover and epidemics requires a basic knowledge on how biotic (mosquito and vertebrate species composition and diversity, phenology, diet, habitats, etc.) and abiotic (geography, climate, etc.) components affect WNV transmission dynamics.
Although having common characteristics, Europe/Mediterranean region is not a homogeneous region in terms of eco-epidemiology for WNV, but rather exhibit a "patchy" pattern in terms of virus transmission and persistence in the field. To define these patterns precisely is the objective of the epidemiological studies carried out in each area. A good model of study is given by the project EuroWestNile, with teams located in different areas of WNV transmission looking at the main factors governing the epidemiology in each location. From their comparison, it is expected to produce a list of "common" and "differential" factors governing WNV epidemiology in each transmission setting, using parameters accurately determined locally. Epidemiological models, diagnostic tools and surveillance programs must be adapted to the specific situation at which they target.

West Nile virus strains in Europe are as virulent as the North American counterparts

Byron E.E. MARTINA, Stephanie M. Lim, Penelope KORAKA, Albert DME OSTERHAUS
Department of Virology, Erasmus Medical Center, Rotterdam, THE NETHERLANDS
<b.martina@erasmusmc.nl>

The severity of West Nile virus (WNV) infection in immunocompetent animals is highly strain dependent, ranging from avirulent to highly neuropathogenic. Reasons for susceptibility to WNV-associated neuroinvasive disease in a minority of human cases remain unexplained. Furthermore, until recently, WNV outbreaks in Europe were limited compared to the outbreaks recorded in the US. It is also remarkable that many of the outbreaks in humans caused by lineage 1 and 2 in Europe, were not preceded by massive bird mortality. Virulence is a multi-factorial process and many aspects need to be studied in order to elucidate the pathogenic force of viruses. Several parameters can be used to describe virulence such as replication rate, immune-interfering properties, lethal dose 50, median survival time, tropism for particular cells or tissues, as well as the viral burden present in infected tissues. In addition, virulence factors in mice differ from those that determine pathogenicity in birds. It is believed that a weak immune response allows WNV replication in the periphery and development of high viremia with an increased chance of infection of the CNS. In addition, to WNV replication in the brain, the cells involved in supporting infection in the CNS and the resultant response to WNV may tip the balance between recovery and severe neuroinvasive disease. Evidence exists that both glia and neurons are involved in WNV pathogenesis as well as virus-related virulence factors.

Development of vaccines against WNV

Sebastian ULBERT
Fraunhofer Institute for Cell Therapy and Immunology, Leipzig, GERMANY
<sebastian.ulbert@izi.fraunhofer.de>

West Nile Virus (WNV) is an emerging pathogenic and mosquito-borne flavivirus with increasing distribution worldwide. During the last couple of years the virus became endemic in several European countries. Birds are the natural hosts of WNV, but also mammals, including humans, can be infected. In most cases, WNV infections remain asymptomatic or lead to flu-like symptoms. However, especially older and immunocompromised individuals are at risk to develop severe neurological complications such as encephalitis or meningitis, which happens in approx. 1% of the cases. Currently available WNV-vaccines include formaldehyde-inactivated virus and viral vector systems, but are only for veterinary use. Despite major research efforts, there is no human vaccine on the market yet. Due to the need to protect older people, any vaccine technology against WNV has to especially focus on effectiveness and safety. The lecture will give an overview on WNV-vaccine development and will present EU-funded research that is being carried out on this topic by the scientific consortia VECTORIE, WINGS and EUROWESTNILE.

ORAL COMMUNICATIONS

REF O37

Impact of vector ecology on virus amplification and spillover into humans and livestock: the case of West Nile virus in Europe

Jordi FIGUEROLA[1], Josue MARTINEZ DE LA PUENTE[1], Annapaola RIZZOLI[2], Alexander PLATONOV[3], Hanna BIN[4], Joaquin MUÑOZ[1], Gioia CAPELLI[5], Santiago RUIZ[6], Roberto ROSA[2], David ROIZ[1], Ana VAZQUEZ[7], Antonio TENORIO[7], Maripaz SANCHEZ SECO[7], Ramon SORIGUER[1]
[1]EBD CSIC, Sevilla, SPAIN; [2]Fondazione Edmund March, S. Michele all'Adige, ITALY; [3]Central Institute of Epidemiology, Moscow, RUSSIA; [4]Central Virology Laboratory Ministry of Health, Ramat Gan, ISRAEL; [5]Instituto Zooprofilattico Sperimentale delle Venezie, Legnaro, ITALY; [6]Servicio de Control de Mosquitos, Huelva, SPAIN; [7]Instituto de Salud Carlos III, Madrid, SPAIN
<jordi@ebd.csic.es>

