

OBJECTIVES

- Identify key factors associated with the highest risk of virus emergence at the 4 stages of emergence
- determine the impact of the transmission route on viral evolutionary trajectories and cross-species transmission
- unravel the mechanisms that govern interactions between a virus, its hosts and the environment to favour/limit cross-species transmission and adaptation to a new host
- evaluate most effective intervention strategies to limit cross-species transmission and spread in the new host
- identify risk patterns of emergence of practical relevance for disease surveillance, control and intervention, and pandemic preparedness

Semi-flexibility clause
to include work on other viruses in area of expertise in response to emergence
MERS-CoV, EBOV, CHIKV

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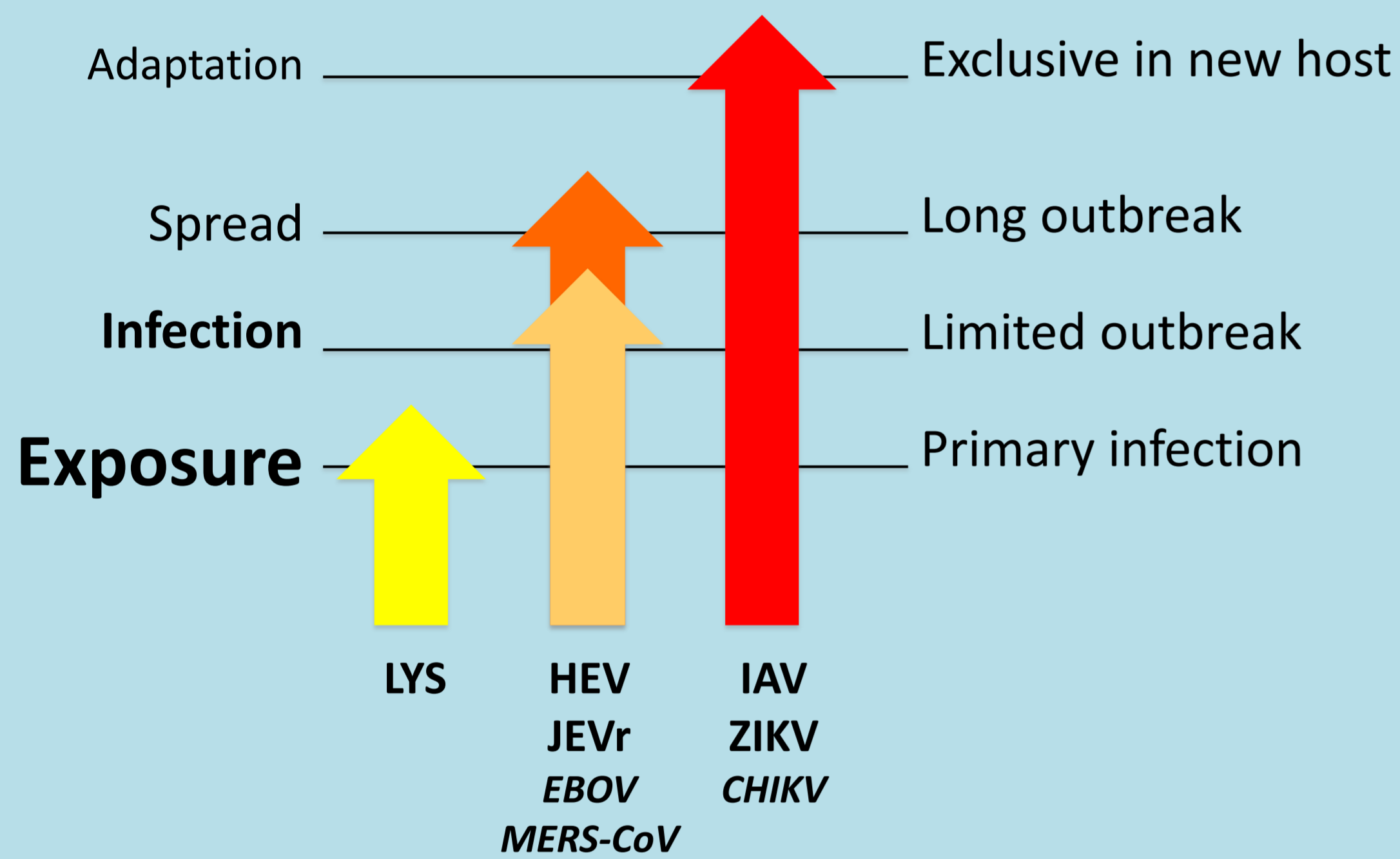
PARTNERS

