SURVEILLANCE — DAY 6			
Time	Activity Description	Intended Learning Outcomes	Relevance
		After completion, trainees will (be able to):	Why this is important for you as:
1540- 1710	Case study : Genomic surveillance and transmission of foodborne pathogens from a One Health perspective (Jose Delgado)	Understand the principles of genomic surveillance in the context of foodborne pathogens, with a focus on <i>Klebsiella</i> species. Practical genomic analysis of NGS sequences to identify genetic determinants of virulence, antimicrobial resistance, and pathogen evolution in <i>Klebsiella</i> populations from animals and humans.	<ul> <li>Bioinformaticians will learn how to integrate genomic data analytical tools (i.e. phylogeny, AMR and virulence gene detection) with epidemiological information and metadata to track the transmission routes and evolutionary dynamics of <i>Klebsiella</i>, supporting outbreak investigations.</li> <li>Microbiologists will develop a practical understanding on how genomic data can help the characterization of <i>Klebsiella</i>, and they will deepen their understanding of the One Health approach specifically applied to this bacterial species.</li> </ul>
		Highlight on the importance of the One Health approach in the context of foodborne pathogens surveillance, recognizing the interconnectedness of human, animal, and environmental health.	<b>Epidemiologists</b> will learn to integrate information from different sources and formats (i.e. genomic data, metadata, epidemiological data) to perform genomic surveillance of <i>Klebsiella</i> infections across human populations, animal reservoirs, and environmental sources, enabling the implementation of effective control measures and public health interventions.

## Details

<u>Case study : Genomic surveillance and transmission of foodborne pathogens from a One Health perspective</u> This course will present a case study for the participants to analyze, and it will focus on genomic surveillance applied to *Klebsiella*. Participants will explore the application of genomic analyses (e.g., phylogenetics, AMR and virulence gene detection) in understanding the transmission dynamics of *Klebsiella* infections within a One Health framework, interpreting genomic data taking into account the interactions between human health, animal health, and the environment. Through case studies and interactive sessions, participants will gain insights into genomic epidemiology, antimicrobial resistance, virulence determinants, and evolutionary trends of *Klebsiella* strains.