Outbreaks of zoonotic diseases are recurrently occurring across Europe. Usually interpreted as the result of virus introductions into new areas, in many cases outbreaks are the result of environmental conditions favouring virus amplification or spillover into humans or livestock. Understanding the risk of emergence of vector borne zoonotic virus implies improving our knowledge of the interactions between vectors and vertebrates. This is specially relevant for West Nile virus, a flavivirus causing encephalitis among humans that has demonstrated its capacity to overwinter in Europe and produce until recent years, reduced outbreaks in humans and horses. The virus is able to replicate in most avian species, and mosquitoes get infected after feeding on viraemic birds. However, most mammal species are dead end hosts. To understand the potential of virus amplification we analysed the blood meal origin of mosquitoes trapped in Israel, Italy,

Russia and Spain. Results show that some mosquito species feed mainly on birds (with a large potential for virus amplification) while others feed on mammals only. Important differences in diet composition also occurred between localities, probably due to vertebrate community composition. In Spain, WNV transmission risk for birds human and horses, was estimated based on mosquito abundance, vectorial competence and blood meal origin. Estimated risk fitted reasonably well interspecific differences in antibody prevalence and virus prevalence in mosquitoes. Vector ecology may contribute to understand risk of zoonotic virus outbreaks across Europe.

REF O38

Characterization of Human West Nile Virus strains isolated in Northern Italy

Luisa BARZON[1,2], Monia PACENTI[2], Elisa FRANCHIN[1,2], Laura SQUARZON[1], Alessandro SINIGAGLIA[1,3], Samuele ASNICAL[1], Enrico LAVEZZO[1], Stefano TOPPO[1], Silke CORBACH SOEHLE[4], Ignazio CASTAGLIUOLO[1], Giulia MASI[1], Sebastian ULBERT[5], Margherita CATTAI[2], Riccardo CUSINATO[2], Giorgio PALÙ[1,2]

[1]Department of Molecular Medicine, University of Padova, Padova, ITALY; [2]Clinical Microbiology and Virology, Padova University Hospital, Padova, ITALY; [3]IOV Istituto Oncologico Veneto, Padova, ITALY; [4]Institut für Labortierkunde, Universität Zürich, Zurich, SWITZERLAND; [5]Vaccine Technologies Unit, Fraunhofer Institute for Cell Therapy and Immunology, Leipzig, GERMANY

<luisa.barzon@unipd.it>

West Nile virus (WNV) is an emerging pathogen that is circulating in North eastern Italy and causing disease in humans since 2008. Aim of this study was the investigation of the spread of WNV strains in north eastern Italy taking advantage of the special surveillance programme for WNV infection that was activated in Veneto Region in 2008 and enhanced in 2010. The pathogenic potential of isolated WNV strains was also investigated. During 2008 2009, several human cases of WNV disease caused by an endemic lineage 1a strain, named Ita09, were identified in areas surrounding the Po river. Since 2010, cases have been recorded in nearby northern areas, where, in 2011, both lineage 1a and 2 were detected. Two novel human lineage 1a strains were identified in 2011 by full genome sequencing and phylogenetic analysis. One of these strains, called Livenza, was responsible of a relatively large outbreak with over 50 human infections in 2012. Both the Ita09 and Livenza strains had a prolin at codon 249 of the NS3 protease/helicase, which has been associated with increased WNV transmissibility and virulence. In vitro experiments demonstrated higher stability and activity of the NS3 protease/helicase with prolin at codon 249 than other NS3 mutants. Pathogenicity studies on the WNV Ita09 strain demonstrated high neuroivasive potential and lethality in mouse models. In the mouse model, different organs were involved by WNV infection with the highest viral load detected in brain, stomach, and gut. Activation of markers of innate immune response was demonstrated in infected organs.