18 partners – 24 teams
8 countries

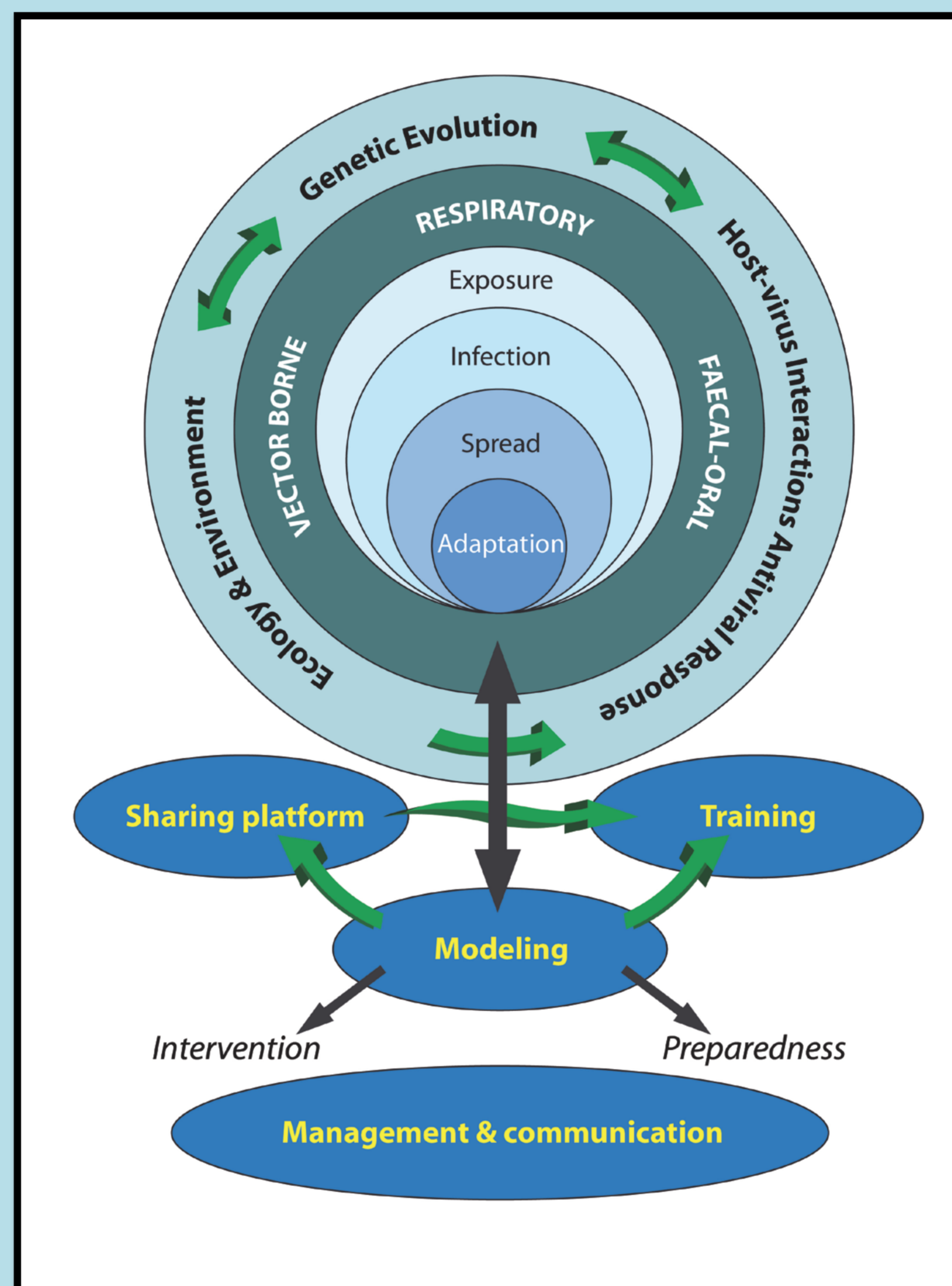
1. Institut Pasteur (coordinator)
2. Istituto Zooprofilattico Sperimentale delle Venezie
3. Katholieke Universiteit Leuven
4. Aix Marseille Université
5. Eidgenössisches Departement des Innern
6. Imperial College of Science, Technology & Medicine
7. Agence Nationale de Sécurité Sanitaire de l'Alimentation, de l'Environnement et du Travail
8. Max Planck Gesellschaft zur Foerderung der Wissenschaften E.V.
9. Universitat de Barcelona
10. Goeteborgs Universitet
11. Philipps Universität Marburg
12. Istituto Nazionale per le Malattie Infettive L. Spallanzani
13. The University of Edinburgh
14. Fondazione Istituto per l'Interscambio Scientifico
15. Foundation Health Sciences e-Training
16. Istituto Superiore di Sanità
17. Alma Mater Studiorum-Università di Bologna
18. Freunde von GISAID e.V.



