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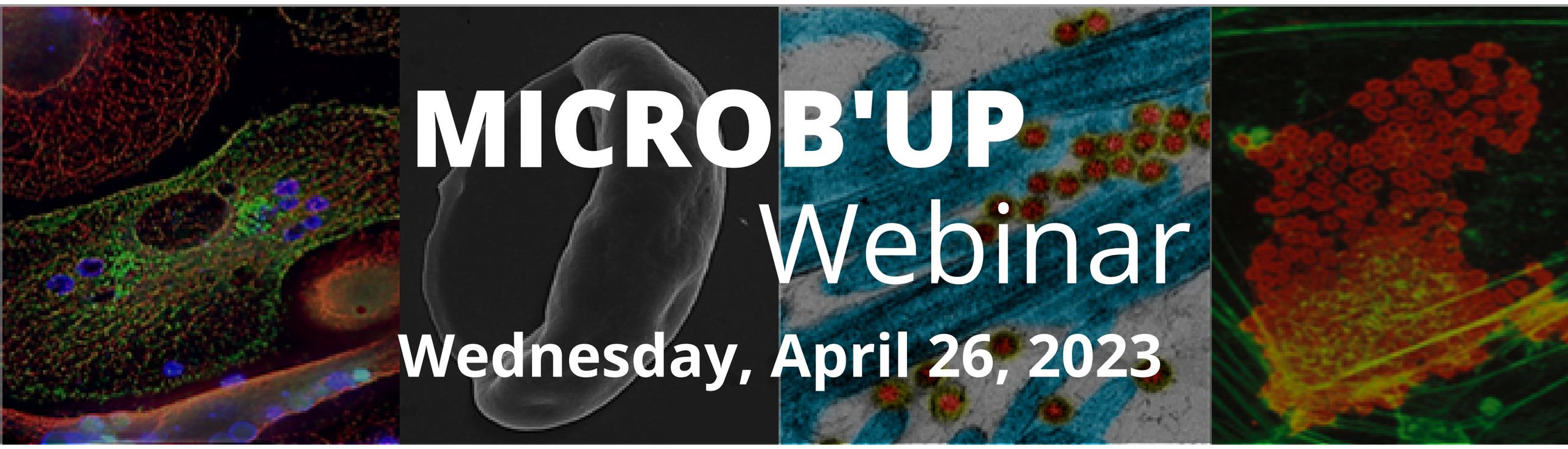

MICROB'UP Webinar

Wednesday, April 26, 2023

26 April 2023

at 11 am GMT+1 (Paris Time)

ZOOM, follow the link bellow

https://u-paris.zoom.us/j/88495777893?pwd=bHhDekdKYytsMG8weVFmSEdHQkFRUT09
ID de réunion : 884 9577 7893 ; Code secret : 172142

11 am

Joao Trindade Marques

Institut de Biologie Moléculaire et Cellulaire (Strasbourg, France)

Mosquito borne viruses: challenges and opportunities

Joao Trindade Marques is an associate professor at the Federal University of Minas Gerais in Brazil and a researcher at the Institut de BiologieMoléculaire et Cellulaire in Strasbourg, France. His research is focused on understanding the factors that affect how mosquito vectors acquire and transmit arboviruses.

11.50 am

Ottavia Romoli

Institut Pasteur (Paris, France)

Limitations of oral RNAi as an antiviral in Aedes aegypti

Ottavia Romoli is a postdoc in the Saleh's lab in Institut Pasteur. She is interested in the mosquito microbiota, how it contributes to the mosquito physiology, how it interacts with arboviruses transmitted by mosquitoes and how it can be used to reduce the transmission of these viruses by mosquitoes.

12.05 am

Shiho Torii

Institut Pasteur (Paris, France)

Identification of Zika virus genes involved in mosquito transmissibility

Shiho Torii, obtained her PhD in Veterinary medicine in Japan and have worked in the Institut Pasteur since June 2021. Her research interest is to elucidate the viral genetic determinants underlying differential transmissibility between African and Asian ZIKV strains by a combination of viral reverse genetics and mosquito transmission assays in vivo.

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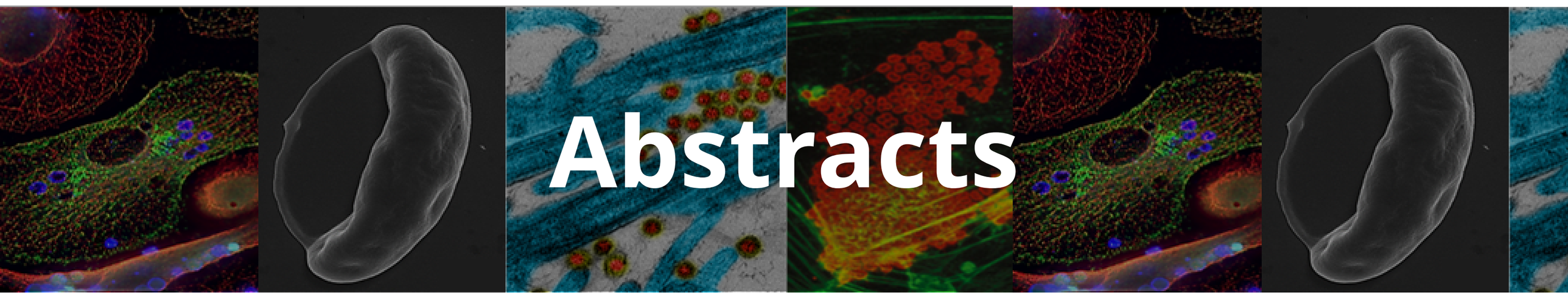