REF O39

Recombinant vaccinia MVA expressing E and prM/M proteins of West Nile Virus for vaccine generation

Gerd SUTTER[1], Martina KASERER[1], Asisa VOLZ[1], Sylvia JANY[1], Stephanie LIM[2], Byron MARTINA[2]

[1]Institute for Infectious Diseases and Zoonoses,Chair for Virology, LMU, Munich, GERMANY; [2]Virosience Lab, Erasmus Medical Center, Rotterdam, THE NETHERLANDS

<gerd.sutter@lmu.de>

West Nile Virus (WNV), a flavivirus, is intrinsically maintained in an enzootic cycle between mosquitos as vectors and wild birds serving as reservoir hosts. WNV can also infect and cause disease in humans and horses. The virus is widely distributed in Africa, Europe, the Middle East, Asia and the Americas and is able to cause neuroinvasive disease with the potential for severe courses especially in the elderly and immunocompromised humans. WNV infections increasingly occur in mediterranean countries with tendency to spread to central and northern Europe. Thus, safe and efficacious vaccines are urgently sought for WNV prophylaxis in humans and animals. Replication deficient Modified Vaccinia virus Ankara (MVA) can be exploited as versatile viral vector in medical and veterinary vaccine development.

Here, we have generated and evaluated recombinant MVA delivering the WNV antigens E (envelope) and prM/M (precursor membrane/membrane) and fulfilling the requirements to undergo clinical testing in humans. The structural proteins of the WNV envelope are highly relevant vaccine antigens for the induction of WNV specific antibody and T cell responses. Infections of human and equine cell cultures with recombinant MVA demonstrated efficient synthesis and secretion of WNV envelope proteins in mammalian cells non permissive for MVA replication. Prime boost immunizations in BALB/c mice induced high levels of WNV specific antibodies. Moreover, vaccinations with recombinant MVA in HLA A2.1/HLA DR1 transgenic H 2 class I/class II knockout mice resulted in the induction and efficient expansion of WNV specific CD8+ T cells. Thus, results from vaccinations in two different mouse models demonstrated solid immunogenicity of MVA WNV vector vaccines. Further evaluation in different animal models is warranted to evaluate protective efficacy against WNV and to demonstrate the potential of the recombinant MVA as candidate vaccines in humans.

REF O40

Sylvatic origin and geographic spread of St. Louis encephalitis virus

Sandra JUNGLEN[1], Anne KOPP[1], Thomas GILLESPIE[2], Daniel HOBELSBERGER[3], Alejandro ESTRADA[4], James HARPER[5], Richard MILLER[5], Isabella ECKERLE[1], Marcel MÜLLER[1], Lars PODSIADLOWSKI[6], Fabian LEENDERTZ[3], Christian DROSTEN[1]

[1]Institute of Virology, Bonn, GERMANY; [2]Emory University, Atlanta, USA; [3]Robert Koch Institute, Berlin, GERMANY; [4]University of Mexico, Mexico City, MEXICO; [5]University of Michigan, Ann Arbour, USA; [6]Institute of Evolutionary Biology and Ecology, Bonn, GERMANY

<junglen@virology-bonn.de>

St. Louis encephalitis virus (SLEV) is the prototypic mosquito borne flavivirus in the Americas. The virus is transmitted between Culex mosquitoes and birds in North and South America. The geographic and ecological origins of SLEV remain obscure.

In an ecological investigation in a tropical rainforest in Palenque National Park, Mexico, we discovered an ancestral variant of SLEV in Culex nigripalpus mosquitoes.

The tentatively named SLEV Palenque strains were distinct from all presently known SLEV strains showing only 94.2 – 95.7% amino acid identity to epidemic SLEV strains and forming a highly distinct phylogenetic clade within the SLEV species. Cell culture studies of SLEV Palenque versus epidemic SLEV (MSI 7) revealed no growth differences in insect cells, but a clear inability of SLEV Palenque to replicate in cells from several SLEV host species permissive for MSI 7 replication (birds, cotton rats, free tailed bats). Only cells from nonhuman primates and neotropical fruit bats were moderately permissive. Phylogeographic reconstruction suggested that the common ancestor of all epidemic SLEV strains has existed in an area between southern Mexico and Panama circa 330 years before present. Expansion of the epidemic lineage occurred in two waves, the first representing emergence near the area of origin and the second involving almost parallel appearances of virus in the lower Mississippi and Amazonas delta regions. We were able to link the emergence of a major epidemic arbovirus with anthropogenic ecosystem invasion during colonial times.