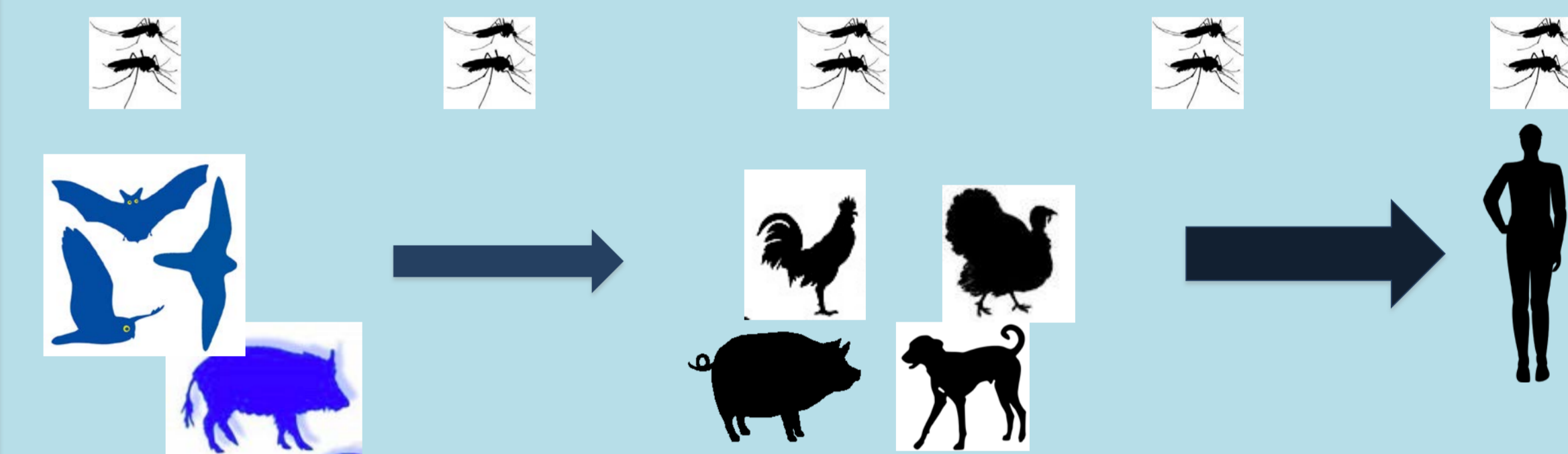
Stages of Emergence



STRUCTURE



Reservoirs and Vectors



Wild reservoir (bats, birds, boars) → Domestic amplifying hosts (poultry, pigs, canids) → Human host

Transmission Routes

- Respiratory : IAV, MERS-CoV
- Faecal-oral : HEV
- Contact : LYS, EBOV
- Vector-borne: JEVr (WNV, USUV, ZIKV), CHIKV

OUTCOMES

- Ecologic, epidemiologic, virologic or host factors that condition virus maintenance and spread in local ecosystems
- Extent and drivers of viral diversity in Europe and globally
- Impact of viral population (quasispecies) structure on cross-species transmission potential and pathogenicity
- Factors that determine cross-species transmission and adaptation from animal reservoirs to domestic hosts and humans
- Viral/host determinants of change of vector, host susceptibility and/or pathogenicity
- Sharing Platforms: sequence databases for Lyssaviruses, Hepeviruses, Flaviviruses (based on GISAID concept & EpiFlu database model)
- Modelling
 - Mapping methods for animal densities & behaviours
 - Transmission models
 - Models for risk assessment and contingency planning
 - Evolutionary epidemic models