Abstracts

Joao Trindade Marques

Institut de Biologie Moléculaire et Cellulaire (Strasbourg, France)

Mosquito borne viruses: challenges and opportunities

Aedes aegypti and Aedes albopictus mosquitoes are the main vectors for dengue virus (DENV) and other arboviruses, including Zika (ZIKV) and Chikungunya (CHIKV). Understanding the factors that affect transmission of arboviruses from mosquitoes to humans is a priority, because it could inform public health and targeted interventions. Furthermore, virologic surveillance of mosquitoes is an important for early detection of potential emerging viruses. Recently, we analysed the viromes of 815 urban Aedes mosquitoes collected from 12 countries worldwide. Two mosquito-specific viruses, Phasi Charoen-like virus (PCLV) and Humaita Tubiacanga virus (HTV) were the most abundant in A. aegypti worldwide. Spatiotemporal analyses of virus circulation in an endemic urban area revealed a 200% increase in chances of having DENV in wild A. aegypti mosquitoes when both HTV and PCLV were present. Using a mouse model in the laboratory, we showed that the presence of HTV and PCLV increased the ability of mosquitoes to transmit DENV and ZIKV to a vertebrate host. By transcriptomic analysis, we found that, in DENV infected mosquitoes, HTV and PCLV block the downregulation of histone H4, which we identify as an important pro-viral host factor in vivo. Our work highlights the importance of monitoring mosquito-specific viruses when performing risk analysis of outbreaks and raises the possibility that strategies targeting the virome of mosquitoes could impact arbovirus transmission.

Ottavia Romoli

Institut Pasteur (Paris, France)

Limitations of oral RNAi as an antiviral in Aedes aegypti

Mosquitoes are vectors for several globally important viral diseases, whose continued spread necessitates novel intervention measures. A mosquito vectorial capacity is dependent upon efficient virus replication and dissemination from the gut to the salivary glands, where the virus must enter the saliva to be transmitted to the next vertebrate host during subsequent blood-feeding. To control viral replication, the mosquito relies on the RNA interference (RNAi)-based response that detects and destroys double-stranded RNA (dsRNA) produced during virus replication. This antiviral RNAi response is directly activated by dsRNA molecules and can act distally from the initial infection site.

We hypothesized that exogenous dsRNA targeting the Zika virus genome (dsZIK) produced by a mosquito bacterial symbiont could stimulate an antiviral response in Aedes aegypti, providing a protection to a subsequent infection with Zika virus. Using Escherichia coli as a proof-of-concept, we monocolonized mosquito by bacteria expressing dsRNA. However, we could not detect a significant effect on viral titers in mosquitoes exposed to bacteria producing dsZIK and challenged with a Zika virus infectious blood meal. We hypothesized that this could be due to three reasons: (i) deficient release of dsZIK by bacteria in the mosquito gut, (ii) deficient uptake of dsZIK from the mosquito gut epithelium, or (iii) degradation of dsZIK in the mosquito gut.

To overcome the possible limitations of dsRNA production or release by bacteria, we inoculated mosquitoes by oral route or by injection route with dsRNA synthesized in vitro and we compared the effects of dsZIK on Zika viral titers. While viral replication was completely abolished in mosquitoes injected with dsZIK, no effect was detected in mosquitoes fed with dsZIK. Moreover, we could not identify 21-nucleotide small interfering RNAs in mosquitoes fed with dsZIK, probably due to the degradation of dsRNA in the mosquito gut previous to the processing by the RNAi machinery. Taken together these results highlight the limitations of the use of oral RNAi as an antiviral in Aedes aegypti. However, they also show the strong antiviral effect of dsRNA, that could be provided to mosquitoes via intracellular members of the microbiota such as mosquito specific viruses.

Shiho Torii

Institut Pasteur (Paris, France)

Identification of Zika virus genes involved in mosquito transmissibility

Zika virus (ZIKV) is a flavivirus mainly transmitted by Aedes aegypti mosquitoes that recently emerged across the Pacific region and Latin America, causing large human outbreaks associated with birth defects and neurological disorders. Phylogenetic analyses show that ZIKV genetic diversity can be divided into an African lineage and an Asian lineage. Although to date, human outbreaks have exclusively been associated with strains from the Asian lineage, a growing body of evidence points towards higher transmissibility of ZIKV strains from the African lineage. To elucidate the viral genetic determinants underlying differential transmissibility between African and Asian ZIKV strains, we used a combination of viral reverse genetics and mosquito transmission assays in vivo. We constructed a set of six chimeric ZIKV strains from two parental strains with different levels of transmissibility by swapping the genome fragments encoding structural proteins, non-structural proteins or untranslated regions. We compared the in vivo transmissibility of the chimeric viruses in mosquitoes experimentally exposed to an artificial infectious blood meal. We detected viral genomes in mosquito head and infectious viruses in saliva and calculated transmission prevalence as the proportion of virus-positive head with a virus-positive saliva. We found that replacing the genome region encoding structural proteins of the low-transmissibility Asian strain with the same region from the high-transmissibility African strain significantly increased transmission prevalence. The reciprocal replacement resulted in the opposite pattern. We concluded that the difference in mosquito transmissibility between African and Asian ZIKV strains is due to genetic variation in the viral structural proteins.

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