SELECTED PUBLICATIONS

Lam et al The genesis and source of the H7N9 influenza viruses causing human infections in China. Nature 2013
 Munier et al Exploration of binary virus-host interactions using an infectious protein complementation assay. Mol Cell Proteomics 2013
 Poletto et al Human mobility and time spent at destination: Impact on spatial epidemic spreading. PLoS Comput Biol 2013
 Shigematsu et al Influenza A virus survival in water is influenced by the origin species of the host cell. Influenza Other Respir Viruses, 2014
 Monne et al. Emergence of a highly pathogenic avian influenza virus from a low-pathogenic progenitor. Epidemiol Infect 2014
 Worobey et al A synchronized global sweep of the internal genes of modern avian influenza virus. PNAS 2014
 Lemey et al Unifying Viral Genetics and Human Transportation Data to Predict the Global Transmission Dynamics of Human Influenza H3N2. PLoS Path 2014
 Wendel et al The avian-origin PB1 gene segment facilitated replication and transmissibility of the H3N2/1968 pandemic influenza virus. JVI 2015;
 Halbherr et al Biological and protective properties of immune sera directed to influenza virus neuraminidase. JVI 2015
 Bedford et al Global circulation patterns of seasonal influenza viruses vary with antigenic drift. Nature 2015
 Pavo et al Frequent hepatitis E virus contamination in food containing raw pork liver, France. EID 2014
 Rogee et al Quantitative proteomics identifies host factors modulated during acute hepatitis E infection in swine model. JVI 2014
 Lin et al High prevalence of hepatitis E virus in Swedish moose—a phylogenetic characterization and comparison of the virus from different regions. PLoS ONE 2015
 Serra-Cobo et al Ecological Factors Associated with European Bat Lyssavirus Seroprevalence in Spanish Bats PLoS One. 2013
 Nouvellet P et al Rabies and Canine Distemper Virus Epidemics in the Red Fox Population of Northern Italy (2006–2010). PLoS One 2013
 Wiltzer et al Interaction of rabies virus P-protein with STAT proteins is critical to lethal rabies disease. JID 2014
 Sambri et al West Nile virus in Europe: emergence, epidemiology, diagnosis, treatment, and prevention Clin Microbiol Infect 2013
 Aubry et al Single-stranded positive-sense RNA viruses generated in days using infectious subgenomic amplicons JGV 2014
 de Wispelaere et al A Japanese encephalitis virus genotype 5 molecular clone is highly neuropathogenic in a mouse model: impact of the structural protein region on virulence. J Virol 2015
 Guery et al Clinical features and viral diagnosis of infection with Middle East Respiratory Syndrome coronavirus: a report of nosocomial transmission. The Lancet 2013
 Cauchemez et al Middle East respiratory syndrome coronavirus: quantification of the extent of the epidemic, surveillance biases, and transmissibility Lancet ID 2014
 Gire et al Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science 2014
 Faye et al. Chains of transmission and control of Ebola virus disease in Conakry, Guinea, in 2014: an observational study. Lancet ID 2015
 Donnelly et al Ebola virus disease among children in West Africa NEJM 2015
 Cao-Lormeau et al Guillain-Barré Syndrome outbreak associated with Zika virus infection in French Polynesia: a case-control study The Lancet 2016

DISSEMINATION

- Interactions with other EU projects (ANTIGONE, PREPARE, SILVER, FLUPHARM, ...)
- Outreach to main stake-holders (WHO, OIE, ECDC,.)

TRAINING

Scientist exchange Program
Training courses and workshops

- Zoonotic features of IAV, HEV, JEVr, LYS
- Virus evolution and phylogeny
- Rabies hands-on course (WHO, IP Int network)
- Training workshop : Genetic analyses of influenza viruses (GISAID-WHO)
- Workshop on Next Generation Sequencing of Viruses (ISIRV-AVG, GISAID)

